SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9249	39617	A	9308	668	826	VNSHSQLLQRE*NT*ESNLQGM *RTSSRRTTNHCSRK*KRIQTNG RTFHAHG
9250	39618	A	9309	497	1042	LPRIPTVLTSGVRRDGWYRRFG RRPSG*PGNWSSSPVEKSATRT LRITGTSAIPSEAITGSSAVVRR VPAGKTTAPTEIKSTPVSANSRS VLSVTLPDTSSSALPLVRLTASR ICSVSKLSSMMISAPAFRASSSS SRFSTSTSTGASGCSQDAFSTA WRTEPEAIIWFSLIRKASESPRR
9251	39619	C	9310	1	3447	
9252	39620	A	9311	570	647	
9253	39621	A	9312	1071	1323	RPPPHRLSGCYHPSHRRPVHGF HHA*RQRQFRR*TVDTLPADAP LPSPHPAHFRPL/TSIFCPVSTMA DNASM*RNSCCRLSARG
9254	39622	B	9313	1	2585	
9255	39623	A	9314	133	357	SSFFQFCEEIHW*LDGDGIESIN YLRQ*GHFHKIDPSYP*AWNVL PFVCVLFHFIEQWFVVLLEEVL HIPCKLYS

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9256	39624	A	9315	1	2680	MLVLPLFQPFMRILDHDDSSID HRPDGNRNATQRHNIGIQSLEV HDNKSNTQPQRQRNNRHQRRA HMPEKQRTDYRRDPLESPKAA AACLFPAIADPNTPPVFTPPASL PTTGM/FDSPPFRNDA*MVMRS LIRSMTVARAVIGVAICNKGLP ATMMALAAQHNIATVLVPGGA TLPAKDGEVNGKVQTIGARFA NGELSLQDARRAGCKACASSV RRSCQFLGTAGTSQVVAEGLGL AIPHSALAPSGEPVWREIARAS ARAALNLSQKGITTREILTDKAI ENAMTVHAAFGGSTNPLLHIPA IAHQAGCHIPTVDDWIRINKRV PRLVSVLPNGPVYHPTVNAFM AGGVPEVMLHLRSLGLLHEDV MTVTGSTLKENLDWWEHSERR QRFKQLLLDQEQINADEVIMSP QQAKARGLTSTITFPWQYAWIL HPDLDPETLLKLLISLRRFWAET PVGKNRITQMTNARHRTGFQG VTIHHTGVQFMGFITRKDSANS GVKQWTLFQQTHRFRHHIQRT FARFQHFLPGFNNGRQRLDVAS VFMEFTTGLMSLDTALNEMLS RVTPLTAQETLPLVQCFGRILAS DVVSPLDVPGFDNSAMDGYAV RLADIASGQPLPVAGKSFAGQP YHGEWPAGTCIRIMTGAPVPEG CEAVVMQEQTEQMDNGVRFT AEVRSGQNIRRRGEDISAGAVV
9257	39625	B	9316	1	2577	
9258	39626	A	9317	2	772	AFGASLAQDKPNTGTG*KSPSH P\LLRVLDIGKICHLARKVGAVS VVDNPFIRPALQNPLALRADLV LHSCTKYLNGHSDVVAGVVIA KDPDVVTELAWWANNIGVTG GAFDSYLLLRGLRTLVPRMELA QRNAQAIVKYLQTQPLVKKLY HPSLPENQGHEIAARQQKGFGA MLSFELDGDEQTLRRFLGGLSL FTLAESLGGVEKLISHAATMTH AGMAPKARAAAGISETLLRIST GIENGENLIADLENGFPA
9259	39627	B	9318	68	1895	
9260	39628	A	9319	1	636	
9261	39629	A	9320	1	942	

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9262	39630	A	9321	479	969	MPSTSQ*I/ISEDFVELNAARYR DEEIQRTPQRYSSRRPTQRHIIV RFTKVEIKEKMLRAAREKGGV AHKRKPIRLTADLSAETLQARR EWGPTFNILKEKNFQPRISYPTK LSFISEGETKSFTDKQMLRDFGT TRPPLKELLKEALNMERNNRY QPQQKHTKL
9263	39631	A	9322	1	652	MGKKQSRKTGNSKNQSASPPP KERSSSRAMEQSWTENDFDEL REEGFRRSNYSELKEEVQTHGK EDKNLEKKLDEWLARIINAEKS LKDLMELKTKARELCDECTSLS SRFDQLEDGVSVMEDEMNEMK SEGKFREKRIKRNEQSLQEIWD YVKKPNLCLIGVPESDRKNGTK LENTLQDIIQENFPNLSGQANIH IQEI\QRTPQRYSLRRATP\RHLI VRFTKVEMKEK\MLRAAREKG R\VTHGKPIRLTTADLSAETLQ AR/RTEWGPIFNILKEKNF\QPRI SYPAKLSFISEGEIKYFIDKQML RDFCHHQGLPLKELLERKALK HGKGNNQ*PPPKERSSSRAMEQ SWTENDFDELREEGFRRSNYSE LKEEVQTHGKEDKNLEKKLDE WLARIINAEKSLKDLMELKTKA RELCDECTSLSSRFDQLEDGVS VMEDEMNEMKSEGKFREKRIK RNEQSLQEIWDYVKKPNLCLIG VPESDRKNGTKLENTLQDIIQE NFPNLSGQANIHIQEIPENATKIL
9264	39632	A	9323	403	410	VFLIRWGGKPLKRKLYFLHCSI TQALV*ACQGKYLG*IVGAKNI KYIDFFITASRYLRMLAQVFE*I LLLREVTRYS
9265	39633	A	9324	174	1252	

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9266	39634	A	9326	1	1049	MHRSDMSCPDKVDILDTTAFRI AINEVKHSKLTSVTVTKVLDMF ISRSSLFPIDDGLLDDGHSDQVG VLNSPTCYSAHQNGERIERFSR KVFVGGLPPDIDEDEITASFRRF GPLVVDWPHKAESKSYFPPKG YAFLLFQEESSVQALIDACIEED GK\LYLCVS*PLLSKDKPSSKYV PWNLSDSDFVMDGSQPLDPRK TIFVGGVPRPLRAVELAMIMDR LYGGVCYAGIDTDPELKYP\KA PGRVAFSNQQSYIAAISARFVQ LQHGDIDKRVEVKPYVLDDQM CDECQGARCGGKFAPFFCANV TCLQYYCEFCWANIHSRAGRE VHIPLVTESAVAAPRIHIPWT
9267	39635	A	9327	2	126	
9268	39636	A	9328	1	1327	IASNSWNASSSPGEAREDGPEG LDKGLDNDAEGVWSPDIEQSF QEALAIYPPCGRRKIILSDEGKM YGRNELIARYIKLRTGKTRTRK QVSSHIQVLARKKVREYQVGIK AMNLDQVSKDKALQSMASMS SAQIVSASVLQNKFSPPSPLPQA VFSTSSRFWSSPPLLGQQPGPSQ DIKPFAQPAYPIQPPLPPTLSSYE PLAPLPSAAASVPVWQDRTIAS SRLRLLEYSAFMEVQRDP*TRT SKHLFVHIRHTDRNPRRFFRTPP LGP\VDVR\QIYDPNFPEKKGGL KELYEKGPPNAF\FLVKFWADL NSTIQEGPGAFYGVSSQYSSAD SMTISVSTKVCSFGKQVVEKVE TEYARLENGRFVYRIHRSPMCE YMINFIHKLKHLPEKYMMNSV LENFTILQVVTSRDSQETLLVIA FVFEVSTSEHGAQHHVYKLVK
9269	39637	A	9329	2	339	
9270	39638	A	9330	1505	1876	TYGCASPSRKPRVMPLVTAQVP ITALRVNSSSIPAQSAVETTSNR PPTTGVPAFRPVRAAV*AVISPQ ISADPTTGGRA*LISAIPSQSVRH GSYSPRLML*RLDSEILLSSQPL TPVKHQRR
9271	39639	A	9331	1	1710	
9272	39640	A	9332	1	1191	

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9273	39641	A	9333	838	1365	STETLSPLPATPGEVTLRHLDV VSAEQQMFSGLVEKIQVTGSEG ELGIYPGHAPLLTAIKPGMIRIV KQHGHEEFIYLSGGILEVQPGN VTVLADTAIRGQDLDEARAME AKRKAEEHISSSHGDVDYAQAS AELAKAIAQLRVIELTKKAM*H RLEKHKSQSGNRLAFFCACDPS
9274	39642	A	9334	3	601	MLSAVGYQP/TLAEEMGVLQE RIPSTKTGSITSVQAVYVPADDL TDPSPATTFAHLDATVVLSRQI ASLGIYPAVDPLDSTSRQLDPL VVGQEHYDTARGGQFILARYQ ELESLL\AILGMNDLSEEDKLVV ARARKIQRFLSQPFFVAEVFTGS PGKYVSLKDTIRGFKGIMEGEY DHLPEQAFYMVGSIEEAVEKA
9275	39643	B	9335	681	1071	
9276	39644	A	9336	203	2189	VASSARRGLPVHGPAPLQGPGN SQDRL/ESGTNRCGLRGPLVKG GKGGRFPSARLIQTVKKGGTPS RDHA\IEPSGY\SVSAGVGE\RTR KGSVFAHEMPDCNVIDKVSLV YGQMTEPPGNCMRVALSGLTM AEKFRDEGRDVLLFVDNIYRYA LAG*ERFATVGR*ASN/AVGIQP TLAEKMGVLQERITSTKTGSITS VQAVYVPANDLTDPSPATTFA HLDATVVLSRQIASLGIYP\AVD PLDSTSRQLDPLVVGQEHYDTA RGG*SI\LQRF\QELKDFMALP/G LSDELSEEDKLVVARARKIQRF LSQPFFVAEVFTGSPGKYVSLK DTIRGFKGIMEGEYDHLPEQAF YMGDMAMTYHLDVVSAEQQ MFSGLVEKIQVTGSEGELGIYS GHAPLLTAIKPGMIRIVKQHGH EEFIYLSGGILEVQPGNVTVLAD TAIRGQDLDEARAMEAKRASG KVKPSIMQSLTPEKIAAILPLQF FPQPADFTGPYVMLTSRRNNRA LSRCDDQTLMPGLAIRGIRHRH QQAGVRILLNNAIEHVVDGEK VELTLQSGDTLQADVVIYGIGIS ADEPLAREANLDTANGIVIDEA CRTCDPAIFAGGDVPITSSLINV VDEIIHDILLTQPVATRYCIVKVI FEAVMILRDSGGAPFCSNGMAT

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9277	39645	A	9337	905	2319	SRQAQWKGVPSTFSVINYHSLQ KRTTNLTHRQLLNLLSTVLYCS CPSIQKLLLMLQTGQPSGVGLV DLPLKAMSRPALPNATAALPTG TRTQPPSTPLLTRLPSSHRLLLH SGF*AAALLGVSEMTIRRDLNN HSAPVVLLGGYIVLEPRSASHY LLSDQKSRLVEEKRRAAKLAA TLVEPDQTLFFDCGTTTPWIIEA IDNEIPFTAVCYSLNTFLALKEK PHCRAFPCGATPFSNPSIFSKRV NNFCRDIAFYYSAGVHVSKGV TCFNLKRWPVKQWAMSMAQK HVLVVDHSKFGEVGPVCMGDL KRFDIVVRECCPEDEYVKYAQT QRIKPDKVSRHPVIIRLREPGLE PVMEFHHPVLPQRTTESAVVHI AHTRKSWRPEHSAPVLIQTSPV ERGPQYIQCYQLSLTSEENNQP DTQTTTKPAQYSSILFLSKYPKV IVDAPDRSTQRGWSSGLATQSN EQACTTKCNSCTANWHQNTTT FNSTANPSTFKPPTSAALRVLSL WTGNHCDWCFIRYWRLTPNW QRFRRVGRTERATTHNRLQAF GGHTQGLSPGPRRWLHEQRFPT TSDTGGHTADDFRKLDPCIQGP YGSHRHSVKSEVNFKEKRYAF APAASFRYTVLIRFCAPPNTGRF LLTGTPLPMLSYRHSFHAGNHA DVLKHTVQSLIIESLKEKDKPFL YLDTHAGAGRYQLGSEHAERT
9278	39646	A	9338	98	596	YSGIIMAQSKLYPVVMAGGSGS RLWPLSRVLYPKQFLCLKGDLT MLQTTICRLNGVECESPVVICN EQPRFIVAHQMRQLNELSENIIL EPAGRTTAPTIAPAALAANRHS PESAPLMLVLATDHVIANEDAV RAPVK\NAIPYPKKGKLVTFGIG LDGRVPRYNM
9279	39647	A	9339	2	437	LECPGRSTANCSPRARATSLLL LTHVHGESRDRAQEMVDLLAQ YEQHGLQLNSRELPDHLPLYLE YLAQLPQSEAVEGLKDIAPILAL LSARLQQRESRYAVLFDLLLKL ANTAIDSDKVAEKIA/VRSAR*Y AAGAGCCLGRRAG
9280	39648	A	9340	152	334	HLSPQYGSIPRVISRMGGKLIIM DHFHYGRDSILLSME*TLALDA NLQFLYVVLLPNYYL
9281	39649	B	9341	1	1401	

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9282	39650	A	9342	86	2063	
9283	39651	B	9343	1	885	
9284	39652	A	9344	1	101	MDDNITYTTFICNPLNLSPQRR MLIITGPNMGGKSTYMRQTALI ALMAYIGSYVPAQKVEIGPIDRI FTRVGAADDLASGRSTFMVEM TETANILHNATEYSLVLMDEIG RGTSTYDGLSLAWACAENLAN KIKALTLFATHYFELTQLPEKM EGVANVHLDALEHGDTMAFM HSVQDGAASKSYGLAVAALAG VPKEVIKRARQKLRELESISPNA AATQVDGTQMSLLSVPEETSPA VEALENLDPDSLTPRQALEWIY RLKSLGKTMPSTRYQKINAHH YRHIWVVGDIHGEYQLLQSRL HQLSFFPKIDLLISVGDNIDRGP ESLDVLRLLNQPWFTSVKGNH EAMALEAFETGDGNMWLASG GDWFFDLNDSEHQEAIDLLLKF HHLPHIIEITNDNIIYAITTCVGN ARRAHAVHFCGDVARLLTCQI NIYRGQFRRLPRTFHRRLLTKL RDLILRLSAGNLQCCPDRAWRD NIHPNTFLRDLFCQATAVVQNR RLRSRIGDRFLGAVERRFGNDL PSSPVEWLTDNGSCYRANETRQ FARMLGLEPKNTAVRSPESNGI AESFVKTIKRDYISIMPKPDGLT AAKNLAEAFEHYNEWHPHRAN PITYQAVCANHYRTLNNGTMT NTG*QYNVYHIYLQPAESVAA APHVDHHRSEHGR
9285	39653	A	9345	1062	1179	PRFVPILAPYAPVRSVCLR*V*T DLPEYGHILFQPADR
9286	39654	B	9346	1	2439	
9287	39655	A	9347	136	629	RSVTPVTDIVKLLEFTRLRLPGY TKSIE*TNITFQCAIAAA*KNSVS TPRGGGTGTNGQALNQGIIVD MSRHMNRIIEINPEEGWVRVEA GVIKDQLNQYLKPFGYFFAPEL STSNRATLGGMINTDASGQGS/ LGVRAVLLGGDILDTQPLPVEL AETLGKSAE
9288	39656	B	9348	1	4653	
9289	39657	C	9349	584	819	

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9290	39658	A	9350	1	765	MQEWGRYTILSGCCNSALKGD VCLLYGFRVAGRRQASELQELT IGYRAQKNRVSSWCYCHFRQM AKAQHIKGFLNRLRKTAKK*GF QLVLLPFSANGK\AQHIKGFLN RLRKTAKKTRDFLTRMPKLGM TMVGVDPALVLCYRDEYKLAL GEERGEFNVLLANEWLASALES QPVATVSGESWYFFGHCTEVT ALPGAPAQWAAIFARFGAKLE NVSVGCCGMAGTYGHEAKNH ENSLGIYELSWHQAMQRLPRN RCLATGYSCRSQVKRVEGTGV RHPVQALLEIIK
9291	39659	A	9351	1	1710	
9292	39660	A	9352	1377	1712	IFRASLNQLLFCGLLAGRNHRQ RSVRALSQRKMVPTDRK*RCA RRAAR*PSARVL*SGE*TDRQH AD*PTIR*RRSWYLRPAVYASV RQSDRLYSDEYHW*PVRLQRY VRR
9293	39661	A	9353	203	1293	VASSARRGLPVHGPAPLQGPGN SQDRL/ESGTNRCGLRGPLVKG GKGGRFPSARLIQTVKKGGTPS RDHA\IEPSGY\SVSAGVGE\RTR EGNDFYHEMTDSNVIDKVSLV YGQMNEPPGNRLRVALTGLTM AEKFRDEGRDVLLFVDNIYRYT LAG*ERFATVGR*ASN/AVGYQ PTLAEEMGVLQERITSTKTGSIT SVQAVYVPADDLTDPSPATTFA HLDATVVLSRQIASLGIYPAVD PLDSTTRQLDPLVVGQEHYHTA RGG*SI\LQRF\QELKDFMALP/G LSDELSEEDKLVVARARKIQRF LSQPFFVAEVFTGSPGKYVSLK DTIRGFKGIMEGEYDHLPEQAF YMVGSIEEAVEKAKKL
9294	39662	B	9354	1	505	
9295	39663	A	9355	604	789	TMVASGSRRMTST*SRGSVNG CRTILRWKRHSSPLKIKRKQKS L*TMPSF*RLPAENSLFEI

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9296	39664	A	9356	1	1514	SVAVLRE*APKIRIQLATMPELA DASSDQQDNGAEMNLVYDRD TMARLGIDVLAANSLLNNAFG QRQISTIYQPMNQYKVVMEVD PRYTQDISALEKMFVINNEGKA IPLSYFAKWQPANAPLSVNHQG LWRAL\TIWFTLPTGKSLC\DPS AAIDRAMTQLGVPSTVRGSFAG TA\QVFQETMNSQVILIAAIAT VYIVLGILYESYVHPLTILSTLPS AGVGALLALELFNAPFSLIALIG IMLLIGIVKKNAIMMVDFALEA QR\HGNLTPQEAIFQACLLRFRP IMMTTLAALFGALPLVLSGGDG SELRQP\LGITIVGGLVMSQLLT LYTTPVVYLFFDRLRLRFSRKP KQTVTDTRWQLWIVAFGFFMQ SLDTTIVNTALPSMAQSLGESPL HMHMVIVSYVLTVAVMLPASG WLADKVGVRNIFFTAIVLFTLG SLFCALSSTIRIILRFVSLLHMR WQFRDLTFWQMRFRTNTPITSG GSDDSLMNQSHQRSVSSSI
9297	39665	A	9357	3218	3337	
9298	39666	A	9358	252	771	RRCQILLSGSLHSSWRTLPGHV *QLASAHRPRF\R*LPGLEPGEL FVHRNVANLVIHTDLNCLSVV QYAVDVLEVEHIICGHYGCGG VQAAVENPELGLINNWLLHIRD IIHGWAYGIHDGLLRDLDVTAT NRETLEQRYRHGISNLKRDVHF TTGRFIQQRTNRQRLRFAQA
9299	39667	B	9359	604	831	
9300	39668	B	9360	1	1104	
9301	39669	A	9361	242	337	LTVIHGVSAKTVILSSAVPIQ*K TVRRVSRR

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9302	39670	A	9362	2208	3411	LAADHRRRNAVQRPCNGGQSV QSTDEAAGRLSHADTHPGRPA RALPGDCRPETLLRTAGVAE*T KALYTLRSEKTRERPMDKQQA SDEKHRRFHDKESDFLA/FVNL WNY/LGEQQKALSSNAFRRLCR TDYLNYLRVREWQDIYTQLRQ VVKELGIPVNSEPAEYREIHIAL LTGLLSHIGMKDADKQEYTGA RNARFSIFPGSGLFKKPPKWVM VAELVETSRLWGRIAARIDPEW VEPVAQHLIKRTYSEPHWERAQ GAVMATEKVTVYGLPIVAARK VNYSQIDPALLHDTIELGTSPAF LITRWGFGRNLSRTSGGPRQEP RRKEIAMELVLKDAQSALTVSE TTFGRDFNEALVHQVVVAYAA GARQGTRAPKTRAAVTGGMPT LYAVGRLSRIPMDT
9303	39671	A	9363	79	559	TLSPGSINPFEKPNS*DSVPMTL/ RRFIEVRVFQQIHHMRQRPAHL W
9304	39672	A	9364	1	655	THWER/A/QGAVMATEKVTVY GFRIVAARKVNYSQIDPALCRE LFIRHALVEGDWQTRHAFFREN LKLRAEVEELEHKSRRRDILVD DETLFEFYDQRISHDVISARHFD SWWKKVSRETPDLLNFEKSMLI KEGAEKISKLDYPNFWHQGNL KLRLSYQFEPGADADGVTVHIP LPLLNQVEESGFEWQIPGL/RRE LVMPD*SCQTVTEFVPANSHSY

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9305	39673	A	9365	1	2082	MDIQEFPDLKGTTSLEILTLTRA GIRLLPSGMCQQLPRLRVLELS HNQIEELPSLHRCQKLEEIGLQH NRIWEIGADTFSQLSSLQALDLS WNAIRSIHPEAFSTLHSLVKLDL T\TSQLTTLPLAGLGGLMHLKL KGNLALSQAFSKDSFPKLRILE VPYAYQCCPYGMCASFFKASG QWEAEDLHLDDEESSKRPLGLL ARQAENHYDQDLDELQLEMED SKP\TPSVQ\CSPTPCPFKPCEYL FESWGIRLAVWAIVLLSVLCNG LVLLTVFAGGPAPLPPVKFVVG AIAGANTLTGISCGLLASVDAL TFGQFSEY/GLARWETGLGCRA TGFLAVLGSEASVLLLTLAAVQ CSVSVSCVRAYGKSPSLGSVRA GVLGCLALAGLAAALPLASVG EYGASPLCLPYAPPEGQPAALG FTVA\LVMMKLLLFSWFVGPLP YHQNWYCDLPRGDFEAVW\DC AHGEATWAWPHLRKTGLLYCP VAFLSFASMLGLFPVTPEAVKS VLLVVLPLPACLNPLLYLLFNP HFRDDLRRLRTPRRRTQGPP*PL CCGREDAGERASC\DSYPQALV APSLMWISFCEAS*SWAGPLEL ETYGFPSVTLISCQQPGAPRLEG THCVEPEGNHFGNPQPSLDGEL LLRAEGSTPASGGLSGGWRLSA LWLGLWLHTCKYPSPFFSSPLF PFLSPPSVNDGCF
9306	39674	B	9366	1	510	
9307	39675	A	9367	88	246	TPMRPMKSPMPTPVSRSGSSSK MG*SSASL*RSIPGLDAGKTPW PAGRSGTWA
9308	39676	A	9368	693	1041	AEGYSQCPNAREGHVDEENED SAPAAQKIP*I*ED*SPHVSQPVP EGEEECVKKQ/GRFSWNTSTS* RQT/TARKKLLADQAEARRSKT KEAHKSYEEHLQAKKEEIIKTL SKEEETKK
9309	39677	A	9369	1	1911	

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9310	39678	A	9370	1	921	MWRSIFLDSRYLLSSRRKILILLI HVTFSGIRALAVPFRLPVEKMS FIFMGDVIHRMLTATQYVAPL MANFNPGYSDNSTVVYFDNGQ QIRKLIKDGLIIRKPVTVHSRAR CRKNTLARRKGRHMGIEFACFC CVFLTPALICMVCAVRLLTRDP YLASGDQPLERATGEHASMHE Y\PGELG\QPPGLYPSSHPPGRA GTLRALSRQDTFDADTPGSRNS AYTEL*DSCVDMETDPSEGPGL GDPCE\GTPPARQGSWEDEEED YEEELTDNRNRGRNKARYCAE GWGPVLGRNKNELEGWGRGV
9311	39679	A	9371	3	740	ELFPFAAAAAAMSMLRLQKRL ASSVLRMWQRTNGLG*TPMRP M*SPMPTPRQQIPEAHQRWAD HP/LSLVTGPFPGSMPEKTPLA\ AGEGAGQHGALGKAGRGTSQ MPGMPGEGQHGLRRIEDFGAG LLQKDTGEI*RRSDRPHVFTAC YLEGEGGMLFQKQGGFFMGTL PQG*RQDKGPQRSFLADQA*RP QGLRTKESTESASEERLPGQRK EEINQRLYSKEGRRPRNKNLPL GSVHTWPLVIT
9312	39680	A	9372	1	2229	
9313	39681	A	9373	3	1560	SGPNSLKFYDWGETVPQPWPIF GLSPAFGFPLCFPRGLGETIFSSR PHIR/RNYPELQKRLNGWLSAA LKTARILTVCVAVMLLLSAWG LFDFWNWLQNGAGQKNP*NIP D/LRIRNSILFL/LSAVGWTVLA\ SLIENRLASDI\HGRPLP\SARTR TLLTLFRNALAVIISTITIMIVLS EIGVNIAPLLAGAGALGLAISFG SQTLVKDIITGVFIQFENGMNTG DLVTIGPLTGTVERMSIRSVGV RQDTGAYHIIPWSSITTFAN\FV RGIGSVGANYDVDRHEDADKA NQALRDAVEDDETRFTSESSPIL RCCQREGLGLKAVVQILLSHGR NGLPGEPASSQGLSAASSTPVF HLALQIDSAPDNIDWVEMLFNK NMVTERLQNVMVLEQCFSDSS SLYRFLTYSYLLAFNVWLLLAP VTLCYDWQVGSIPLVETIWDM RNLATIFLAVVMALLSLHCLAA FKSRVTASIPGCIKAHAVENVL TTKSKTRIYPEVVVQSGLQKQK GKGSVMFIEAAGL

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9314	39682	A	9374	3	276	VRQYR/LGN/MHQQRMAEMID ARQQQAFGEEGACWGGCPKHR VMLDASGKPGLNDLCAGYQRD VRHLPRYLKAMADLLAHGRPA SDIMHAHLLV
9315	39683	A	9375	102	916	RSLLAIFNHW*\KRDL\GKFLVW NIKW/AFAKFCRSAGQTSGRSVI VEHNGEIYACDHYVYPQYRLG NMHRQRMAEMIDSRQQQAFGE DKFKQLPAQCRSCNVLKACWG GCPKHRFMLDASGKPGLNYLC AGYQRYFRHLPPYLKAMADLL AHGRPASDIMHAHKKVFKRGT ACSGFQKGGPLFRSRTGYCPTL RKKAPCPKTGLLGKKWTPQRR NSSGKSCAKRRGDPPLLENRFN GSRVQRKPQWNSCTGHPENNF FPNYGGTPYPQRMWPL
9316	39684	A	9376	338	1155	SIFISIGNLAANDLSPSRIARLQK ILHSYVPEEIRDGNQVRVTSWD GRKWGELEGDTYDRVLVDVPC TTDRHSLHEEENNIFKRSRKKE RQILPVLQVQLLAAGLLATKPG GHVVYSTCSLSHLQNEYVVQG AIELL\PINTASRYRWKI*LTSEG FSWTHFVSSQSCPGWGAGNTK TSLA\ILALCTSAKCVGWT*YPP QSLKQEYQRVYSVGCTRNWKL GPVAEMHSRSCLHPVRVFLQFS AIRSRRFAVLLSNCGASAWFPT SLINPYPIS
9317	39685	C	9377	157	453	
9318	39686	A	9378	486	1195	ARPQQYEQVPGKAEASEWERG SSAPTGPGGHAAAAAGGVGGG EGSPPALHGRGARAG/GAGICM GLRQQLNR*AMDLTGAGGPAR AGAAGAVARGGGRHQGPGAG GRGRGLGFAAGTAEPRGAPHR PLQRALPPIRREPGERHRAPRAG AAPQCGSARPRQPRAPQSLRAG ALPEAHAQGQGPARTHPAEPGP AARRAQQSLCRHWD*GRGRPG PPDALRGGAASDFRLSARTPICR
9319	39687	A	9379	10	1278	

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9320	39688	A	9380	1	1305	MECVCVKEKEREEKEGKEEEE EDEAVAERGGKGERRGERRGE RKREKETYTEKNRYRDTKRDR DRERKEPYEIPSSLIGHGDPKDE LDRNLALKQVKTYWVIQFSKSI EVIEKRMAVLNEQVKEAEGSS AEYKKEIEELKELLPEITEKTED AKESQTTGNVAELALKATL\GG GSSVS/SIASRKPTDGASSSNCV TDISHFVRKKRKPEEQSPWKDD AKKVKQELEVNGGSGDAVPSG NEVLENMEEEAENRVESRAAV EGTVEAGATAESTAYMYDIPA MYQENTAVSKTDEVSDLIHKL AQTDLLAQERAGKRASPQDGG SAEGQAQSDRQEATKQRHKQE AGDRHYDKQMLEYQGAHELY SSREKRKEKKKKPPHGRLPPTP VALHGAKRRLLTKRLFNASPN KPKGHSTQFSVMSQAEQQPVL
9321	39689	A	9381	67	458	WDMANSGCKDVTGPDEESFLY FAYGSNLLTERIHLRNPSAAFFC VARLQ\QEGVKSGMYVVIEVK VATQEGKEITCRSYLMTNYESA PPSPQYKKIICMGAKENGLPLE YQEKLKAIEPNDYTGKGSEENE
9322	39690	A	9382	139	710	WDMANSGCKDVTGPDEESFLY FAYGSNLLTERIHLRNPSAAFFC VARLQDFKLDFGNSQG\KTSQT WHGGIATIFQSPGDEVWGVVW KMNKSNLNSLDEQEGVKSGMY VVIEVKVATQEGKEITCRSYLM TNYESAPPSPQYKKIICMGAKE NGLPLEYQEKLKAIEPNDYTGK VSEEIEDIIKKGETQTL
9323	39691	A	9383	1	731	MANSGCKDVTGPDEESFLYFA YGSNLLTERIHLRNPSAAFFCV ARLQLLIESPRMSRLAKFWPRT HAVILSKTERTSFWPLKPQKWE SGSDTPYSQTRKDFKLDFGNSQ GKTSQTWHGGIATIFQSPGDEV WGVVWKMNKSNLNSLDEQEG VKSGMYVVIEVKVATQEGKEIT CRSYLMTNYESAPPSPQYKKIIC MGAKENG\LRLKYQEKLKAIEP NDYTGKVSEEIEDIIKKGGTTKL
9324	39692	A	9384	41	333	MFCNTDLGT/LLCTDVVARGLD IPQVNWIVHYDHPDDPKEYIHR VVPAFVDLNVNGNEGKQKKRG GGGGFDYQKIKKVEKSKIFKHI SKKSSDSRQLSH

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9325	39693	A	9385	3	1852	SKQKPMNVGLSETQNGGMSQE AVGNIKVTKSPQKSTVLTNGEA AMQSSNSESKKKKKKKRKMV NDAEPDTKKAKTENKGKSEEE SAETTKETENNVEKPDNDEDES EVPSLPLGLTGAFEDTSFASLCN LVNENTLKAIKEMGFTNMTEIQ HKSIRPLLEGRDLLAAAKTGSG KTLAFLIPAVELIVKLRFMPRNG TGVLILSPTRELAMQTFGVLKE LMTHHVHTYGLIMGGSNRSAE AQKLGNGINIIVATPGRLLDHM QNTPGFMYKNLQCLVIDEADRI LDVGFEEELKQIIKLLPTRRQTM LFSATQTRKVEDLARISLKKEPL YVGVDDDKANATVDGLEQGY VVCPSEKRFLLLFTFLKKNRKK KLMVFFSSCMSVKYHYELLNYI DLPVLAIHGKQKQNKRTTTFFQ FCNADSGTLLCTDVAARGLDIP EVDWIVQYDPPDDPKEYIHRVG RTARG\LNGRGHALLILRPEELG FLRYLKQSKVPLSEFDFSWSKIS DIQ\SQLEKLIEK\NYFLHKSA\Q EAYKSYIRAYDSHSLKQIFNVN NLNLPQVALSFGFKVPPFVDLN VNSNEGKQKKRGGGGGFGYQ KTKKVEKSKIFKHISKKSSDSRQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9326	39694	A	9386	1	2703	MAQQATLCSMKGCMRALVAQ LKSESEDLQQTVQAKREVPKSK VPAAEKRESGPKQAAVNAAVQ RVQVLPDVDTLLHFATESTPDG FSCSSSLSALSLDEPFIQKDVEL RIMPPVQENDNGNETESEQPEE SNENQDKEVEKPDSEKDLLDDS DDDDIEILEECIISAMPTKSSRK AKKLAQTASKLPPPVARKPSQL PVYKLLPAQNRLQAQKHVSFTP GDDVPRVYCVEGTPINFSTATS LSDLTIESPPNELATGD/GVRA/S IQSGKSHKPFRVKK/IMDQVQQ ASSTSSGANKNQVDTKKKKPTS PVKPMPQNTEYRTRLPNNEDR VRGSFALDSPHHYTPIEGTPYCF SRNDSLSSLDFDDDDVDLSREK AELRKGKESKDSEAKVTCRPEP NSSQQAASKSQASIKHPANRAQ SKPVLQKQPTFPQSSKDGPDRG AATDEKLQNFAIENTPVCFSRN SSLSSLSDIDQENNNNKESEPIK EAEPANSQGEPSRQLSQQNLTK QASLSKNASSIPRSESASKGLNQ MSNGNGSNKKVELSRMSSTKS SGSESDRSERPALVRQSTFIKEA PSPTLRRKLEESASFESLSPSSRP DSPTRSQAQTPVLSPSLPDMSLS THPSVQAESSEKAKSEDERHVS SMPAPRQMKENQVPTKGTWR KIKESDISPTGMASQSASSGAAS GAESKPLIYQMAPPVSKTEDV
9327	39695	A	9387	2	193	QSSE*NIQGPCNVWSSR*RWER SKGRRHLSSASRPLSALSTLRFT SVSQHAAKRVVVIRPQGQ
9328	39696	A	9388	395	761	SMQKKPRPIAHRQRCRAAMAA/ GQQPQIPITTGTGVVYPGAITM ATTTPSPQMTSDCSST\SASPEPS LPVIQSTYGMKTDGGSLAGNQ MINGEDEMAMYDDYEDDPKS DYSSENEAPEAVSAN
9329	39697	B	9389	1	477	

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9330	39698	A	9390	167	890	LSGARSSQGRLPWGRGDAVSTS TSRRNPRTGASDERNNHEPGKN SPYLQAQ\VRIGGKGTARRKKK VVHRTATA\DDKKLQF\SLKKL GVNH\ISGIE\EVNM\FTNQGTSG STFNNP*KVQAISWAANTFHPL PGPCWRPKPADKKWLPQPSLN PSLGAG*S*LRFKGRLARSFLPP NNP\VDGKATHLPTG\KDDDD\ KVPRSLWRILMRLPKNEGKLEL RSTS*R*NLEEVT\GSRYFKIMT AF
9331	39699	A	9391	2	315	GAASLLRAGPGSSGSDP\PLSSR FVERRGALYRSPMNQENPPPYP GPGPTAPYPQYGWQGGPQEPP KTTVYVVEDQRRDELGPSTCLT ACWTALCCCCLWDMLT
9332	39700	A	9392	263	680	LLLPALVTSAPLPPAGLATCPCP RLAQLGIGRAAPQKRSPRRRNP EASRGRPPDGVWRAPLR/VPPT PRETEPQRRGDPGLRNPCLSQA SPGAPQFSGP/PPGSPGTRPVRA* SPPGPSWVGPGPLHLTSPLPNRL DNGRV
9333	39701	A	9393	2	537	SGARLLLTCSETGAASLLRAGP GSSGSDP\PLSSRFVESRGALYR SPMNQENPPPYPGPGPTAPYPP YPPQPMGPGPIGGPYPPPQGYP YPRIPTVRLAGWTSGSLLKTTV LLWVGRPKEEMKLGTIHLPSQP AGTGLCLLLSLGTWFTLTRTRP RPFLFLASSAANLLTGVPCPHLF
9334	39702	A	9394	3	470	PKAKKEAPAPPKAEAKAKALK AKKAVLKGVHNHT\QKKKIHTP LTFQRPKSLRLRRQPKYPRKSA PRRNKLDHYAIIKFPLTTESAM KKIEDNNTLVFIVDVKANKHQI KQAVQKLYDIDVAKVNTLIRPD GEKKAYVRLAPDYDALDVAN KIGII

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9335	39703	A	9395	1	1144	MLYQVLMVDTCGTRGEGAFLK YRKPACPTALGFMFPRSHGLTA DTVLVSSLSRWFLWRRLLLLLL LLLLNLPLQKAVHRKATPESAI ADCSGPRDCAPWVKFAMLELH SFKCPAGEYWSKDVCCKNCSA GTFVKAPCEIPHTQGQCEKCHP GTFTEKDNYLDACILCSTCDKG DFYGKKTAVHEALCDNIDTRT VMEEMRALVSQCNLYMAARK AERRRPNRALLENIAMYLTHM LKIFGAIEEESPLGFPVGGPGTN LNPIENGGMDKFLTTVSVLRKT HRVSNGQNSVCRSVSYWKPKC TFCSLTHITYIRYLELRLTLESTV MPYLQVLSEFREGVRKIAREKK VLEVLQLSDALR\VTSCLSLGSG LKTMKEPCLLF
9336	39704	A	9396	1	639	MDGDEKTSFICAVHNGIFREWK QTGTCSPIKKGQLLLRVECHGK IKAQGGQMYIKAALFTRAKTW NQPKCPS\MIDWIKKMWVHIY/ TCEYYTAIKKKIMSSVETWMEL EAIILSKLTQEQKSKFRTFSLYSS RVFQRTQDVPYHNKLNEEADK PTTNKKGLILNLRLVNTPIGRK NTGKLSAIKEKLLKRPKRKHLS KIYTLKNDSDLIKDKNI
9337	39705	B	9397	1	825	
9338	39706	A	9398	2	285	HEENRPFVCEH/AGCGKT/FAN KPSLTSDAVVH/DPGKKKMKL KVKKSREKRSLASHLSGYIPPK RKQGQGLSLCQNGESPNCVED KMLSAVPVLTLG
9339	39707	A	9399	2003	2344	PFVGVFWFLFFFFSVFVFTFVPP EYYVLPAPPPHRSVFLVFGKRV VFFFPLPC/CDFRSRLTPPFVCAP P\PPPLPFVSVPCVPSLSCGDVC AADKKNKKKFLNTTRWKKKT
9340	39708	B	9400	3	113	
9341	39709	C	9401	48	182	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9342	39710	A	9402	2	752	VWWNSRRRPVKRRRLLASPYS ACSGRSAGFLDNCAMCAARLA AAAAAQSVYAFSARPLAGGEP VSLGSLRGKVLLIENVASL*GTT VRDYTQMNELQRRLGPRGLVV LGFP\CNQFGHQENAKNEEILNS LKYVRPGGGIEPNF\MLFHKSE VN\GAGAHPLFAFLREALPAP\S DDATALMTDPKLITWSPV/CRK DPGKIKFFLGPPGNFFEKFLGGP CTVLPLRRYSRRF\QTIDIEPDIE ALLSQGPSCA
9343	39711	A	9403	1	1128	
9344	39712	A	9404	7	378	ARCDHPTAFVVCYRFYPWPAG HVDAAVH*YVCARATDSFIAV WRTLLKGTIIILHESSIHDNFNLT SQKLWAFVPNKAPRTSGIICWP EIQSAFQGGGNLYFTIPIVDRNS TNYVLRQVRLLGN
9345	39713	A	9405	318	616	DPAGFPGCWKPLFYDLHYRSQ LHQLCLQAGRTPGQFGHQHRF WWQFCT*ELPSALQPLPEGNLV SCNEQSFGAPATGTNPGEPVHP AALGTWLYLLPPC
9346	39714	A	9406	1	145	MEYYAVIKKDEFMSFAGTWM KLETIILSKLTQE\QKPTPLMFSL ISGS

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9347	39715	A	9407	1	2052	MVLVVVAVVVVVLVVAVIVV VVVVVAAVVVGAVVVVVVVV MVVVVVVVVVEEDNQHKTGA INNNNTAKNPQQSPFHSPATST GAEATQMRRNQKTNPHNMTK QVSLTPPKITLAHQQWIQTKKK YLIYLKKHSGVNKIPRNPTYEG CEGPFQGELQTTAQQNKGGHK QTEDHSMLMDRKNQYCENGH TAQAVPNPYTLLSQIPEDAEWF TVLDPKHAVFCIPVHPDSQFLF AFEDPSNPMSQLIWTVLPQGFR NSPHLFGQALAQDLSQFSYLDT LVLRYMDDLLLATHSETLCHQ ATQALLNFLATCGYKVSKPKA QLCSQQVKYLGLKLSKGTRTLS EERIQPILGYPHPKTLKQLTAFL GITGFCQIWIPRYSKIARPLNTRI KETQKANTHLVRWTPEAEVAF QALKKALTHAPVLSLPVGQNFS LYVTEK\TGIALGVLT/PGTSAQ LAELIALTRAPELGEGKRVNIY ANSIGREREFLTSKGTLVKHQE AIKRLLLAVQKPKEVAVLHCW GHQKGKEREIEENRQADIEARR AARQDPPLEMLTEGPLAFELA MATARAELSLAIHHCCLPPPPQ TRCWLPSLRIRQGVCCIPDPAR AITLTAWPKIPFLGIRKAKNPRS EKTRLATILEAACCHFGSGPPPS WELWEQGPPVTVQTHILRSHL
9348	39716	A	9408	2	350	YKVSKPKAQLCSQQVKYLWLK LSKGTRALSEERIQPILAYPHPK TLKQLRGILGITGFCRIWIP\R*S SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
9349	39717	A	9409	1	749	MNQSDQEMTGAFVHMKSYTG LISGVAVKMERHIYQDRRIAIEK EFNSCRTGCMGDWSFTITQIRL LENTGIRVFKDNLVEEAEWFTV LDLMDAFFCIPVHPDSQFLFAFE DPSNPASQLTWTVLPQRFKNSP HLFGQALAQDLSQFSYLDTLVL RYMDDLLLAAYSETLCHQATE ALLNFLATCGYKVSKPKAQLCS QQVKYLGLKLSKGTRDLTTFLP VNEEKIE/P*LSTSNCSKLRCSRG TSRGSLG
9350	39718	A	9410	118	174	
9351	39719	A	9411	577	3018	

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9352	39720	A	9412	310	1964	TFRLTEPTQMRRNQKTNPHNM TKQGSSIPPQKNHTSSPAMDPN QEEIPDLP\EKNSGVNKIPRNPT YEGCEGPFQGELQTTAQQNKG GHKQTEDHSMLMDRKNQYCE NGHTAQAVPNPYTLLSQIPEDA EWFTVLDPKHAVFCIPVHPDSQ FLFAFEDPSNPMSQLIWTVLPQ GFRNSPHLFGQALAQDLSQFSY LDTLVLRYMDDLLLATHSETLC HQATQALLNFLATCGYKVSKP KAQLCSQQVKYLGLKLSKGTR TLSEERIQPILGYPHPKTLKQLT AFLGITGFCQIWIPSILTAKGDL WLSDNHLLKYQVLLLEGPVLQ LRTCATLNPATFLPDNEEKIEH NCQQVIAQTYATRGDLLEVPLT DPDLNLYTDGSSFVQKGLQKA GYAVVSDNGILESNPFTPGTST QLAELVALTWALEFGEGKRVN INTGSKYAYLVLHAHASIWRER EFLTSEGTPIKHQEAIRRLLLVV QKPEEVAVLHCWGHPKGKERE IEGNCQADIEAKRASRQDPPLE MLIERHLVWGNPLWETNPQYS
9353	39721	A	9413	3	370	RCCPCPRVHHMHISARAEIRPPP RPPPFLLLLVFLFQTGPCSHPGC SPPPAHPSCSSWPQWPG/CSSPV SVLLAKPAACLIAAAVSANPRL LFKPCCRTASNWAHRQVTLCQ WSELSSCFWPE
9354	39722	A	9414	191	1375	EWPEGGGRYSSVPSAVHHART CLAAELSGTSRPQEPRALPPETG VATAEAEKSNQPAAISK\PNGQ GAPLQR/RSPRLSPSPGAAQVPA LPMQDMSEGSSSPSPPGGHIWL ASLTPCSLALWNSCCQSPGSQP RGRDEGDCLVRATEPSATGPDP RRTRLCSISASLVVRNTPDPGIS DRRPGISDRRPGTSDRRPGTSDR RPGISDRRPGTSDRRPGTSDRRP GTSDRRPGTSDRRPGISDRRPGT SDRRPGISDRRPGTSDRRPGISD RRPGTSDRRPGTSDRRPGISRLP RDWIPAAAASRENSNSADARN RCSSPSRKCQTPTSHRMRGSAG SVGSSAGHTAGGTGLPTPSRCS QALQVFPAVLGKRGFLSWERS LKQRDIRGPDFSSTALI
9355	39723	A	9415	3	523	

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9356	39724	A	9416	1	846	MLCDFQDGSTSRHVNEPSNNPS PQPWSEDQGQASATVPCAKSV MHRLKKFTIEYLVMKFLKAVS HAIQMEMLAPKGPSPIPEDASV KEENICRAFSDALLYKIEDIDNK DWNNPQLCSDY/VKDNAYTSF QIQEMET\ILKELKFEVGGPLPL HFLRQASKAGKADVEQHTLAK YLMELTLIDYDMMHYHPSKAA TAASCLSQKVLGQGKWNLKQQ CYTGYTQNEVLEVMQHVAKN VLKVNENLTKFIAIKNKYASNK FLKISMIPQLNSKAIKDLAFPLM GGS
9357	39725	A	9417	72	1340	CPPFSVRVPPWAGLALLPSPSL MALLRRPTVSSDLENIDTGVNS KVKSHVTIRRTVLEEIGNRVTT RAAQVAKKAQNTKVPVQPTKT TNVNKQLKPTASVKPVQMEKL APKGPSPTPEDVSMKEENLCQA FSDALLCKIEDIDNEDWENPQL CSDYVKDIYQYLRQLEVLQSIN PHFLDGRDINGRMRAILVDWL VQVHSKFRLLQETLYMCVGIM DRFLQVQPVSRKKLQLVGITAL LLAPKYEKMFSPNIEDF\VYITD NAYPS\SQIREMETLILKELKFEL GRPLPLHFLRRASKAGEVDVEQ HTLAKY\LMELTLIDYDMVHY HP\SKVAAAASCLSQKVLGQGK WNLKQQYYHKDTQENEVLEV MQHMAKNVVKVNENLTKFIAI KNKYASSKLLKISMIPQLNSKA VKDLASPLIGRS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9358	39726	A	9418	1	1875	EPEKQQLYDIPASPKKAGLHPP DSQASGQGVPLISVTTLRRGGY STLPNPQKSEWIYDTPVSPGKA SVRNTPLTSFAEESRPHALPSSS STFYNPPSGRSRSLTPQLNNNVP MQKKLSLPEIPSYGFLVPRGTFP LDEDVSYKVPSSFLIPRVEQQN TKPNIYDIPKATSSVSQAGKELE KAKEVSENSAG\QIPHGSPDGQ/ RSPSPEPDRLSGSSSDSRASIVSS CSTTSTDDSSSSSSEESAKELSL DLDVAKETVMALQHKVVSSVA GLMLFVSRKWRFRDYLEANID AIHRSTDHIEESVREFLDFARGV HGTACNLTDSNLQNRIRDQMQ TISNSYRILLETKESLDNRNWPL EVLVTDSVQNSPDDLERFVMV ARMLPEDIKRFASIVIANGRLLF KRNCEKEETVQLTPNAEFKCEK YIQPPQRETESHQKSTPSTKQRE DEHSSELLKKNRANICGQTLPN LEEKDKPILEQRLDENKDLGTM NPGPLIPQPSSQQTPERKPRLSE HCRLYFGALFKAISAFHGSLSSS QPAEIITQSKLVIMVGQKLVDT LCMETQERDVRNEILRGSSHLC SLLKDVALATKNAVLTYPSPAA LGHLQAEAEKLEQHTRQFRGT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9359	39727	A	9419	1	2013	MGLKSWGGMGLGTAFGKGLR GEKAWCVSGRYHWRYSQWSG TLTQGPWVWRVHSLSDRVYDV PTQHRGPVVLKEPEKQQLYDIP ASPKKAGLHPPDSQASGQGVPL ISVTTLRRGGYSTLPNPQKSEWI YDTPVSPGKASVRNTPLTSFAE ESRPHALPSSSSTFYNPPSGRSR SLTPQLNNNVPMQKKLSLPEIPS YGFLVPRGTFPLDEDVSYKVPS SFLIPRVEQQNTKPNIYDIPKAT SSVSQAGKELEKAKEVSENSAG \QIPHGSPDGQ/RSPSPEPDRLSG SSSDSRASIVSSCSTTSTDDSSSS SSEESAKELSLDLDVAKETVMA LQHKVVSSVAGLMLFVSRKWR FRDYLEANIDAIHRSTDHIEESV REFLDFARGVHGTACNLTDSNL QNRIRDQMQTISNSYRILLETKE SLDNRNWPLEVLVTDSVQNSP DDLERFVMVARMLPEDIKRFAS IVIANGRLLFKRNCEKEETVQL TPNAEFKCEKYIQPPQRETESH QKSTPSTKQREDEHSSELLKKN RANICGQNPGPLIPQPSSQQTPE RKPRLSEHCRLYFGALFKAISAF HGSLSSSQPAEIITQSKLVIMVG QKLVDTLCMETQERDVRNEILR GSSHLCSLLKDVALATKNAVLT YPSPAALGHLQAEAEKLEQHTR
9360	39728	A	9420	3	645	DFHTN/K/RVCEEIPIILSKKKLHN RRAGCVTHLTNQIQRGPVRGISI KLQEEEKERRDNYVPKVSALD QEIIEVDPDTKEMLKLLDFGSLS NLQQQKATRVYAVVQISAPMF LLWALPLSVAPLITDFKMFVTT SYLISLFLIINSSANPIIYFFVGSL RKKRLKESLRVILQRALADKPE VGRNKKAAGIDPMEQPHSTQH VENLLPREHRVDVET
9361	39729	A	9421	312	694	LTPAPRKNVTEKYYMCLGNDF HTN/K/RVCEEIPIILSKKLHNRR AGCVTHLTNQIQRGPVRGISIKL QEEEKERRDNYVPKVSALDQEI IEVDPDTKEMLKLLDFGSLSNL QVTRPTVGMNFKMPRGAV
9362	39730	A	9422	3	383	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9363	39731	A	9423	304	1862	RMLEATSKMRKGVPSSIQ/SSQ GNSYTLIPSAKSDNLSDSSHSEI SSRSSIVSNCSVDSMSAALQDE RCSSQALAVPESTGALEKTEHA SGIGDHSQHGPGWTLLKPSLIK CLAVSSSVSNEEISQEHIIIEAAD SGSWEVGTSCSSSSHDNFQSLP NPKSWDFLNSYRHTHLDDPIAE VEPTDSEPYSCSKSCSRTCGQC KGSLERKSWTSSSSLSDTYEPN YGTVKRRVLESTPAESSEGLDP KDATDPVYKTVTSSTEKGLIVY CVTSPKKDDRYREPPPTPPGYL GISLADLKEGPHTHLKPPDYSV AVQRSKMMHNSLSRLPPASLSS NLVACVPSKIVTQPQRHNLQPF HPKLGDVTDADSEADATLGNK CKLLYMSDVRNPVPAVKDVLV QKYTSFNFFHPQEALDRRREEL ALPEGASGEACLSTRSLKRSGV QALAQQTHSRNFLPEKQPFSAQ AAGILHGSINHNTRGPCLLEGT KMMTGVLYRAYLLCIAYSRDLI VDEQIMNGLRKAI

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9364	39732	A	9424	1	1335	MTFKNPKYPFVSNLAKQKGMS VIKVNGKLQQSNPNRTTNGPDP SGMKVWVSPQGKNPQPTEVLA EGKGNTEWVVEEDTRNFGFGI QKHTDIGIKYDSSTGIYDLDFN VVLDRRASEEGITLTAALAADR ETPSENCLPSPVNPTAQGEEGIH PDPIIVLEQEDPTTAPHPQRLCQ QQQCQRPLCRLQPVWPHIVDLT PLTEIGSEEPVGELNFKHIRFEV SEDNMTFDASDQGPFFENYWQ LVLSATPGDVTWNGALGLHTP KSSSPDTCSAQQASQCWELSPG GRRIGTLLLPQESGASWLPPGV TSSLAAVRVIMNCGDKATPRN GGVRTLKKLSSLPLSKAGGKVL YGEINPEQEVQASLSFAALLES YGIFMETEFLVACLISQGGQLR NQDFSSSIYSLAPGPLDPSSVRA GAQRTAPPWGISPRSC/PVIKVN GKLQQSNPNRTTNGPDPSGMK VWVSPQGKNPQPTEVLAEGKG NTEWVVEEDTRNFGFGIQKHT DIGIKYDSSTGIYDLDFNVVLDR RASEEGITLTAALAADRETPSE NCLPSPVNPTAQGEEGIHPDPII VLEQEDPTTAPHPQRLCQQQQC QRPLCRLQPVWPHIVDLTPLTEI GSEEPVGELNFKHIRFEVSEDN MTFDASDQGPFFENYWQLVLS ATPGDVTWNGALGLHTPKSSSP DTCSAQQASQCWELSPGGRRIG
9365	39733	A	9425	56	235	
9366	39734	A	9426	1	515	
9367	39735	A	9427	138	830	AWAQLPSALGSTRVSPPPSARS QPPWRRRHK/CLLETEPLQGTD EDAVASADFSSMLSEEEKEELK AELVQLEDEITTLRQVLSA\KER HLVEIKQKLGMNLMNELK\QNF SKSWH\D\MQTTTAYKRTHDTL SHAGQKATAAFSNVGTAISKKF GDMSYSIRHSISMPAMRNSPTF KSFEERVETTVTSLKTKVGGTN PNGGSFEEVLSSTAHASAQSLA GGSRRTKEEELQC
9368	39736	A	9428	3	381	LLETEPLQGTDEDALASADFSS MLYEEEKEEVKAELVQLEDEIT TLRQVLSAKERHLVEIKQKLG MNLMNELKQ\NFSKSWHDMQT TTAYKKTHETLSHAGQKATA\A FSNV\GTAISKKFGDMRRK

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9369	39737	B	9429	79	426	
9370	39738	A	9430	1	570	
9371	39739	A	9431	1	1677	MLESVNVRLEDLITGPCWEAG WNAGYAFLVVAVEDFTIGKLF DKLEGTKLCLKNALPRVITQTE SHRQRLLQEAAANWHSWLIKV QKMKAVYHILNMCNIDVTQQC VIAEIWFPVADATRIKRALEQG MELSGSSMAPIMTTVQSKTAPP TFNRTNKFTAGFQNIVDAYGV GSYREINPAPYTITFPFLFAVMF GDCGHGTVMLLAALWMILNER RLLSQKTDNEIWNTFFHGRYLI LLMGIFSIYTGLIYNDCFSKSLNI FGSSWSVQPMFRNGTWKTGTH DPHLAVLFKMGHVEGRDCVLR IVLAKIGYRNGFLRKIWNLASN KLTFLNSYKMKMSVILGIVQM VFGVILSLFNHIYFRRTLNIILQF IPEMIFILCLFGYLVFMIIFKWCC FDVHVSQHAPSILIHFINMFLFN YSDSSNAPLYKHQFNFGDVFV HQAIHTIEYCLGCISNTASYLRL WALSLAHAQLSEVLWTMVMN SGLQTRGWGGIVGVFIIFAVFA VLTVAILLIMEGLSAFLHALRL HWVEFQNKF\YVGDGYKFSPFS FKHILDGTAEE
9372	39740	A	9432	3	933	GTWPVSSAASIYAGTGGLG\SQI SMSCSTSFWGGLGSGGLATEM AGGLAEMGGIQNEKETMQSLN DHLDYLDRVRNLETENWRLES KIQEYLEKRPHVRDWGHYFKTI KELRAQIFANTVDNVHIILQIDN AQSSMRQELAMRQSVESNIHG LCKVIDDTNVTLLQLETEMGAL KEELLLMKKNHEEEVKGLQVQ IANSGLAVEVDAPKSQVLAKM EQLNRILLYLESKLAQNWAEG QRKVQEYKDLLNIRVKLEAEIA TYRRLLEDSEGLNLGDALDSSN SMQTIQKTTTRQIVDSKVVSEIS DTKVLRH
9373	39741	A	9433	3	698	

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9374	39742	A	9434	2	479	PRVRESTTVVTTQSAEVGAAET TLTELRRTVQSLEIDLDSMRNL KASLENSLREVEARYALQMEQ LNGILLHLESELAQTRAEGQRQ AQEYEALLNIKVKLEAEIA/TTY RRLLEDGEDFNLGDALDSSNS MQTIQKTTTRRIVDGKVVSETN DTKVLRH
9375	39743	A	9435	1	618	AEHLLKPLPADKQIETGPFLEA VSHLPPFFDCLGSPVFTPIKADIS GNITKIKAGYDTN\QPRFRTLKT ILEGEKEMYGAKGPKVGATLA LMWLKRGLRFIQVFLQSICDGE RDENHPNLIRVNATKAYEMAL KKYHGWIVQKIFQAALYAAPY KSDFLKALSKGQNVTEEECLEK IRLFLVNYTATIDVIYEMYTQM NAELNYKV
9376	39744	A	9436	1	1569	
9377	39745	A	9437	211	368	ERNSLSQLQWDNPTPPATRRPS HSSLRGEHAQ*GLLSFFERLSCT LSRFMPI
9378	39746	A	9438	1435	1703	
9379	39747	A	9439	1	913	MKNYNCWRRVFLFVVTPIPMG HIKHRQGPNKQQRGQKRDEQR MRKENRGHRKGCTWCGGGTE GTGWGKYEKSEVERGLVRYER KRRAYSGIQQYAAAALPTVYN QNLLTQQSIGAAGSQKEACAY AVMSLASRAPVYRSFDSEKAG DREVQRTMLELLNQLDGFQPN TQVKVIAATNRVDILDPALLRS GRIDRKIEFPMPNEEAR\ARIMQ IHSRKMNVS/TDTTLVALQMAL NVYNGKQAPYASCHIFELYQE DNGFLLEHTGFVSYDNPVSAQ AAIQSMNGFQIGMKRLKVQLK RSKNDSKPY
9380	39748	A	9440	3	438	
9381	39749	A	9441	1	247	AIAAIDSDSSDGSRQSEWKFWK GFTILDAIKNIYDSWEEVKMST LTEVWKKLIPTLMDSFEDFI\EE VTVDVWECTVLQTQI

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9382	39750	A	9442	93	726	TSLGLSLCPRQCKRCPHLSLQQ EEPDPANLEVDHDFFQDKVWP HLALRVP\AFETLKVQSAWAGY \YDYNTFDQNGVVGPHP\LVVN MYFATAFSGHGLQQAP\GIGRA VAEMVLKGRFQTIDLSPFLF\TR FYLG\EKIQ\ENNIILRHVCSGIG LPLACNPWLCLKSLVCWLPIFP KVLCPGLLSPSPVSSSSQAGHW HPIWAGQGTGSEAEGQ
9383	39751	A	9443	1	849	MSGALDVLQMKEEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYIINLKRTWEKFLLAAR AVVAIENPADVSVISSGNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIQAAFREPRLLVVTDPRA DHQPLTESSYVNLPTIALCNTDS PLRYVD/ICNNKGAHS\DPEEIE KEEQAAAEKAVTKEEFQGEWT APAPEFTATQPEVADLSEGVQV PSVPIQQFPTDDWSTQPATENW SAAPTAQATEWKMQQQSTILE AESSPHQTPNLPAPWSRTSQPPE
9384	39752	A	9444	1	1575	
9385	39753	A	9445	1	2325	
9386	39754	A	9446	1	1149	
9387	39755	A	9447	85	1041	REIVTMSGALDVLQMKEEDVL KFLAA\GTHLGGTNLDFQMEQ YIYKRKSDGIYIINLKRTWE\KL LLAA\RAIVAIENPADVSVISSQE ILGQKGCAESFAAATG\ATPICW ARFTPWNLSLTQIQGSPSGEPR AFLLVTDPQGLNHQPSHGGNL NV*PTLPLALVNPD/SPLRRYVD I\AIPCNNQGSSLQWGLMWW\M LASGSFCAMRGT\ISREHP\WEV\ MP\DLYFYRDPEEIEKEEPGCCL RSQVTKEEFQGEWTAPAPEFT\ VTQPEVADWSEGVQ\VPS\VPIQ QFP/TTEDWSAQPATEDWSAAP TAQATEWVGATTDWS

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9388	39756	A	9448	1	762	MGKVKVGVNGFGCIGRLVIRT ACNSGKVDIIAINDPFIDLSYMV YMFQYDPTHGKFHGTVKAENG KLVINGNPITIFQEPDPSKIKWG DAGTEYVMESTGIFTTMENAG AHLQWGAKRPQG\LQNIIPATT/ GAAKAVRKVIPELNGKLTGMA LRVPTANVSVVDLTYHLEKPA KYDDIKKVVKQASEGPLKGILG YTGHQVVSSDFNSDTHSSTFNA GAGTALNDHFVKLISWYDNEF GYNNRVVDLMAHMASKE
9389	39757	A	9449	93	660	DTMGKVKVGVNGFGRIGRLVT RA\AFNSGKVDIVAINDPFIDLN YMVYMFQYDSTHGKFHGTVK AENGKLVINGNPITIFQE\RDPSK IKWGDAG\AE\YVVESTG\VFTT MEK/ALGAHLQGGSQKGHSSL APSCLMPPMFVMGVN\HEKDD NSLK\IISN\ASCTTNCLAPLAK\ VIHDTLVSGEGLKDHRALP
9390	39758	C	9450	554	715	
9391	39759	A	9451	193	472	RRVGVWRRPQFQQSRCSHGPN QGSAPWLNPTGAFGKETDLLL\ DDSLVSIFGKRRL\KRFSMVG/D RMASKNALNAQPDGPGLTCSL APNIISQL
9392	39760	A	9452	1	864	GTRMGLAGVCALRRSAGYILV GGAG/WSVLAPRAAAARRCSE GEWASGGVRSFSRAAAAMAPI KVGDAIPAVEV\FEGEPGNKVK PGKSLFKGKKGVLFGVPGGPPP LGCS\KTHLAKGLWEQG*RLCK AKGKSRVVALF*VVNDALCDW AQWGQAPQGGKARFGLLAESP LGPFGK\ETDLL\LDESLVSHLL GIRRLK\RFS\MVVQDGIV\KAL\ NVEPDGTGLHLAAWAPNIIFTA LEALGPDLLPLPPPYSSPCPALC LGPLQFGNVGQISAINTLWVLR PKQKKKKS
9393	39761	A	9453	1	239	QCCSGGTHGNPAIGDR\MQKQI LPWAPAQMKIRFMAPPERKYS VWIAAPILASLSTSSRMWISKQE YDESGPSIVHRKCF

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9394	39762	A	9454	2	801	ASAPRAQSLAFADPPPVHTRRQ LTMDDDIAALVVDNGSGMCKA GFAGDDAPRAVFPSIVGRPRHQ GVMVGMGQKDSYVGDEAQSK RGILTLKYPIEHGIVTNWDDME KIWHHTFYNELRVAPEEHPVLL TEAPLNPKANREKMTQIMFETF NTPAMYVAIQAVLSLYASGRTT GIVMDSGDGVTHTVPIYEGYAL PHAILRLDLAGRDLTDYLMKIL TERGYSFTTTAEREIVRDIK/EE AVLRRPGLRARDGHG\ASSSSL EKSYELPDGQVITIGNERFRCPE ALFQPSFLG\MESCGIHETTFNSI MKCDVDIRKDLYANTVLSGGT HQFPLPCRPGC*KKITALEP\AT MKI\RIIA\PPEAQSTPLWNRGAP IL\ASLVHLPAKMWDQKSREYD ESGPLPFVHRK\CFQLLPGEELR
9395	39763	A	9455	3	108	
9396	39764	A	9456	1	1430	MKFLIFAFFGGVHLLSLCSGKAI CKNGISKRTFEEIKEEIASCGDV AKAIINLAVYGKAQNRSYERLA LLVDTVGPRLSGSKNLEKAIQI MYQNLQQDGLEKVHLEPVRIP HWERGEESAVMLEPRIHKIAIL GLGSSIGTPPEGITAEVLVVTSF DELQRRASEARGKIVVYNQPYI NYSRTVQYRTQGAVEAAKVGA LASLIRSVASFSIYSPHTGIQEYQ DGVPKIPTACITVEDAEMMSRM ASHGIKIVIQLKMGAKTYPDTD SFNTVAEITGSKYPEQVVLVSG HLDSWDVGQGAMDDGGGAFIS WEALSLIKDLGLRPKRTLRLVL WTAEEQGGVGAFQYYQLHKV NISNYSLVMESDAGTFLPTGLQ FTGSEKARAIMEEVMSLL\QPL NITQVLSHGEGTDINFWIQAG\V PGA\SLLDDLYKYFFF\HHSHGD TMTVHGIQTQMECLLLLFWAV VSYV\VADME\EMLPRS
9397	39765	A	9457	2	631	
9398	39766	A	9458	1	406	PTVCERELCVFAFQTLGVMNE AADEIATGAQVVDLLVSMCRS ALESPRKVVIFEPYPSVVDPNDP QMLAFNPRQLKFMHTPHQFLL LSSPPAKESNFRAAKKLFGSTF AF/HLHGAMYGSGIYLSPMSSIS FGYSA
9399	39767	A	9459	7	257	

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9400	39768	A	9460	2	649	
9401	39769	B	9461	50	607	
9402	39770	A	9462	627	1665	EQAGQALSTAPVGDGHELLCE VGSSSFRDVLGTSMGLCGGY/G GAS/GMGGITAVTVNQNVLSPL NLEVDPNMQGMHTQEKEQVK TLNKSASFVDKVLFLEQQNKM LETNWSLLQQQKPAQSNMDN MFESYINNLLGQLEILGQEKLK LEAELGNMQGLCMFFVKEDFK KKYEDEINKPTEMENEFVLIKK DVDDAYMNKVELEFRLEGLTD EINFLRQLYEEEIPELQSQILDTS VVLSMDNSRSLDMDSIIAEIKY EELQTLAGKHWDDRRLTKTKIS EMNRNISRLQAEIEGLPQRPEQ RASLESVIADAEQRGELAIKDA KTKLSELEAAQQRAKQDMAHG
9403	39771	A	9463	2237	2656	LSCSLFSGFAGTRFFGTSILRLPL MYCPVNDSGTAIIASSGPSATTS PP*TPAPGPMSITWSAARIASSS CSTTITVLPRSRRWISVPNRRSL SRWCRPIDGSSSTYITPTRPAPI WLARRIRCASPPESVSAERESV
9404	39772	A	9464	3	2790	EFVLIKKD\VDEAYINKVELESR LEGLTDEINFLRQLYEEEIRELQ SWISDTSVVLSMDNSRSLDMNS VIAEVKAQYEEIANRSQAEAES MYQIKDEELQSLAGKHGDNLR CTKTKISEMNRNISRLQAENEG LKGQRAFLEAAIADAEQCGELA IKDANAKL/SELEAALQRAKQD MAWQLR\LMNVRLALDIEIATY KKLLEGEESRLESGMQNMSIHT KTTSGYASGLSSACGGLTSPGL SYGLGASSFSRT

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9405	39773	A	9465	2	1516	SAIPTSTPASTMSIRVTQKSYKV STSGPRAFSSRSYTSGPGSRISSS SFSRVGSSNFRGGLGGGYGGAS GMGGITAVTVNQSLLSPLV\LE VDPNIQAVRTQEKEQIKTLNNK FASFIDKVRFLEQQNKMLETK WSLLQQQKTARSNMDNMFESY INNLRRQLET\LGQEKLKLET\E L\GNMQGLVEDFKNKYEDEINK RTEMENEFVLIKKDVDVDEAY MNKVELESRLEG\LTDEINF\LR QLYEEEIRELQSQISDTSVVLSM DNSRSLDMDSIIAEVKAQYEDI ANRSRAEAESMYQIKYEELQSL AGKHGDDLRRTKT*DLLR*TRN ISRLQAEIEGLKGQRASL\EAAI ADAEQRG\ELAI\KDANAKL\SE LEAALQRAKQDMARHLR*VTR ELD*TFKLGPGTFEI\ATYRKLL EGEESRL\ES\GMQNMSIHTKTT GGYAGGLSSAYGGLTSPGLSYS LGSS\FGSGAGSSSFSRTSSSRAV VVKKIETRDGKLVSESSDVLPK
9406	39774	A	9466	1410	3244	PPCRRSHPRPPLRGEQKPRPSQP PFAVPAAPAPQV*\PQMIDLCNV GFQFYRSLEHFGGKPVKQEPIK PSAVWPQPTPTPFLPTPYPYYPK VHPGLMFPFFVPSSSPFPFSRHT FLPKQPPEPLLPRKAEPQESEET KQKVERVDVNVQIDDSYYVDV GGSQKRWQCPTCEKSYTSKYN LVTHILGHSGIKPHACTHCGKL FKQLSHLHTHMLTHQGTRPHK CQVCHKAFTQTSHLKRHMMQ HSEVKPHNCRVCGRGFAYPSEL KAHEAKHASGRENICVECGLDF PTLAQLKRHLTTHRGPIQYNCS ECDKTFQYPSQLQNHMMKHK DIRPYICSECGMEFVQPHHLKQ HSLTHKVLRGLWWGGRGLGK RSGALSRALGSRTPVPLCTLPR GGLQGEIQAQESEFSPVCNHSP GVIQAELKQGPSGVPEILPQLNS CPTKGTCRYYPEGSRLPSAGTI NKGPRLGFSRKGDHSLTSGAPL YVGKESKVHFRAYEDPGVKEH KCGICGREFTLLANMKRHVLIH TNIRAYQCHLCYKSFVQKQTLK AHMIVHSDVKPFKCKLCGKEF NRMHNLMGHMRLA\RNGKPLK RLYCPSKFTLKGNLTRHMKVK

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9407	39775	A	9467	1	1309	MRIQQLCGHLWQQKKISLELM SSFHKILKNKMGCGVTPDSKEL LKYLSYCNSYPLTGSPQEAPVS DVPLPVSKCSHCSVQLIMCLRP EHIPNSPGIKGQGIKQHEEKHPT LLHLDASHLMTCFVVEMTLYV LIAGFKSLCSIHSYPPRTLRHLC EKVWDSLLENERRHEKRGPAN FLHRLPAEHQWGIVQSSNIMAG LSARLQLFLEHRPFPVFELTAN GCPTKGLQGEIQAQESEFSPVC NHSPGVIQAELKQGPSGVPEILP QLNSCPTKGTCRYYPEGSRLPS AGTINKGPRLGFSRKGDHSLTS GAPLYVGKESKVHFRAYEDPG VKEHKCGICGREFTLLANMKR HVLIHTNIRAYQCHLCYKSFVQ KQTLKAHMIVHSDVKPFKCKK SFTAQGNSAPQEDAGSQGE/PV CLL/CPNWGQRKGRAWRHLRH
9408	39776	A	9468	3	4804	KRLENIQKTLEVAFSEAVWMQ PSVVLLDDLDLIAGLPAVPEHE HSPDAVQSQRLAHALNDMIKE FISMGSLVALIATSQSQQSLHPL LVSAQGVHIFQCVQHIQPPNQE QRCEILCNVIKNKLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSISTREKLVL TTLDFQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
9409	39777	A	9469	2	1844	
9410	39778	A	9470	3	772	VPNPYTLLSQIPEEAEWFTVLD LKDVFFCIPVHPDSQFLFAFEDP LNPMSQLTCTVLPQGFRDSPHL FGQALAQDLSQLSYLDTLVLQ YVDDLLLAACSETLCHQATQA LLNFLATCGYKVSKEKAQLCS QQVKYLGLKLSKGTKALSEECI QPILAYPHLKTLKQLREFLGITG FCRIW/NFQALLLERPVLQLCTC ATLNPVTFLPDNE\EEYNCQQII SQTYATRGDLLEVPLTDPDLNL YTDGSSFVEKGPQKA

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9411	39779	A	9471	1	6504	MWGSDRLAGAGGGGAAVTVA FTNARDCFLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSDQGENVAEINRQVGQKL GLSNGGQELHAVSLEQHLLDQI RIVFPKAIFPVWVDQQTYIFIQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADAEYKKLHS YGRDQKGMMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSIFSFQSEKKQETSWG LTEINAFKNMQSKVVPL
9412	39780	A	9472	2	1658	
9413	39781	A	9473	1	617	MCSWTAPVSSILTHPNWPVLR MAGLTGCASVAMKKKIEHNCQ QVIAQTFTTRGDLLEIPLTDPGL NLYTDGSSFVEKGLRKAGYAV VSDNGILESNPLTPGTSAQLAEL IALTWAPELEEGKRVKRKKAI WREREFLTSEGTPIKHQEAIRRL LLAVQKPKEVAVLHCRGH/QE GNCQVDIEAKRATRSQVARGH KICDFPSCSYR
9414	39782	C	9474	587	715	
9415	39783	A	9475	96	269	
9416	39784	A	9476	1	1398	
9417	39785	B	9477	1	1152	
9418	39786	A	9478	3	241	
9419	39787	C	9479	202	534	
9420	39788	A	9480	108	199	
9421	39789	A	9481	125	352	
9422	39790	A	9482	2	325	RRSLALSPRPDCGLQWHNLGSL QAPLPGFTPFSCLSLPSSWDYRR PPPRPANFLYFLVETGFHLVSQ/ SGLDLLTS\DPPASASQSAGITG VSHRARPQNLFFKVRCPE
9423	39791	A	9483	184	383	LGLQ\WRNLGSLQAPLPGFTPFS \CLSLPSSWDYRRPQPRPANFFF FVFFLVKTGFHLVSQG\G\LDLL TS*SHPASAFQSAG\IIGVSHRRP AITLQF
9424	39792	A	9484	1	416	MGRSFLGGGSTLMLLGGGQLH ILTPSFPSWTETGNYTCEFCGKQ YKYYTPYQEHVALHAPIRNSA KDDHRSASILSENRGSHQ/SHAS CHHHYHCHYYHQHHHCLHHH SYHHHHCHHHRGMWRNWDTV LWIHQTQPVQD

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9425	39793	A	9485	3	534	GRRQRRSRHLLHRRQDRQSAP GSGSKIPQK\KVKLAADEDDDD DDEEDDFDDEETEEAPVKKSIQ DTPARNAQKSDQNGKVSKPSS TPRSKGQESFKKQEKTPKTPKG PRSVEDIKTKMQASIEKAHGTV LGTTVGNIPLRGGNQEKFHGAA GVWFGKFGVQRKIQQKQLQKD VTSGS
9426	39794	B	9486	44	924	
9427	39795	B	9487	41	2197	
9428	39796	B	9488	67	1507	
9429	39797	A	9489	134	311	
9430	39798	A	9490	5	1545	EKIQINTI/KNDKGILPLDPTEIQI TIREYYEHLYAHKLENLEEIDK FLDIYTLPRLNQEELESLNRKPN TACSNLRDGSLLLGDGHGSSIQ AAIEVVGAGSVATKGRGRQDD TDPSNRYHRPPYSQEEKEQCITL LLSWCLGDSQGPQCRPQLSLQE LRREFTVSLHLARKLLSEVRGQ AHRFVSPPNAAGAGDGQTPNPF WPPLTDLAPQAESHLPGVNLYL LPLGEQLPDVSLTFQAWRRLSV KCTAVRAYQTTRVVETSSCRL HVKGASNASTHRSPKEVTQGT NKSERRTRETQRAIRERNMAGC CTCATDVLVTLQSLMEGLALQ PQRTRALLLGSASIKASCAVTII LMSENLGKGCSKKSEGMVRRY AKHKKQEIKPYYQRKSPSLERG QEEKKVGREDREGSENQYLYG PSNISEARNRLPECGRMGLGYV ARLFLGDRRSSTPSFASYDPSSL VTYGHRRSCRVSDIRVPRLGPN VGGPCKGTGIDLQCEREKKNEE
9431	39799	A	9491	32	2123	
9432	39800	A	9492	1	911	MSTLKGLIIKIIISVMIASEFILEE RIKTGLNAAKHCFAAPSQAASH TISRPIPMPIRSASACSTPTHTPQ DSLTGVGGDVQEAFAQSSRRN LRNDLLVAADSITNTMSSLVKE LNSEVGSETESNVDSEFARTQF EDLVPSPTSEKAFLAQIHARKP GYIHSGATTSTMRGDMVTG\DA NPYVQPEDENYENDSVRQLEN ELQMEEYLKQKLQDEAYQMPL VPTKKEIHMEDFLSSLPEGAIAQ CPRTFIPDCRRKGASYSQTDDES NMKTGDDGEPCGHTEEEDSSL AAASPKRGTTTPSSS

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9433	39801	A	9493	2	2233	
9434	39802	C	9494	477	737	
9435	39803	A	9495	2	746	GQATHFMAKEV*QWAHAHGIH WSYRVPHHPEAAGLIEWWDCL LKSRLQCQLGDNTLQAWGKVL QKAVYALNQCPIYGTVSPIDRI HGSRNQRVEVEVEVAPLTITPS DPLAKFLLPGLTTLCSAGLQVL VPEGGMLPPGDTTTIPLNRKLR LPPGHFGLFLPLSKQAKMRVTA LAVVIDLDYQDEISLPLHNGDK EEYARSTGDPLERLLVLPCPVIE VNGKLQQHNLGRTTNGPDPLG MKVWVSPPG
9436	39804	A	9496	70	532	HVALLMPLQNSRSFSGYGFAYP ARNTFSKTTIHGLKECLIHHHGI PSSIASDQGTRFLPKEV/RKWAH AHGIHWSYHVPHYPEAASP/HS DPLAKFLLPVPTTLCSAGLAVL VPEGGMLPPGDATMIPLNLSSR SHLGMPTTSLKVVRMCSKDKY
9437	39805	A	9497	51	408	CVPEPRTPSLGFQT/HPAAHAPG AQAPGSAH/DRLSSAGPGSRAA PRAPWRPWTIGYSESQPTVL\RP GQPWPGRGVSGSSAPSVPSALR GPPRSSRPSCCTWWCLWRCRH RDLGRDINFTL
9438	39806	A	9498	3	618	SSCAFSHRSSRPSRCHTVRRSTA PCAAS*HSSRAPKRHWALPGSS G*S/WRETPSTHW*P*TLPRWRT ALRPSQ*PRPRVFRVRKPCSSRP PTITRCALASAQ*SCAA\PTSSLA QRKSSRSPRRTATTWGTARRSR AHAVPAGRSPAPSASPAPPQAP RAWSAAAPASPSRLSSAGRGRQ AAPRAPWRLRGPPRSCRPTCCT WWCP
9439	39807	B	9499	215	293	
9440	39808	C	9500	1	1170	
9441	39809	C	9501	25	481	
9442	39810	A	9502	27	265	
9443	39811	A	9503	2	326	GRVGGRVGSDLGRGDMAKRT KKVGIVGKYGTRYGA/SRVRK MVKKIEISQHAKYTCSF\CGKT KMKRRAVGIWCCGSCMKTVA GGAWTYNTTSAVTVKSAIRRL KELKDQ

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9444	39812	A	9504	2	1125	RVGRPPLPPRPTHPRRKPLPPNN VTGKPGSAGIISSGPITTPPLRST PRPTGTPLERIETDIKQPTVPAS GEELENITDFSSSPTRETDPLGK PRFKGPHVRYIQKPDNSPCSITD SVKRFPKEEATEGNATSPPQNP PTNLTVVTVEGCPSFVILDWEK PLNDTVTEYEVISRENGSFSGK NKSIQMTNQTFSTVENLKPNTS YEFQVKPKNPLGEGPVSNTVAF STESADPRVSEPVSAGRDAIWT ERPFNSDSYSECKGKQYVKRT WYKKFVGVQLCNSLRYKIYLS DFLTGKFYNIGDQRG\HGEDHC QFVDSFLDGRTGQQLTSDQLPI KEGYFRAVRQEPVQFGEIGGHT QINYVQWYECGTTIPGKW
9445	39813	A	9505	2	385	REAGSGGNDNFARRRNFSG\RG G\FGG\SRGGVWIWVAVGDGY NGFG\NDGSNFG\GGGSY\NDF WENTNKSGLQNFGPHEGGEIFG GQKLLAPYGGWRPNTFAKPTK PQGG\YGG\SSSS\SSYGKWPEDF
9446	39814	A	9506	945	2313	TRVLLESRAGSQQSEGEASWQ RGYARPSCQAAISFPEHRRALR ALWAGDCRVADAGPGSSSSTPP SPPSLPKTSVSLGFLCFKKSLAA SCASGRERQLEA*VWASQPLSP TQWSEGQLGVRVWASQPLSPT QWSEGQ/PGGPSVGISTSLTYPV EGRT/GWGPECYVFCMLHRLPE QHDCTFDHMGRGREEAIMKM VKLDRKVGRSCQRIGEGGQED DVVASILVSMQPHSPRTPSPHLP YSKFKDFSSCNCARQGWKEMG ACVQRPSAVLGGTRPVSVQAK QPLPCFLLGASALGSCGTGLGV KDRDIDRIVVMSVMKILRGNQR PSGDEQARGQRAREGLGGLGV RRACREQWAVLCPLVHRNWV CVSSFLIASQSNSPQQQHNCCY ANNSPQQEEGMVGRQAETFLL GGVRNRKPWVGVGRGLQGSH QQHIQGAVSSPSSPKKGVSKRE
9447	39815	A	9507	3	684	

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9448	39816	A	9508	15	513	RIRLEGLWGSSKTMNLCSKCFA DFQKKQPDDDSAPSTSNSQSDL FSEETTSDNNNTSITTPTLSPSQ QPLPTELNVTSPSKEEYSQSENE ASPVKRPRLLENTERSEETSRSK QKSRRRCFQCQTKLELVQQEL G\MCRCGYVFCMLHRLPEQHD CTFDPHGAVAGR
9449	39817	A	9509	818	1455	SDYITRDGASFTKALLTWKNPV PNFFWKKDTFKLWGEVIRSTM WKT/DQSPSAAWMGGFGAQPP QGQAPPPVIPPPNQAGYGMASY QTQILPSPHILAVFMLPERGPNP DPKRGFLDLARKNLGNWVSTIT FLSRFPGVQVLQEFVVPGTMPL LRPLELPMHFNPHFSTALASLIA DELYLLPQLSVSQMGESFPSFD MMAICAQASTNRLWMP
9450	39818	A	9510	1	1132	MMEDDGQPRTLYVGNLSRDVT EVLILQLFSQIGPCKSCKMITEH TSNDPYCFVEFYEHRDAAAAL AAMNGRKILGKEVKVNWATTP SSQKKDTSNHFHVFVGDLSPEI TTEDIKSAFAPFGKISDARVVK DMATGKSKGYGFVSFYNKLDA ENAIVHMGGQWLGGRQIRTNW ATRKPPAPKSTQENNTKQLRFE DVVNQSSPKNCTVYCGGIASGL TDQLMRQTFSPFGQIMEIRVFPE KGYSFVRFSTHESAAHAIVSVN GTTIEGHVVKCYWGKESPDMT KNFQQVDYSQWGQWSQVLGN PKPSD\RYMANGWQVPPYELY GQPWNQQAFGV\DQSPSAAWM SGFGA\QPP\QGQAPPP\VIPPPN QAGYGM\ASYQTQ
9451	39819	B	9511	1	1212	
9452	39820	A	9512	1	1032	

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9453	39821	A	9513	17	976	SGRP/GGPGGPGMGKPRCF/RGE VFGIVIRGPGFPPGGRGRGR\GR GARGGKGPRIKGLGCPSTKLG\ RLVKDH*RSKFPWRRSIYSYSG PLKESE\IIDF\FLGGLLSKDEVFE RLCQVQEPEPVPGQRHQGSRHF VAI\GNYQWPTVGSGVLKCSQE /VWPTAHPVGPIILAKLLHSSPC AEGYWGEQSIGKAP/HTVPCQ/ VWTGRCGSVLVRPHPWHPRGS GIVSAPVA\KKLLMMAGIDDCY T\SARGCTATLG\NFAKAT\FDAI SKTYSYLTPDLWKETVFTKSPY QEFTDHLVKTHTRVSVQQTQA PAVAYNIGFLYKKNKVN
9454	39822	A	9514	1	866	
9455	39823	A	9515	1	1793	MAAAAVSGALGRAGWRLLQL RCLPVARCRQALVPRAFHASA VGLRSSDEQKQQPPNSFSQQHS ETQGAEKPDPESSHSPPRYTDQ GGEEEEDYESEEQLQHRILTAA LEFVPAHGWTAEAIAEGAQSLG LSSAAASMFGKDGSELILHFVT QCNTRLTRVLEEEQKLVQLGQ AEKRKTDQFLRDAVETRLRMLI PYIEHWPRALSILMLPHNIPSSL SLLTSMVDDMWHYAGDQSTD FNWYTRRAMLAAIYNTTELVM MQDSSPDFEDTWRFLENRVND AMNMGHTAKQVKSTGEALVQ GLMGAAVTSPRSRRGGWWPLG EMPYANQPTVRITELTDENVKF IIENTDLAVANSIRRVFIAEVPII AIDWVQIDANSSVLHDEFIAHR LGLIPLISDDIVDKLQYSRDCTC EEFCPECSVEFTLDVRCNEDQT RHVTSRDLISNSPRVIPVTSRNR DNDPNDYVEQDDILIVKLRKGQ ELRLRAYAKKGFGKEHAKWNP T\AGVAF\EYDPDNALRHTV\YP KPEE\WPKSEYSELDEDESQAP YDPNGKPERFYYNVESCGSLRP ETIVLSALSGLKKKLSDLQTQLS HEIQSDVLTIN
9456	39824	A	9516	3	176	FFFFFAETNSK*ITYQNIHIMVEI FQNSIFWDLYTKDKQIRGQEAA RREKRGLGRPL
9457	39825	A	9517	1485	1679	RVGDAGHDDPGKPGPPGAGHR PEG*TGAHSLRAGLPACRAEPA GPGRAREGSKAPGHCAEELLQ

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9458	39826	A	9518	1	232	FFFFETESCSVAQAGVQWCDLG SLQTLPTG/SSRHSPASAFRVARI TGARYHVRLIFVFLVQTGLHHL GQADFDLLTS
9459	39827	A	9519	1	2408	GTLVTKVAPVSAPPKVSSGPRL PAPQIVAVKAPNTTTIQFPANLQ LPPGTVLIKSNSGPLMLVSPQQT VTRAETTSNITSRPAVPANPQT VKICTVPNSSSQLIKKVAVTPV KKLAQIGTTVVTTVPKPSSVQS VAVPTSVVTVTPGKPLNTVTTL KPSSLGASSTPSNEPNLKAENSA AVQINLSPTMLENVKKCKNFLA MLIKLACSGSQSPEMGQNVKK LVEQLLDAKIEAEEFTRKLYVE LKSSPQPHLVPFLKKSVVALRQ LLPNSQSFIQQCVQQTSSDMVI ATCTTTVTTSPVVTTTVSSSQSE KSIIVSGATAPRTVSVQTLNPLA GPVGAKAGVVTLHSVGPTAAT GGTTAGTGLLQTSKPLVTSVAN TVTTVSLQPEKPVVSGTAVTLS LPAVTFGETSGAAICLPSVKPV VSFCWDHI\CKPVIGTPVQIKLA QPGPVLSQPAGIPTGSSS\KQLFS LFHVVQQPSGGNEKQVTTISHS STLTIQKCGQKTMPVNTIIPTSQ FPPASILKQITLPGNKILSLQASP TQKNRIKENVTSCFRDEDDIND VTSMAGVNLNEENACILATNSE LVGTLIQSCKDEPFLFIGALQKR ILDIGKKHDITELNSDAVNLISQ ATQERLRGLLEKLTAIAQHRMT TYKASENYILCSDTRSQLKFLE KLDQLEKQRKDLEEREMLLKA AKSRSNKEDPEQLRLKQKAKE
9460	39828	A	9520	1	637	MLSNVKRGRKLPNGTWAHDL VTPPTASLLLLLTEPAMPSVAFC HSILIVTKGGVKRTRVPPPNNSS GARTGNPLKVKHISFKTGDELIF LDPHTTQTFVDTEENGTGNDQT FHCLQSPQR\MNILNLDPSVALG FFCKEEKDFDNWCSLVQKEILK ENLRMFELVQKHPSHWPPFVPP AKP\EVTTTGAEFI\DSTEQL\EEF DL\EEDFEILSV
9461	39829	A	9521	3	176	
9462	39830	B	9522	1	792	

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9463	39831	A	9523	2	486	NGHVGLGVKCSKEVATAIRGAI ILAKLSIVPVRRGYWGNKIGKP HTVPCKVTGRCGSVLVRLIPAP RGTGIVSAPVPKKLLMMAGIDD CYTSARGCTATLGNFAKATFD AISKTYSY\LTPDLLKE\TVFTKS P*QELTDHLVKTHTRVSVQRT QAPAVATT
9464	39832	B	9524	1	2991	
9465	39833	A	9525	3	263	KHENWSTARQSLHACSRVTWQ NRLRLSNKWMPSHVLCLLPS/H MTLQPANLSSLLITPPEFGPKIA SPICTSCSVNFPRTLISPFSHC
9466	39834	A	9526	1022	1201	
9467	39835	C	9527	1	924	
9468	39836	A	9528	2	837	WKNCLEKRSMLTMHRILES*D* RQE/ILERHDAKYHSPKAEEKQ MKHKAGSQIVKKEEAKLALAL EGFCRFRNHHQTGFSPAGATQR GPLVAILSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGTTGFPTGKRAWPPFRL FLPHKGFADWGPTINQDFRLLG QPSVARFLNFSQGPAGEGQSAV ARLPGHPFITQPYPILPGYAAAG MQALARRRPILMFDSLSSNFCH SSAYYHLFRRSNQAFKGTNNCL KKITPRPATHRSTVVIH
9469	39837	A	9529	3	1137	APAPSPVGSGSCCLSHMFFHPPS RANRAFVD\YAPMDEIQNAEIN SQVRRYLEGTLDEIDVRNPSVT TMLSQPGPPSPGHTPTHALLAS EPHVNGCKTVSTVHEDYSGSSE SSNDESDSEDTDSDDSSIPRNRL QSVVAVPKNSTLPMEETSPCSS RSSQSYRHYSDHWEDERLESRR HLYEEKFESIASKACPQTDKFFL HKGTEKNPEISFTQSSRKQIDNR LPELSHPQSDGVDSTSHTDVKS DPLGHPNSEETVKAKIPSRQQE ELPIYSSDFEDVPNKSWQQTTF QNRPDSRLGKTELSFSSSCEIPH VDGLHSSEELRNLGWDFSQEKP STTYQQPDSSYGACGGHKYQQ NAEQYGGTRDYWQANGLLGS
9470	39838	A	9530	1	1857	

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9471	39839	A	9531	1	989	MEDWKVRGHQEKTLAFEVQSF SCSERETTLVLLLRSPAVPQLLL HGLCGPDLSTKAAQCHFKAIW QSLGNTLGAVSDQATPGHVKS LPPGALISRQGRGQFCSVDAVF LLHDSPELPSSLPHGASLPLASS DKQAEQTWLGAVGSVQCTSIT ACPRDLEDRPHLTEHPPAGVHC GQNPCPCHLIFTLYSKSLPLDLA CRIWDVFCRDGEEFLFRTALGI LKLFEDILTKMDFIHMAQFLT\R LPEDLPAEELFGPSIATIQMQSR NKKWAQEPGHELEWPDRSFRP RVLACPMGSREHRLQPACSGST GQGHTKALFPETCCQSPIFQDA
9472	39840	A	9532	2013	2270	
9473	39841	A	9533	3	744	
9474	39842	A	9534	190	991	SVLSNKQNHCSQTAPPPPPPAA SGSRGWVVWGLFWGLAAILEGS TGADWSQLPHSCCPSLLVPHVL SVVPLRPPHRDFPVEDVFTLPV YFSSDWLNEFWDALDVDDYRF VYAGPAGSWSPFHADIFRSFSW SVNVCGRKKWLLFPPGQEEAL RDRHGNLPYDVTSPALCDTHL HPRNQLAGPPLEITQEAGEMVF VPSGWHHQVHNLDDTI\SINHN WVNGFNLANMWRFLQQELCA VQEEVSEWRDSMPDWHHHCQ VIMRSCSGIKL
9475	39843	A	9535	1	885	MKRRAVMGPPQVQAWKALDL WESSQVMEGKAVVPMGRNPM MRKATQGQLENSPALEKLLPPL QGNVGFAFTKEDLTEVRDLLL ANKVPAATRAGAIGPCEVTVPA QNTGLGPEKISFFQALGITTKIS RGTTEILSDVQLIKTGDRVGAS EATLLNTPNISPFSFGLVIQQVF NNGSIYNPEVLDITEETLYSGFL EGVRNVAS\CLQTGYPPVASVP PSII/NGYKGCLALSVETDYTFPP AEKIKTFLADPSAFVAAAPVAT TATAAPAAAAAPTKFENEESEE LDEDMGFGLFD

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9476	39844	A	9536	65	988	RTAVMPREDRATWKSNYFLKII QLLDDYPKCFIVGADNVGSKQ MQQIRMSLRGKAVVLMGKNT MMRKAIRGHLENNPALEKLLP HIRGNVGFVFTKEDLTEIRDML LANKVPAAARAGAIAPCEVTVP AQNTGLGPEKTSFFQALGITTKI SRGTIEILSDVQLIKTGDKVGAS EATLLNMLNISPFSFGLVIQQVF DNGSIYNPEV\LD\ITEETLHSRF LEGVRNVASVCLQIGYP\TVAS VPHSIINGYKRVLALSVETDYTF PLAEKVKAFLADPSAFVAAAPV AAATTAAPAAAAAPAKVEAKE
9477	39845	A	9537	1	993	MREIALTQTRQCGKKIGAKVGI RGSEVPAPAYWVAREDVGSGS GLGGGWYVPCAVLVDLEPVT MDSLRSGPFGLIFRPTTSSLKLIE NADKTFCIDNEALYDIYSRTLK LPTPTYGDMNHLLSATMSGVT MCLGFPGQLNADLQKLSVNMV PFPRLHFFMPGFAPLTSRGSQH YQALTVAELTQQMFYAKNMM AARDPRHGRYLTAAAIFQGRM PMREVDEQMFNIQDKNSSYFA DWFPDNVKTAVCDIPPRG\LKM SGSFIGNNAAIQELF\QCVSEQF TAMFRRKA\FLHWYTGEG\MDE \MEFT\EAESNMND\LVSEYQQY QDATAQGGGG
9478	39846	A	9538	231	881	SSLSGTKVGSLPFRLLHWMPVS YSSVTTRYYHRAGAEEGKDRII FVTKKDHETPSSAELVADDPND PYEEHGLILPNGNINWNCPCLG GMASGPCGEQFKSAFSCFHYST EEIKGSDCVDQFRAMQECMHK YPDLYPQEDEDEEEEREKKPAQ QAEETAPIEATATKEEE\DQVNE GHKALSTSPFGVDLLQKALSSP SKKVSFCCPVHYNIQNNLF
9479	39847	A	9539	1	804	

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9480	39848	A	9540	2	3337	SSLLEKMTSSDKDFRFMATSDL MSELQKDSIQLDEDSERKVVK MLLRLLEDKNGEVQNLAVKW LGVPLGAFHASLLHCLLPQLSS PRLAVRKRAVGALGHLATACS TDLFVELADHLLDRLPGPRVPT SPTAIRTLIQCLGSVGRQAGHRL GAHLDRLVPLVEDFCNLDDDE LRESCLQAFEAFLRKCPKEMGP HVPNVTSLCLQYIKHDPNYNY DSDEDEEQMETEDSEFSEQESE DEYSDDDDMSWKVRRAAA
9481	39849	B	9541	1	3178	
9482	39850	A	9542	190	284	LNAQPGTRRLWPAEIRPPPRRL GKGGQQVSHHPPISCFYCECEE KRLCVNTHVWTK*T
9483	39851	A	9543	62	280	
9484	39852	A	9544	1	1452	
9485	39853	A	9545	2	998	ITAGATPEERVICFVEYYLTAFH EGRKGALAKKPYNPIIGETFHC SWEVPKDRVKPKRTASR/PLLP AVMNTQWPMTLPKSYKLRFVA EQVSHHPPISCFYCECEEKRLCV NTHVWTKSKFMGMSVGVSMI GEGVLRLLEHGEEYVFTLPSAY ARSILTIPWVELGGKVSINCAKT GYSATVIFHTKPFYGGKVHRVT AEVKHNPTNTIVCKAHGEWNG TLEFTYNNGETKVIDTTTLPVY PKKIRPLEKQGPMESRNLWREV TRYMRLGDIDAATEQKRHLEE KQRVEERKRENLRTPWKPKYFI QEGDGWGILQSPLESTLMGLEV
9486	39854	A	9546	12	740	HFFLYKKLIPFVLKNCMFHFSP VRGTVVTNDRWGAGSICKHGG FYTCSDRYNPGHLLPHKWENC MTIDKLSWGYRREAGISDYLTI EELVQPLVETVFSAGNPLMD\IG PHLDGTI\SVVFEERLRQMGSW LKVNGEAIYETYT\WRSQ\NDT VTPDVWYTSKPKEKLVYAIFLK WPTSGQLFLGHP\KAILGAT\EV K\LLGHGQPLNWIFFGDKMGIM \VELP\QLT\IHQMPCKWG\WAL A\LTNVI
9487	39855	B	9547	1	627	
9488	39856	B	9548	47	504	

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9489	39857	A	9549	2	379	VDLVREFIERQ/HAKNRYYYYH RQYRRVPDITECKEEDIMCMYE AEMQWKRDYKVDQEIINIMQD RLKAFQQQSYRATQQGHPQAA SGGGSWRPLLQIFSLAASSASV RPGTSWQNCRPPGPDLGKQ
9490	39858	B	9550	49	707	
9491	39859	A	9551	3	1162	
9492	39860	C	9552	342	581	
9493	39861	A	9553	3	513	LLPHKPLAGFFKAYLPSEPPRV YVSSFWPQ/EYKPDTHQELFLQ EEIS/LLEDLNQVIENRLENKI/A FIRQHAIRVRIHALLLARGLDPF IGPRRDWLVYPAVTGAVAFGF VEGLDPSQEHPRFQGTQDNVSK DESTRKEQSVRLVGCGADDRK PRDLQILDRDRKGPELVQ
9494	39862	A	9554	1	1365	
9495	39863	A	9555	771	1536	PRPLSLWSREAGKGVQDCYIDN SQLCRKCDLCPTGSPQSLPPYAS IPPTPSPTIK/DPPSTQMV/QKET DKGVNNEPKSGNIPQLCRLQAV GGGEFGPARVRVPFSLSDLKQI KIDLGKFSDNPDGYIDVLQGLG QCFDLTWRDIMLLLNQTLTPNE KSAVITAAREFGNLLYLSQLRH WPVTLQPSAVPTPDSGTYDTKE CKIVQSVEMSMEVMIAVMSVQ RQQGKQTQQQPLLVVVRSAEP AEESVPHKSSTRGAS
9496	39864	A	9556	220	249	P*N**PSTLTTGTGSTTT*QIRM KVN*MGN/DSPQGKNTPKMYS GEFSPVRVHVPFSLSDLKQIKID LGKFSDDPDGYIDVLQ
9497	39865	A	9557	2	385	
9498	39866	A	9558	84	849	PRPLSLWSREAGKGVQDCYIDN SQLCRKCDLCPTGSPQSLPPYAS IPPTPSPTIK/DPPSTQMV/QKET DKGVNNEPKSGNIPQLCRLQAV GGGEFGPARVRVPFSLSDLKQI KIDLGKFSDNPDGYIDVLQGLG QCFDLTWRDIMLLLNQTLTPNE KSAVITAAREFGNLLYLSQLRH WPVTLQPSAVPTPDSGTYDTKE CKIVQSVEMSMEVMIAVMSVQ RQQGKQTQQQPLLVVVRSAEP AEESVPHKSSTRGAS
9499	39867	A	9559	66	197	RQWKG*KFVFQKM*DLGKYLQ RQLFCLSSLVQPPWPVPTEIYP
9500	39868	A	9560	1	2340	
9501	39869	B	9561	1	1776	

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9502	39870	A	9562	1	1349	
9503	39871	B	9563	107	769	
9504	39872	A	9564	329	2042	
9505	39873	A	9565	511	1631	HFGNHERTSKVMGNVPRKTKT PLRRILENWEQFDPQTLRKKRLI FFCSAAW\PPEGSINYNTILQLD LFCRKGKWSEVP*VQTFFSLRD NSQLCKKCDLCPTGSLQSLPPY PSIP\TPSPLNKDPPSTQMVQKEI DKRVNSEPKSANIPQL*PLQAV GGREFGPARVHVPFSLPDLKQI KTDLGKFSDNPDGYIGVLQGLG QFFDLTWRDI\MSLLNQTLTPNE RSATITAARELGDLWYLSQVN DRMTTEERERFPTGQQAVPSAD PH*DTESEHGDWCCRHLLTCVL EGLRKTRKKAVNFSVMSTVTQ GKEENPTAFLERLREALRKHTS LSPDSIEGQLILKIKFITRSAADI RKQTSKVHLRPGAKLKTPY
9506	39874	A	9566	15	178	
9507	39875	A	9567	3	826	RQLGTRNFLNGTKAKAFELSYL EKVPEGKDTVHKQSLLHHVGT MGGENFPDSSDLYSEIGAITRSA KDDFDQLQDNLCQMERRCIAS WDHLKAIAKHEMKPLLKQRMS ELLKDCAERIIILKIVHTRIINRF HSFLLFMGHPPYAIREVNINKFC RIISEFALEYRTTRERVLQQKQK RANHRERNKTRGKMITDSGKF SGSSPAPPSQPQGLSYAEDAAE HGEHEGCAENLVPLQESPAHTF SIVSAVFLLIP*HPVY*FKSVTPF LGKEQPL
9508	39876	A	9568	1	670	

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9509	39877	A	9569	1	2426	MPKPSLEAGSCPRLEFPVEDAQ PVIKGEEFTPPPPNSYLALGDIST EEWDLEVAQEYQERMPPQRAA LICVFSWNLGRSLPAPAMRRPC QNFCVALSTFAGDPEPESEAEP EAEAGAGQVADEAGQDIASAH EGAETEVEQALEQEPEERASLS EKERQNEGVNERDNCSASSVSS SSSTLEREEKEDKLSRDRTTGL WPAGVQDAGVNGQCGDILTNK RFMLDMLYAHNRKSPDDEEKG DGEAGRTQQEAEAVASLATRIS TLQANSQTQDESVRRVDVGCL DNRGSVKAFAEKFNSGDLGRV FNAPQGLGWSQVPRGQPTFTK KKKTIRLFWNRN/VGLLTGH/G KNNRRCREFLWSKLEPIKVDTS RLEHLFESKSKELSVSKASKLV RPLFILTSACPFLSFPWKAPLHS STRQLHRGLSAQERWRCSGIRG MECLNGKGPLESRNPAYRKSE GTRQTGAGDMKDGVWQGVPA TPDTPQGMCTVCTVSFAIMDGL NVNSVGPLPFHEVAEPLLDLKE GIDQLDYTLGFFFLVSMLSGGG LLGGSASAKAFELSYLEKVPEV KDTVHKQSLLHHVCTMVVENF PDSSDLYSEIGAITRFHSFLLFM GHPPYAIREVNINKFCRIISEFAL EYRTTRERVLQQKQKRANHRE RNKTRGKMITNCVRHCVRMFS GSSPAPPSQPQGLSYAEDAAEH
9510	39878	B	9570	164	346	
9511	39879	C	9571	160	339	
9512	39880	A	9572	54	212	SFPSVVLWKDLQNLKIQVPGLI LLGVGLISVPGGRI*LLRTGSRK PISQVCP
9513	39881	C	9573	48	185	
9514	39882	A	9574	2	551	ADRRGAVYPRSRDGGGVRGPC AMATSVLCCLRSCKDRGTGHIP LKDMLSVHMDTQHMGTDVVI VKNGRKIFGTGGCLASAPLHQN KSYFEFKIQSTGIWGIGVATQK VNLNQIPLGRDMHSLVMKNDG ALYHNNEEKNRLPANSLPQEG D/VVDDSAILDCQFSEFYHTPPP GFEKILFEQQIF
9515	39883	A	9575	3	655	

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9516	39884	A	9576	131	1066	SHSSSAAAHPLGLLPIAAQSLA VFIEPWSQASSRGQLQ/VSAPGI WGIGVATQKVNLNQIPLGRDM HSLVMRNDGALYHNNEEKNRL PANSLPQEGDVVLCWSNNGHS LCKEESLSPILPTSDGEERRRKR KKRKRKKRKQKQQQQQEAAA PAEADAEATAAEAAVEEAAAR KEEEEEGEEGEGNGEEEEEKAA AAARGDWSQQEKACKSSLQAI LFGHAKLEPGRLPRPTQCRVEA TVLVGTNSPLDNPLWSISWSLW QKPVGTSQQQPLGLWTREFPLE GHLLTRNETFTEATPLIPEIGML SQMMSEEHI
9517	39885	A	9577	1	2363	ELQRDIEKHSTGVASVLNLCEV LLHDCDACATDAECDSIQQATR NLDRRWRNICAMSMERRLKIE ETWRLWQKFLDDYSRFEDWLK SSERTAAFPSSSGVIYTVAKEEL KKFEAFQRQVHECLTQLELINK QYRRLARENRTDSACSLKQMV HEGNQRWDNLQKRVTSILRRL KHFIGQREEFETARDSILVWLTE MDLQLTNIEHFSECDVQAKIKQ LKAFQQEISLNHNKIEQIIAQGE QLIEKSEPLDAAIIEEELDELRR YCQEVFGRVERYHKKLIRLPLP DDEHDLSDRELELEDSAALSDL HWHDRSADSLLSPQPSSNLSLF ASLQPLRSER\SGRDTPG\SVDSI PL\EWDHDYDLSRDLESAMSRA LPSEDEEGQDDKDFYLRGAVG LSDVMIPESPEAYVKLTENAIK NTSGDHSALESQIRQLGKALDD SRFQIQQTENIIRSKTPTGPELDT SYKGYMKLLGECSSSIDSVKRL EHKLKEEEESLPGFVNLHSTET QTAGVIDRWELLQAQALSKEL RMKQNLQKWQQFNSDLNSIW AWLGDTEEELEQLQRLELSTDI QTIELQIKKLKELPESCWDHR\K AIILSINLCSPEFTQADSKESRDL QDRLSQMNGRWDRVCSLLEE WRGLLQDALMQCQGFHEMSH GLLLMLENIDRRKNEIVPIDSNL DAEILQDHHKQLMQIKHELLES

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9518	39886	A	9578	2	3248	ENAVGSWTDDLTQLSLLKDTL SAYISADDISILNERVELLQRQW EELCHQLSLRRQQIGERLNEWA VFSEKNKELCEWLTQMESKVS QNGDILIEEMIEKLKKDYQEEIA IAQENKIQLQQMGERLAKASHE SKASEIEYKLGKVNDRWQHLL DLIAARVKKLKETLVAVQQLD KNMSSLRTWLAHIESELAKPIV YDSCNSEEIQRKLNEQQELQRD IEKHSTGVASVLNLCEVLLHDC DACATDAECDSIQQA
9519	39887	A	9579	2	194	CSTSLMIREMQIKTTVRYHLTS ARMAIIKKSK\NSRCWHGCGEH GTLLHCCNLWKERNVSYVSA
9520	39888	C	9580	105	215	
9521	39889	A	9581	1	210	MNSHFLKEDIQMANKHMEKCS \TLLMIREMQIKPTVRYHLTSAR MPIIKKSK\NSRCWHGCGEHGT LLHC
9522	39890	C	9582	48	182	
9523	39891	A	9583	3	225	
9524	39892	A	9584	1	549	
9525	39893	A	9585	367	971	GVCLLGAPAGRRGSLLSLGSLR GQGSYLSKNVAVPSEATTVREL HP**TSLQRPPSDPGGWVVLGF P\CNQFGHQENRQ\NE\EILNSLK VRSGPGGGFEAQLHGSSRKCEV \NG\SGAHPLFAFLR\EALP\VPS DDGPRAL*PTPKLI\TWFSGVFA TIVAWNFFEKFL\VGPDGVPLR RYSR\AFQTIDIEPDIEALLSQGP
9526	39894	A	9586	1	129	
9527	39895	A	9587	1	406	PTVCERELCVFAFQTLGVMNE AADEIATGAQVVDLLVSMCRS ALESPRKVVIFEPYPSVVDPNDP QMLAFNPRQLKFMHTPHQFLL LSSPPAKESNFRAAKKLFGSTF AF/HLHGAMYGSGIYLSPMSSIS FGYSA
9528	39896	A	9588	2	634	SSNRSHIVKLPVNRRLKFMHTP HQFLLLSSPPAKESNFRAAKKL FGSTFAFHGSHIENWHSILRNGL VVASNTRLQLHGAMYGSGIYL SPMSSISFGYSGMNKKQKVSAK DEPASSSKSSNTSQSQKKGQQS QFLQSRNLKC\IALCEVITSSDL HK\HGEIWGCPPI/SDHVCTRFFF VYEDGQVGDANINTQEGGIHK EILRVIGNQTATG

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9529	39897	A	9589	3	3623	FGVCARGCLDSAGPWTMSRAL RPPLPPLCFFLLLLAAAGARAG GYETCPTVQPNMLNVHLLPHT HDDVGWLKTVDQYFYGIKNDI QHAGVQYILDSVISALLEDPTR RFIYVEIAFFSRWWHQQTNATQ EVVRDLVRQGRLEFANGGWV MNDEAATHYGAIVDQMTLGLR FLEDTFGNDGRPRVAWHIDPFG HSREQASLFAQMGFDGFFFGRL DYQDKWVRMQKLEMEQVWR ASTSLKPPTADLFTGVLPNGYN
9530	39898	B	9590	1	3839	
9531	39899	B	9591	1	513	
9532	39900	A	9592	1	233	KQELNEPPKQSTSFLVLQEILES ENKGDPNKPSGFRS\VKAPVTK VAASIGNAQKLPMCDKCGTVL QQASAAAFSLSV
9533	39901	A	9593	3	469	LTVARSEHKVWSPLVTGEGKR HPYKMNLASEPQEVLHIGSAHN RSAMPFNASPASSTTARVITNQ YNNPAGLYSSENISNFNN\ASSL VIDKESEVYKMLQEKQELNEHP KQSTSFWVLQEILESEEKGDPN KPSGFRSVKAPVTKVAASIGNA
9534	39902	A	9594	1	1146	MTTQQIDLQGPGPWGFRLVGR KDFEQPLAISRVTPGSKAALAN LCIGDVITAIDGENTSNMTHLE AQNRIKGCTDNLTLTVARSEH/ KKVWSPLVTEEGKRHPYKMNL ASE\PQEVLHIGSAHNRSAMPFT ASPASSTTARVITNQYNNPAGL YSSENISNFNNC/ALESKDWLPA GVEANSRPLDHA\QPP\SSLVID KRILKVYKMLQEKQE\LNE\PPK QSTSFLGFCQEIL\ES\EEKGDPN KP\SGFRSV\KAPVT\KVA\ASIG KCSRKFAFCVDKCWHLGFLGV F\LKLR\DRHRHP*VFMCCT\DC GHQT*KQKGPFLLWMDQ\IYCE ESMAPGSEVNTHPEG\YESGST VFPPSGAQQDLDPLFLPAGLLL KLFLLKCSGPLSLS
9535	39903	A	9595	65	353	

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9536	39904	A	9596	1	1974	MNGVPVGAQKRVDKEEVKNG AIAELFSEDWSDCAYKANEVSR IRPLEESELLYPILGQSKLFVLSG EWSQSSEEASEEVAVTLIYQLA ESPTVICAQIWQGCAKQALEKL EEKRTSQGDPKESPTMLPTFLL MNLLSLAGDVALQQLVHLEQA VSGELCQRRVLREEQEHKTKDP KEKNTSFETTMEEELGLVGAA DDTEAELIRGFCKMELLDGKQT LAAFVPLLLKVYNNSGLYSNPD LSAAASPTLGKFCMISTTFCNSQ PHLLFTMLEKSPLPIVRSNLIVA TGDLAIHFPNLVDPWTPHLYAH LQDPAQPVWKTVGLVMT\HLIL KDMVKVKGQSKAL/RKMLGNF DCFGDKLSDESIFSSFLSVMGKL QHGAKPEGKAIIDEFEQKLQAC HARGLDGIEELEINQAGSQRAP TAKKPSTVCRHQPLASAASDN DFVTPEPRRTTHRHPNTQQRAS EKKPKVVFSSDESSIKTEVEGLG YNIKLRVATQRLSFVWVMNIA EGESAVLVTVAWPECEVAVMG SLGSAARGTGKRLQGEGNLQL NFVTIATKLEVSWTELGGGCVS ALFASVGTKREKAGFYQGCSF ASNIMKRGRVKEVEDVQKRLI KMTVEFNLAWSSLPPHMAMN GDQGGDRVTHESFLRCMTLMR .
9537	39905	A	9597	785	5049	ACRSRMAPQMYEFHLPLSPEEL LKSGGVNQYVVQEVLSIKHLPP QLRAFQAAFRAQGPLAMLQHF DTIYSILHHFRSIDPGLKEDTLEF LIKGVYGSGVVSRHSQELPAIL DDTTLSGSDRNAHLNALKMNC YALIRLLESFETMASQTNLVDL DLGGKGKKARTKAAHGFDWE EERQPILQLLTQLLQLDIRHLW NHSIIEEEFVSLVTGCCYRLLEN PTINHQKNRPTREAITHLLGVA LTRYNHMLSATVKI
9538	39906	C	9598	134	382	
9539	39907	A	9599	117	235	KIAAPQLHVFLPFLFFCMRPFAF WQPLPEPLELRP\RLSD
9540	39908	B	9600	1	732	
9541	39909	C	9601	1	420	
9542	39910	B	9602	110	928	

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9543	39911	A	9603	1	868	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPEARKITRRWRIG EAADLVGVSLRLSEMPRKQGD YRTRIWKFEDGLSNVLVIQLNK LIICVMCLDLALKGLRVLLVEG NDPQGTASMYHGWVPDLHIHA EDTLLPFYLGEKDDVTYAIYFT CWPGLDIIPSCLALHRIETELMG KFDEGKLPTDPHLMLRLAIETV AHDYDVIVIDSAPNLGIGTINVV CAADVLIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPDD PTGNRTVQLTWQPLPEPLEL\C*
9544	39912	A	9604	1036	1119	
9545	39913	C	9605	1	513	
9546	39914	A	9606	1	890	MSKSESPKEPEQLRKLFIGGLSF ETTDESLRSHFEQWGTLTDCVV MRDPNTKRSRGFGFVTYATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYGKIE VIEIMTDRGSGKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQRGRS GSGNFGGGRGGGFGGNDNFGR GGNFSGRGGFGGSHGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNNQSSNFGPMKGGNF GGRSSGPYGGGGGQYFAKPRNQ/ GGYGGSSSSSSYGSGRRF
9547	39915	A	9607	1	286	
9548	39916	A	9608	1	1674	
9549	39917	B	9609	531	744	
9550	39918	A	9610	1	818	YNRAMFHPHAVNKIALSLNNK NP\RSKVLFLELLAAVCLVRGG HKLFYLAFDNFKEVCGEKQRFE KLMEHFRNEDNNIDFMVASMQ FINIVVHSVEDMNFRVHLQYEF TKLGLDEYLDKLKHTESDKLS\ VQIQAYLDNVFDVGALLEDAE TKNAALERVEELEENISHLSEK LQDTENEAMSKIVELEKQLMQ RNKELDVVREIYKDANTQVHT LRKMVKEKEEAIQRQSTLEKKI HELEKQGTIKIHKKGDGDIAILP VVASAHCPWGQKW

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9551	39919	A	9611	1	937	MALLTLKQQQNEDLQDISHFTT TRTPRQGTPVQKEKSEETRLEW ARRMLRRDQHSTKGKVVKRM RGFLVGLVYCDKQSGALESLLC LWNVSGNTTLSSLVEIGSKAAL GLVCGEKQRFEKLMEHFRNED NNIDFMVASMQFINIVVHSVED MNFRVHLQYEFTKLGLDEYLD LLDTKSTDRKQTLLHYISNVVK EQYHQVSLFYNELHYVEKAAA VSLENVLLDVKELQRGMDFTK REYTMHDHNTLLKEFILNNEGK LKKLQDDAKIAQDAFDDVVKY FGENPKTTPPSVFFPVFVRFVKA YKQAEEE/NMELRKKQEQALM EKLLEQEALMEQQDPKSPSHKS KRQQQELIAELRK\RQVK\DNR HVYEGKDGAIEDIITVSLENVLL DVKELQRGMDFTKREYTMHD HNTLLKEFILNNEGKLKKLQDD AKIAQDAFDDVVKYFGENPKT TPPSVFFPVFVRFVKAYKQAEE
9552	39920	C	9612	47	286	
9553	39921	A	9613	1	423	

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9554	39922	A	9614	1	2015	MPSVSKAAAAALSGSPPQTEKP THYRYLKEFRTEQCPLFSQHKC AQHRPFTCFHWH/FPQTRRRRR\ PLGRRDGTFNYSPDVYCSKYNE ATGVCPDGDECPYLHRTTGDT ERKYHV\RYYKTGTCIHETDAR GHCVKNRLHCAFAHGPLDLRP PVCDVRELQAQEALQNGQLGG GEGVPDLQPGVLASQAMIEKIL SEDPRWQALLPVALLRHRVAH FSDANFVLGSYKTEQCPKPPRL CRQGYACPHYHNSRDRRRNPR RFQYRSTPCPSVKHGDEWGEPS RCDGGDGCQYCHSRTEQQFHP EGPVRESGVRGVFCVQSRRPW LQTPVSGTQLKWSWHHVGHSR TINPEGDKPSRLGPAPENIKRGN DFACDGRADAAGMAPHVCVFP IYKSTKCNDMRQTGYCPRGPFC AFAHVEKSLGMVNEWGCHDL HLTSPSSTGSGQPGNAKRRDSP AEGGPRGSEQDSKQGVRAHGV YVFEQNHLAVFAAVHPPAPSVS SSVASSLASSAGSGSSSPTALPA PPARALPLGPASSTVEAVLALE PTPSSPTSSAVQGVAGELGMGS GGQGCWSHVVGALAAVPAWT HSGDLEWDPSTIRTRVNVGGGP AARPAMTLAREPQLLVVGGCP TRNCSGPAASPQQLLDDAGQG GRGERDSSQRPLRPQTTHRQDT
9555	39923	A	9615	2	609	IHSLCVSPCLSPCHCLSLSPASLL VSFFCCLFLMTLFPSLCVCGSLP VHLLPSL/HFLSQVLNEYFHNV CELDLVFNFYKVECFPLKSPVV PESKEIGSQVDGQSRMEQRSPA HTNRENDIAREGGSEETHSKPG KGNLEFRFRCSHLQLGECPIPP WQKERTIAQGPEPEARAAVPA GRHDTRHAVNAGCALIGSLRRP WGGA
9556	39924	A	9616	60	277	
9557	39925	B	9617	43	354	
9558	39926	A	9618	3	309	GGGQGRPGAGGQGRSDGGGQ GSPGGGSQGSPGGSGGVGQGS RGGQGKPGGGGGQGSPDGGGR PLAGGASGRRGSRGQAQ/CPISV SATHLAF
9559	39927	A	9619	36	363	

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9560	39928	A	9620	1	512	MLMPGLSACVRDCVAFLQAVV LGDPSPAAQCQDTWTLAASAD GTCKAVGTEDGSVYFISVYDKE SPQVVHKAFLSESSVQHVVYD QQGIFLLVGTAEGKVFIINANSS SSFQIIGFT/DGGQRHFTDIHSVS FRNRHSGSDGAFLASRSREKQV GDVHTAYITATSFHNLC
9561	39929	A	9621	1	822	MKLGV/QVVITDHEKLDQIRQR ESD\ITKERIQKILATGANVILTT GGIDDMCLKYFVEAGAMAVRR VLK/RIAKASGATILSTLANS\KA HTSASIILRGANDIMCGEMERSL HDALCVVKRVLESKSMVPGGG AVEAALSIYLENYATSMGSQKE LAIAEFARSLLVIPNTLAVNAA QDSTDLVTKFRAFHNEAQVNP EHKNLKWIGLDLSNGERGDNK QAGMFEPTIVKVKSLKFATEAA ITILRIDDLTKLHPESKDDKHGG YEDAVHSGALND
9562	39930	B	9622	625	1162	
9563	39931	A	9623	202	402	
9564	39932	A	9624	350	652	SAGGYPDGQGVHPGPPELFAAL GRLGHTLREHGHHLLRYHRPG HMGRRPLPCRMGHREPGSLH* QDCPRAWQWCWPHRPGHLQD VPPPGIHLQRLSQPGP
9565	39933	A	9625	83	1503	SWNTPYNHWATKQ/LSSHYSR GGAKYEGEAVKQSLVESYTHP NSNETERSANIDTVMNWFTKE DFDFVTLCYREPDNVGHRFRPE AENRKLMIQQIDRTIRPWDDHR EEETQCQQDPLSNYIKFMDLVK FDIVGYGGFGMPLPKLGQEEAL YQALKNAYPHLHIYKKEGFPEH FHLAKHDRVLPIVMYANFGYSI NGISLLYFYTHLCDKYFNVHFF HEPLSLWRAQTTPSLSHRYISLV RHMDATNLDASEAQLPGSPYP DSAPGPANLDSTQDLPQRRLSW PYPRPRPPNAHPGPALQPAPRTL LLTLPPGPAPSLPPRTALGPPPL QSRPGFRPVSRQRCGPAHFMAP EENAGTELLLQSFERRFLAART LRSFPWQGGGGRAERPAGLAG VQGQTGWVSVLKPPALLPREFL GSPRSGPRDPVPVPGAWPKSLA PLLPRELAAEDEGVSTALGGQT RARCGVQFTIIFTTF
9566	39934	B	9626	1	1177	

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9567	39935	A	9627	1	283	
9568	39936	A	9628	1	708	MPKGKEAKGKKLALAPAFVKK QEAKKVVNPLFEKRPKNFGIGQ DIQPKRDLTCFVKWPRYIRLQW QRSILYKQLK\PETKQEKKWRL LAQAE/SVGKGDLPMKRLPVFR AGVNTVTTFVDNKKAPLVVTT HDMDPIELTVFLPVLCHKMGA TCCIIKGKARLGCLVHRKTYTT VDFTQVNSEDKGALAKLVEAI GTNYNARYDETHCHWDGNVL GPKSVAHIAKLEKAKAKELAT
9569	39937	A	9629	1	836	GTRPKMPKGKKAKGKKVAPAP AVVKKQEAKKVVNPLFEKR\PK NFGIGQDIQPKRDLTRFVKWPR YIRL\QRQRAILYKRLKEPPAIN\ QFTQAL\DRQTATQLLKLAHK\ YRP\ETKQEK\KQRL\LARAEKK AA\GKGDVPTKRPPV/LFRAGV KQPSPPLVE\NKESFSLVVISH\D VDPIELVVFLP\ALCRKMGVPY CIIKGKARLGRLS\HKKTCTTVA FTQVNSEDKGALAKLVEAIRTN YNDRYDEIRRHWGGNVLGPKS VARIAKLEKAKAKELATKLG
9570	39938	A	9630	3	119	
9571	39939	B	9631	1	711	
9572	39940	B	9632	97	942	
9573	39941	A	9633	1	588	
9574	39942	A	9634	1	1029	
9575	39943	A	9635	1	1031	MADQKEARHSASQWKCFVGFL SFRGHMQVAWEADRCKGPGRP LLAEALQDLWPSPRRSQRDPVP ERPCRRPQQSPLPRFGSLSAPLH RENNFIKDFPQLADGLLVIPLPV EEQCRGVLSEPLPDLQLLTGDIR YDEAMGYPMVQQWRVRSNLY RVKLSTITLAAGFTNVLKILTKE SSREELLSFIQHYGSHYIAEALY GSELTCIIHFPSKKVQQQLWLQ YQKGFLGEPKKILGSSLPRRTQF LWKNNHLITKQTVSILSCGEAFI LRKGQQISFSSDSQLLSELEFLR PGAGDQSLPTHLVKVIPFPPQFS L/LCEMGTFILFCNINCAWGRG RGERYSQSC

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9576	39944	A	9636	3	4091	FASASAVSAAASSSSFATAATA AAARSTAAPPAMAAAGARLSP GPGSGLRGRPRLCFHPGPPPLLP LLLLFLLLLPPPPLLAGATAAAS REPDSPCRLKTVTVSTLPALRES DIGWSGARAGAGAGTGAGAA AAAASPGSPGSAGTAAESRLLL FVRNELPGRIAVQDDLDNTELP FFTLEMSGTAADISLVHWRQQ WLENGTLYFHVSMSSSGQLAQ ATAPTLQEPSEIVEEQMHILHIS VMGGLIALLLLLLV
9577	39945	A	9637	2	398	SDARVDALNKIKIWERIKKHLE GHSTNLSLDIAKLKEQIFEASQA HLTLMPGTGVLEGAADRLSAS NPLKWIKTLGSSVISMMIVLLIC VVCLCVVCRCRS*LLREVAHRD KAAFAFIALQIKEGEHVGNST
9578	39946	A	9638	201	495	WKKTLMPGTGVLEGAAN/GLA AINPLKWIKTLGDSVISMMIVLL IC/VCLCIVCRCRSRLLREVAHC DKATFAFIISEKMWYFGFCFCN NSLRVIASSCIH
9579	39947	A	9639	3	409	GIYILHQKKTWEK\LLLAACAIV AIENPADVSVISSRKTGQKATPL FAAVTGATLVAGCFTPRTFSNQ ISAAFREPQLLVVTDPRADHQP LTEASYINLPTIALC\TDSPLHYV GLAIQCNNKGAHSGGLTCNLS
9580	39948	A	9640	3	438	
9581	39949	A	9641	288	489	SFRPLSVLGDCVVRGPTKPSGK CSPASRSLFVRRHILLLHPQGLH NLDQNKATPPPQPL\GHQTCAC
9582	39950	C	9642	23	411	
9583	39951	A	9643	1	209	SPSTTAVCCPPRPSIDFHSSGSSR VSAALLIQ/QRFPLPLWIGLKAR HCSCGLRQRQVSWQETEEDGK AG

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9584	39952	A	9644	28	925	PEAGTRSWREPDPEDLRRFLLS AACRSFPQWLPGGGGGQVSSC SDTDVPYLLLAVKSEPGRFAER QAVRETRRKPTS\GIRLLFLLGS PVGEAGPDLNSLVAWESRRYS DLLLWDFLDVPFNQTLKEP/VL WLPGWAGPCPTGSFVLRAQDD AFVHTPALLAHLRALPPASARS LYLGEVFTQAMPLRKPGGPFY VPESFFEGGYPAYASGGGYVIA GRLAPWLLRAAARVAPFPFED VYTGLCIRALGLVPQAHPGFLT AWPADRTADHCAFRNLLLVRP LGPQASIRLWKQLQDPRLQC
9585	39953	A	9645	1	1612	MIFVVIILMVVLSPEGGSGLDSS PFLSEANAERIVQTLCTVRGAA LKPYPPTGPNFRYSHGVPPHLF AYFPPGSTVSQDNSFISPQLQHI FERVRQSADFMPRWQMLRVLE EELGRDWQAKVASLEEVPFAA ASIGQVHQGLLRDGTEVAVKIQ YPGIAQSIQSDVQNLLAVLKMS AALPAGLFAEQSLQALQQELA WECDYRREAACAQNFRQLLAN DPFFRVPAVVKELCTTRVLGME LAGGVPLDQCQGLSQDLRNQIC FQLLTLCLRELFEFRFMQTDPN WANFLYDASSHQVTLLDFGAS REFGTEFTDHYIEVVKAAADGD RDCVLQKSRDLKFLTGFETKAF SDAHVEAVMILGEPFATQGPYD FGSGETARRI\QDLIPVLLRHRL VSP\PEGDLWPWHRKL\AGAFL ACAHLRDHIACRDHKPGHLPPL LGQSPARRSHCRQPPHQRGTPG WIPHDSLHGGFSPQSRPYPAVV PLIPSPSALGQRSPLGLPSLAWL SSLAQELRIPGAGELPTSCPRSC TSPLESEVSEN
9586	39954	A	9646	930	1123	GVRRDGSSASVTVGQPCRDTSL AFETVAGPYLA*KT*TSGKPGS D*RASKVAGGVQNGTRTTAT
9587	39955	A	9647	719	1346	

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9588	39956	A	9648	1	823	MKKVLIAALIAGFSLSATAAETI RFATEASYPPFESIDANNQIVGF DVDLAQALCKEIDATCTFSNQA FDSLIPSLKFRRVEAVMAGMDI TPEREKQVLFTTPYYDNFALFV GQQGKYTSVDQLEGKKVGVQ NGPTHQKFIMDKHPEITYVSDE SYQNAKL\DLQNGCAARAAPG SRRYGGWTIQASTARPSDVLLT ADSVSFAVRSRGAAATAYHRC CLSGVMVNAATACEHSTASQG RASRTVTDSADPHPRSVRRRAS FRRSGRGFCGTVR
9589	39957	A	9649	583	730	
9590	39958	C	9650	333	439	
9591	39959	A	9651	2	171	
9592	39960	A	9652	1	826	MGGLFWRSALRGLRCGPRAPG PSLLVRHGSGTIMGVFVAVGTI PVPSRVPCIEADTLKPGGPSWT RERTLVAVKPDGVQRRLVGDV IQRFERRGFTL\VGMKMLQAPE SVLAEHYQ\DLRRKPFPPCPSSR YMSSGPVVAMVWEGYNVVRA SRAMIGHTDS\AEAAPG\TIKGV DFSVHISRNVIHASDSV\EGAQR EI\QLWF\QSSELVSWA\D\GGQH SSIHPGLRLRAALTTPSPTQDPT YPPLARTPSPTSKPALSPNPLTS PVSPLAPPQAQREF

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9593	39961	A	9653	144	1650	NCETTTKGSAILRNVDPSTLLPL RRAGSSPGLM\PVEEEMEIDEEK QMKGFLDDSERMAFLVSLHLG AAERWFILQMEVGEPLSHENKS FLRRSQGIYDSLSEIDILSAVLC HPKQGQKSVRQYATDFLLLAR HLSWSDAILRTRFLEGLSEAVT TKMGRIFLKVAGSLKELIDRSL YTECQLAEEKDSPGNSSQVLPT ACKRNNEEAMGNELSSQQQTE EHQHVSKRCYYLKEHGDPQEG LHDHLGQSTGHHQKAHTNNVA ATKKVVQQLQLEAGLNSVKVS QAATEPQTIISPPNALQEPSGIE WEQFPKAQIPSEPQENLCPFVST MNSIKGLHEDYQGNAGKVLST VPGRRYALQNLGTAIVQGEER KQSSLCPGEEGKRHELRSGSHS LVMKHAMVLFNVGFETKDQIH LPTRLGMAEVETLCIYAKQLPH KLIAKLRLLKGTRPLSLNNEHIL THPGLEGWLHTEFFRILSINNKY HLSAYLVQSIVLHVMGFHRKT
9594	39962	A	9654	8	440	VFERSTPPTLETVRSKQEWETR LNGVRIMKKNVRDQFNSHIQL VRNGAKLSSLPQIPTPTLPPPPSE TSCFRCFNPVPLWLLGCPSPLG RQTGEDPGEAADPVPTVQ*GPD DQHSSADQDSTYHHGRPDHGG TYPVGCCTTGRT
9595	39963	C	9655	89	389	
9596	39964	A	9656	1	184	
9597	39965	B	9657	1	942	
9598	39966	A	9658	424	614	NDGPDWGGRRRETDVNRKRGF KISKTLYLYSDIYSCHVHFYYIG NVCIESLYSNVRK*NYVYY
9599	39967	A	9659	1	717	
9600	39968	A	9660	103	374	
9601	39969	A	9661	1590	2051	SYPVSEERSQAEQPSSNPYSHFT STPIRDRLHASGVSTQSLSGSSD ALLHWAGHNAHGYAQCRSPLL VFPNPEPCPFPAQPAFLTPSWLP WQK*PWLGFPCQPPRSTHAPCR LHPTSP\GLGGVKASAETPRPQP VD/ETGEDPGEAADPVPTVQ

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9602	39970	A	9662	1	2912	MAQALPWLLLWMGAGVLPAH GTQHGIRLPLRSGLGGAPLGLR LPRETDEEPEEPGRRGSFVEMV DNLRGKSGQGYYVEMTVGSPP QTLNILVDTGSSNFAVGAAPHP FLHRYYQRQLSSTYRDLRKGV YVPYTQGKWEGELGTDLVSIPH GPNVTVRANIAAITESDKFFING SNWEGILGLAYAEIARPDDSLE PFFDSLVKQTHVPNLFSLQLCG AGFPLNQSEVLASVGGSMIIGGI DHSLYTGSLW\YTPI
9603	39971	A	9663	1	902	MSAKEKGKFENMAKADKVHY VREMKTYIPPKQETKKKFKDPN APKRPPFS/SEYCPKIKG\EHPGQ STGDVAKKLGEMRTNSAADDK WPYEKKAAKLKEKYRKDTAV YRAKGKPDAAKKGDVKAEKS KKRKNEKDEEDEEEDEEEDEE DDDNEYADNECTGFSGFVYKT FNSPVHNSLFLNVEIHALGFDEL LESIFCILLVVEVFSLQKGVAML EEVVVNGERSGRSLPWLPAAPS LPVPVPLGLRHPPSQSDNHSLQ LTFLTALRLLRPRLGAVLEETV EDGRTKTNLPDENSVPFSPET
9604	39972	A	9664	146	733	LNMGKGDPKKPRGKMSSYAFF VQTCREEHKKKHPDASVNFSEF SKKCSERWKTMSAKEKGKFED MAKADKARYEREMKTYIPPKG ED/TKKKFKDPN\APKRPPSAFF LF\CSEY/RAPKIKGEHPG\LSIG\ DVAEETGEEMW\NNTAADDKQ PYEKKAAKLKEKYEKDIAAYR AKGKPDAAKKGVVKAEKRSTR PRIPDL
9605	39973	A	9665	30	359	
9606	39974	C	9666	418	555	
9607	39975	B	9667	550	1717	
9608	39976	B	9668	1	1705	
9609	39977	B	9669	328	484	

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9610	39978	A	9670	5	1215	IIVLPKMSMPVVSAQLTITSIPP WAVE/WGNVTLSVQGIPQNLIS YNWLRGATTNQVTRILNFNFFS HGYTLGPAHTGRETGRADGSLI IIDVRASDNGIYTLHLISSGE\KV AIMLCYLSLLVAPWHFHKTPR WRFPWGPRAASQRASCSQPQS WSSGCSK/VSQAALYIQKIPEQP QKNQDLLLSVQGVPDTFQDFN WYLGEETYGGTRLFTYIPGIQR PQRDGSAMGQRDIVGFPNGSM LLRRAQPTDSGTYQVAITINSE WTMKAKTEVQVAEKNKELPST HLPTNAGILAATIIGSLAAGALL ISCIAYLLVTRNWRGQSHRMAT TEKPELGPAHDAGDNNIYEVM PSPVLLVSPISDTRSINPARPLPT PPHLQAEPENHQYQQDLLNPDP APYCQLVPTS
9611	39979	A	9671	1	558	EGGLRTPSNPYHVDISQTKPCH *TNHCIQKEYSKNYGKYEEGNE MFFKEFNQYLTSALNITLESSIL LQIKHIIRNCLLSVEPAISTKHLP \YQSFQLFGFDFMVDEELKVWL IEVNGAPACAQ*ACTSLCFYKW EVGSAVGIVCGYKCSHFDCCEG GCHSDRRPLGGLYLAGGFAESL PFLFPRV
9612	39980	A	9672	1	534	MVGVDVTFKVISREERQTQRL GSSSPKRCPLEQEFEHEYSSFFG RNCLLSVEPAISTKHLPYQSFQL FGFDFMVDEELKVWLIEVNGA PACAQSPAKSL/CATSSSLFLSPP PWTCQQHSRQPTALAELLSCH GWTRGAGQACLWAFVLSVTC VWNPHHHYHHHHQPYRGWLL LYQNIL
9613	39981	A	9673	624	805	SGGHPGHWLPPNPMASPGATT PVGEG/ELQYASLSFQMVKPWD SRGQEATDTECSEIKIHR

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9614	39982	A	9674	1	1005	MENRRKVKGEWIAVPQPVKEL RGVLNAATTLSKTREILRGKCF QLTSPTGNEPSHLSWTPRKRSR DGHPGCPDPLAASGARPLRSSS AFAAAAADSGSTVQVWDKGV LRVADVWSTIEPVTHVNLGWA AKVGPIISHGSAVISAFSKEGMF RIFSERKTLLAKLRDFQNTQLR KLFSEMEKAAGRSQSGVSFGQ KGLGDRACEEMSENPQKGRKK PKAPQEVSFRENGNWKTP\SIFF SPKTPRKKKSFS\KEELMS\SD\L EETRWQAPSIPKRKKSTPKEET VNDPLE\AGHK\SGSKKKRKFS K\EEPV\SSGPEEAAGKSSSKKK KKFHKASQED
9615	39983	A	9675	1	2742	
9616	39984	A	9676	1	405	MADIPQEARQYRHKQAYAYSI QGEGVEDDDERIVRFHTRWPL QNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFYQKVGDN SIDSWKNAGR/VLKDSDKFDAN DPILKDQTQEWSGSATFTGSVF LAFGCYSK
9617	39985	A	9677	3	642	GKGLFDDEDEESDLFMEAPQD RQAGASVKEESSSSKPGKKIPA GAVSVFLGDTDVFGAASVPSLK EPQKPEQPTPRKSPYGPPPTGLF FFSAPHSKPSKTRKVQSTADIFG DEEGDLFKEKAVASPEATVSQT DENKARAEKKVTLSYSKNLKP SSETK\TQKGLFSDEEDSEDLFS SQSASNLKGASLLPGKLPTSVS WFDDEDEEDNLLGVQ
9618	39986	B	9678	175	1422	
9619	39987	A	9679	1	3096	MVTHQQPAARKPNMTSKKPKP MGPKAHGIFSGTRKNNLEIYMD QTRTGIAKTKLSKNNKSGGMT LPDFKLYYKAIVAKIACGGSMY NSDTDEDEETEPSSSGQQIIENSI TMNKMKLLKAKMKNMNLSKK HITQVSDEEEDDDGCDLFADSE KEEKDIEDIEENTRPKRSRPTSF ADELAARIKGDAVGRVDEEPTT VSYEDDRRGKNQDAYTEGGLS TIKTVNCSSSL\PSGEAKLRKTL/ KEKKERRTPSDDE
9620	39988	A	9680	1	2925	
9621	39989	A	9681	2	688	
9622	39990	A	9682	1	1005	
9623	39991	B	9683	1	588	

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9624	39992	A	9684	1	2763	
9625	39993	A	9685	2	1075	NSDEELLFSHKLQKDNDPDVDL FAGTKKTKLLEPSVGSLFGDDE DDDLFSSAKSQPLVQEKKRVV KKDHSVDSFKNQKHPESIQGSK EKGIWKPETPQ\AHQVSLHLKP NEPSTRIGKIQANLAINPAALLP T\AASQIS\EVKPVLP\ELAF\PSS EHRRSHGL\ESVPVLPGSGEAG VSFDLPAQADTLHSANKSRVK MRGKRRPQTRAARRLAAQESS EAEDMSVPRGPIAQWADGAISP NGH*PQLRAASGEDSTEEALA AAAAPWEGGPVPGVDTSPFAK SLGHSRGEADLYDSGDIFSRAP GSQ/SVERPNPRQRSRDLPPPGW KQRPRSGKQPRKRPSP*QPKHP LPKGRTSSPW
9626	39994	A	9686	1	4086	VTPRAAWLGLGFRGSAVLGLC WQPRSPPSRAAGMMNRTTPDQ ELVPASEPVWERPWSVEEIRRS SQSWSLAADAGLLQFLQEFSQQ TISRTHEIKKQVDGLIRETKATD CRLHNVFNDFLMLSNTQFIENR VYDEEVEEPVLKAEAEKTEQE KTREQKEVDLIPKVQEAVNYG LQVLDSAFEQLDIKAGNSDSEE DDANGRVELILEPKDLYIDRPLP YLIGSKLFMEQEDVGLGELSSE EGSVGSDRGSIVDTE
9627	39995	A	9687	1930	5781	RAKSPANIIMTGSNSHITILTLN VNGLNSPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNLTQSR
9628	39996	A	9688	1	3654	
9629	39997	A	9689	1	5127	
9630	39998	A	9690	1	3663	

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9631	39999	A	9691	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
9632	40000	A	9692	1	3489	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLTDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTEIITNYLSDH SAIKLELRIKNPTQSRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIPLNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKTDRPLARLIKKKR EKNQIDTIKNDK
9633	40001	A	9693	1	3235	
9634	40002	B	9694	1	3300	

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9635	40003	A	9695	1	2563	MKAEIKMFFETNENKDTTNQN LWDAFKAEEVESLNRPITGAEI GAIINSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEEI LPNSFYEASIILIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNILLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTSNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS RTPKAMATKAKIDKWDLIKLK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKKHMKKCSSSLAIREMQI KTTMRYHLTPVRMAIIKKSGNN
9636	40004	B	9696	1	3420	
9637	40005	A	9697	1	3579	MPGHNLKWKLNRGTVLIETGI QLSTSTILGSASEPPSAPIPKAQV SSTEKLRNCIDDLKPFPALASEL SRRAKALQIAGFPPMKVPRDTI SKVCLDKTVGKLCHSGEESRK CTLICNNKHYPIQDNLQGYKTQ NKFLNKEILELSALRRNAERRE RDLMAKYSSLEAKLCQIESKYL ILLQEMKTPVCSEDQGPTREVI AQLLEDALQVESQEQPEQAFV KPHLVSEYDIYGFRTVPEDDEE EKLVAKVRALDLK
9638	40006	A	9698	1	4371	

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9639	40007	A	9699	1	1825	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQI DAIKNDKGDITTDPTEIQTTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPITGAE IVAIINSLPTKKSPGPDGFTAKF YQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSINVIQHINRAKDK NHMIISIDAEKAFDKIQQPFMLK TLNKL\GIKYLGIHLTRDVKDLF KENYKPLLKEIKEDRNKWKNIP CSWVGRINIVKMAILPKNILITL QLLLVLPELSTLIPLWLPALAGQ
9640	40008	A	9700	1	4449	
9641	40009	A	9701	824	3693	AWKGTTDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YT/FFSAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNNLLL NDYWVHNEMNAEIKMFFETNE NKDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
9642	40010	B	9702	1	2858	
9643	40011	A	9703	1	3354	
9644	40012	B	9704	288	3301	
9645	40013	A	9705	1	3457	
9646	40014	A	9706	1	4794	
9647	40015	B	9707	1	3384	
9648	40016	A	9708	1	3345	
9649	40017	A	9709	1	3780	
9650	40018	A	9710	1	3720	
9651	40019	A	9711	1	3894	

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9652	40020	A	9712	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ
9653	40021	A	9713	1	3780	
9654	40022	B	9714	1	3855	
9655	40023	A	9715	1	3345	
9656	40024	A	9716	965	4362	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEYTFFSAPHHTYSKI DHIVGSKALLSKCERTEIITNYL SDHSAMKLELRIKNLTQNCSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTNQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELKEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREKNQIDT
9657	40025	A	9717	1	3921	
9658	40026	A	9718	1	3988	MTGSNSHITILTLNINGLNSAIK RHRLASWIKSQDPSVCCIQETH LMCRDTHRLKIKGWRKIYQAN GKQKKAGVAILVSDKTDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDIYRTLHPKSTEYTFFSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRIKNLTQS RSTTWKLNNL
9659	40027	A	9719	32	583	GPHGAFTHGRR/RFGRDPYEGP RRTGKRKQKSARGCIVDANLSI LNLVIVKKGEKDIPGLTDTMVP CHLGPKRASRICKLFSLSEDDD VHQCVVRKALNKEGKKPRTKA PTTKYLVTPHVLQHEWWHIAL KKQRIKENKEVAAEYAKLLAK RMKEAKEKHQEQIAKRRRLSSL RASTSKSESSQK
9660	40028	A	9720	318	605	

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9661	40029	A	9721	1	649	MGLKGQGVEGGLLRQSGSVSL QPLSREDLGRSQSESLGPEFQGL WEWLPVERVERENLSDYCVLG QRPMHLPNMNQLASLGKTNEQ SPHSQIHHSTPIRNQVPALQPIM SPGLLSPQLSPQLVRQQIAMAH LINQQIA/S*PAPGSPASSSHQPA VPEPS/IPSPEQLSQSQPTLPWKS LQISTSKSEMS*RGPVCPKLSLQ EWHSTAHRNLKTWKKD
9662	40030	A	9722	15	272	KPQWPGIPSGPPPPGSCFKC*KS GHWAKECLQPRIPPKPCPICAGP HWKSDCSTHLAATPRAPGTLA QGSLTDSFPDLLGLAAEG
9663	40031	A	9723	96	531	VQPADLLRPLHTDTCNIWCQRP GTEGLLRETGPLSS/PLTP/MRRS TYDLRSSDQPKEHLTDFKSGSC FKCRKSGHWTKECQQPRIPPKP CPICAGPHWKSDCPSCPAATPR APGTLAQDSLTDSFPTDPKGSLI DYFPDLLCLVAED
9664	40032	A	9724	3	567	GRLQTGADPAWRVHGTWRSTS AADAIDQMWP\PVMRTWRLNE RHYGGLTDLGKAETAAKHGEA QVKIWSNISKDRRYADLTDDQL SSCESLKDTIASALPFWNKEIVP QIKEGKWVLIAAHGNSLRGIVK HLEGLSEEAIMELNLLTGIPIVC KLDKSSKPIRCMEFLGDEGTLC KAMEAVAAQGKAKK
9665	40033	A	9725	2	801	GGVPHPQPAAMAAYKLVLIRH GESAWNLENRFSGWYDADLSP AGHEEAKRGGQALRDAGYEFD ICFTSVHLY\AIRTLWTVLEMPL\ SEMWLPVVRTWRLNERHYGG LTGLNKAETAAKNGEAQVKIW RRSYDVPPPPMEPDHPFYSNISK DRRYADLTEDQLPSCDRLKDTI ATALPFWNEEIVPQIKEGKRVLI AAHGNSLRGIVKHLEGLSEEAI MEL\NLPTGIPIVYELDKNLKPI KPMQFLGDEETVRKAMEAVAA QGKAKK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9666	40034	A	9726	3	573	VAPVVQVWKEMHKLLPFSPDS V\VTHGDISIDSGIFDQDKLIGRI DVGRVGIACGCQDVAIVWNYL AACSVDRNTCRIMRPNCRPEVE ETPGLKEEKELSQPKEGEATDL KKEVEKISSSEEEETVNLKEEVE KIPPPEEETMDLKEEKEEIPPPEL RDQKLMHVLKDLEPVSAVPHK DSLFHGQLTTVPV
9667	40035	A	9727	2	685	TLYCRVFLLDGTEVSVDLPKHA KGQDLFDQIVYHLDLVETDYF GLQFLDSAQVAHWLDHAKPIK KQMKIGPAYALHFRVKYYSSEP NNLREEFTRPKITKMDFKKSKL TLVVVEDDDQGREQEHTFVFR LDSARTCKHLWKCAVEHHAFF RLRTPGNSKSNRSDFIRLGSRFR FSCFS/ERENAHSTGNSPALRER PGDGSVSREGRWVDEGWPQRP GGRGQNALCSVP
9668	40036	A	9728	1	419	MSKFGRATRGLRKPEVGDVIRT IVRAGLAMPGPPLGPVLGQRRA SINQFCKEFNERTKDIKEGIPLL TKIFLKPDGTFEIKIGQPTVSYF VKAAAGIEKGARPT/DLSSEEFA AFQKEQAIFLAAQKKADLATQ EEAAKK
9669	40037	A	9729	97	826	SQLPRIMSKLGRAARGLRKPEV GGVIRAIVRAGLAMPGPPLG\N VLGQRGVSINQFCKEFNERTKD IKE\GIPLPTKIL\VKPD\RTFEIKI GQPTVSYFLKAAAGIEKG\ARQ TGKEVAGLVTLKHVYEIARIKA SGLRAFALQDVPLSSV\VRSIIGS ARSLGTSRGERTSSSEELAAFQ KERAIFL\AAQK\EADFGLPKKE AAKEIDPLPHQLPDFQKEVSLQ KLCPRGGRRSHQYDDGFHDFE
9670	40038	B	9730	273	418	

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9671	40039	A	9731	69	1565	RRRRFQASGAAAMLSSRAEAA MTAADRAIQRFLRTGAAVRYK VMKNWGVIGGIAAALAAGIYV IWGPITERKKRRKGLVPGLVNL GNTCFMNSLLQGLSACPAFIRW LEEFTSQYSRDQKEPPSHQYLS LTLLHLLKALSCQEVTDDEVLD ASCLLDVLRMYRWQISSFEEQP HFQDGLVQLRVGVVCRHYPEK WEAASWTSQNCGADDAHELF HVITSSLEDERDRQPRVTHLFD VHSLEGHPLTLDHCLHHF\TQSE SVRDVVCDNCTKIEAKGTLNG EKVEHQRTTFVKQLKLGKLPQ CLCIHLQRLSMVQP\GTPLKRHE HVQFNEFLMMDIYKYHLLGHK PSQHNPKLNKNPGPTLE/HAGW AGSPHTSSESARGPQNTDFYEW RLLPIFIANAVSADALPSPSCSR LQLLHIPLPADGQLSSTMGDMA LWDTLFIYRRSPPSARNPLSTSN QWLWVSDDTVRKASLQEVLSS SAYLLFYERVLSRMQHQSQEC
9672	40040	A	9732	1	1393	PLQLQPRHIGAQIQLGPLLQRV QAIRLGSFHMVLSLW/VMQSAR VEILEPPPRLQRMYGKAWRISL CPQGLSTVMRSELTASSTPQVQ EILPPQSPEYLGPKGITERIHKIM HVKGLAKLPANRNQPSPGVSG KRLVNCVSASAVDSEPAAVPEP DVCAGIVIKKQCFPVIARCNKT KQVDSIPHRAYAKPSPFFPAVV VVTSESKDPRVKQNPTHPLLAE GSNAAHFHKTKISQSLKWLPVG YLNSTTYEYRDLTKGLSLLCSL LLGVEADIPSMAGLHVRHLMQ VPQQPCIAFAVSSPLHQGGKET EDAWSFHIPSTIHRWPTSPSVQL SSLRASTQLLCLHINLAKCFIWG ILAQVLSCHHHRITQFVGMLTF VCAGDSSKLSPDIRTLVRRLTS YLVSASVLLKSKQMALCSASRI LDVSVSPGDHVASEARARCAP DLVAPRPMPHQNQGSLEWTEE
9673	40041	A	9733	44	282	FSCLILHDAFPCLILHDAFPCSL CSVTGSLVLSRVPLRGTHQKSA IATSTKIALSNM/KILKHHTDAY FKKQQLFFDVSKK

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9674	40042	A	9734	3	381	EQQGQR/SQWWRGAARVSRTV KRVLCE/VVECPLKSACPDVDM YWAALQRLASLLKADGNLVT MAALHSHYMVGSKKFFGLHPE KETVEKAMQEAGCQVQRCA/SI SCSETCSINDGICFVAACKGPSV
9675	40043	A	9735	2	209	CRHSTQHCVS/HHGHSQYK/DS HQHYSHYHHHNHPHHHHQSPY LHHHHYDCHLHHHHHNDHYH RHISVYDI
9676	40044	A	9736	197	3348	RVVQTDMIKGMLETSLLKISLD QAFIRICLNSTCFRPKGKLVIK/C EKSINSASLVSTSQRISCRPKTHI SKNYGNNFLNSSLLTQKQEVH MREKSFQCNESGKAFNYSSVLR KHQIIHLGAKQYKCDVCGKVF NQKRYLACHRRCHTGKKPYKC NDCGKTFSQELTLTCHHRLHTG EKHYKCSECGKTFSRNSALVIH KAIHTGEKSYKCNECGKTFSQT SYLVYHRRLHTGEKPYKCEEC DKAFSFKSNLERH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9677	40045	A	9737	1	1665	MAGACWLMAFQYWVLKLLVV KSA/SWPRQSSLKWNWNFKGC QDLETWGKKETRKFYGYRRNE EAQKYSCRIPRKPD*WCHCWQ W**WLMAFQYWVLKLLVVKS AYGLVKALSNGIGISKVAKTW KPGGKKRLENFMAIEEMKKHR STHVGFPENLTNGATAGNGDD GLIPPRKSRTPESQQFPDTENEE YHRDFSKLCLGSAANGVVHVE VKMCVYNGKGERQEEKMKGLI SMNLVVEEEMKKHESNNVGLL ENLTNGVTAGNGDNGLIPQRKS RTPENQQFPDNESEEYHSLGDK SKTSFQNSNNNNNKQQEQQQQ NPTFSNTRKLTKLYKAPIPPSIL SGCPNINDSNWQEIEHGMQTA GLPTRPLSHGLQQKGAAFRCLG CKCSEPFTGSLILQKAKTNTQK WQATYPKSQNEQLVPSVGKSY RCSTPAQPMKTAVGHKPCKAT GAELPKALGAQPLHPCALDVG QGFKKGNFGAVGLNGLLGLEF HGVSGVLLVGPGDGGLISEGVV REDLMCGVWSAGTWSVGTAE RCLEKPGALHVIEGPLDSWDGP VMPNGPVKSRQSSCLDGPGRC CSEILTGQSHGNKKPARASSKS SQSINDRPLAVLTNQYQCEQLA SERQPSSNSCSIRIDSA
9678	40046	A	9738	1	115	RRTARGPQQTSTDGLGTSPCRN ASEHTADILELSTLIV*RRQ*ICL CLDFLYY/LIPEGRCFCRACDLV HNF\DTIILQQHRTLTSQGVDDF LKAKATFKASDFIDALVLSKVA SPRILIQGGRMGA*DQVSDQAS VYGRCSSSGAEAAKRPKSAWL\ LLGYDSRASGLY*ILYNLTKHP D/YRECCQPVMQES*S*RRTAR GPQQTSTDGLGTSPCRNASEHT ADILELSTLIV
9679	40047	A	9739	1	506	MVIVGLAAGVLLVGPGDGGLIS EGVVREDLMCGVWSAGTWSV GTAERCLEKPGALHVIEGPLDS WDGPVMPNGPVKNHKGEQQE VPSKHPQMALEICLCLDFLYY/L IPEGRCFCRACDLVHNF\DTIILQ QHRTLTSQGVDDFLKAKATFK ASDFIDALVLSKVASPGS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9680	40048	A	9740	1	380	KFSRPSVNMLRIVKPCITRG/YP NLKSVNKLIYKHGRGKINKKRI ALTDNTLIDQSHGQYGIICIEDLI HELY\LWPFKLSSPQSGMKKKT THFVENGAAANREGQIHRLLIR MNCGVYRDYFSNLVS
9681	40049	A	9741	3	279	
9682	40050	B	9742	23	197	
9683	40051	A	9743	2	402	CGDRGALRPPSCAGRSGPGPPR PPRPPRPLPWHPAPPAHGAPLA RPGARARRSEKPPSEKPRLRRSS PRAQEEGPGEPPPPELALLPPPP PPPPTPA\PRRPRRP\PGPGRAAG ALGDVPEAAEAYLERVPPSSC
9684	40052	A	9744	1	660	
9685	40053	A	9745	1	1035	
9686	40054	A	9746	1	2575	MRAAGGAMLCGKQGRWDPEG EGAHPGFIPKLACSSQGVFRQL HLRTAVTAAVSRHFPQPSWRY DPGPQFLGEKSGFKPRCPGVAV CQFQSMNAFIHWFRNKAWASS CDRIKIPVPPEATFVEPNCLPGEI GQLLRQLQSGRNLKEWLREQF CDHPLEHCEDTRLHDAAYVGD LQTLRSLLQEESYRSRINEKSV WCCGWLPCTPLRIAATAGHGS CVDFLIRKGAEVDLVDVKGQT ALYVAVVNGHLESTQILLEAGA DPNGSRHHRSTPVYHASRVGR ADILKALIRPAACDRSVSITADT HFRYLIKVVPAMFRSRKAIPFLS SCTAWRCADELQFIQPVPLVDT SGSGKTVSNVITESHNSDNEED DQFVVEAAPQLSEMSEIEMVTA VELEEEEKHGGLVKKILETKKD YEKLQQSPKPGEKPSATGWHG ECLGTRNRAQGALVGWGWLY SERHSGMLRAITLKYKGGGRQ GIQA/AWKSETFRSRAAPENPL GRWGFALLSKIIS*RQVL\KLHF SLSPQARVNSRFPGSGKAGLGL WMEGARPSGHVPKERVVAGK RPQVPTKAHHTCVRETAGNQE GNGEGALQQEQRLGVAEAGSN GEGALQQEHRITDCAVEPLKAE LAELEQLIKDQQDKICAVKANI LKNEEKIQKMERSLFESAWKKE KDIVSKEIEKLRTSIQTLCKSAL

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9687	40055	A	9747	2	1739	MKGLYTDAEMKSDNVKDKDA KISFLQKAIDVVVMVSGEPLLA KPARIVAGHEPERTNELLQIIGK CCLNKLSSDDAVRRVLAGEKG EVKGRASLTSRSQELDNKNVRE EESRVHKNTEDRGDAEIKERST SRDRKQKEELKEDRKPREKDK DKEKAKENGGNRHREGERERA KARARPDNERQKDRGNRERDR DSERKKETERKSEGGKEKERLR DRDRERDRDKGKDRDRRRVKN GEHSWDLDREKNREHDKPEKK SASSGEMSKKLSDGTFKDSKAE TETEISTRASKSLTTKTSKRRSK NSVEGDSTSDAEGDAGPAGQD KSE\VPETPEIPNELSSNIRRIPRP GSARPAPPRVKRQDSMEALQM DRSGSGKTVSNVITESHNSDNE EDDQFVVEAAPQLSEMSEIEMV TAVELEEEEKHGGLVKKILETK KDYEKLQQSPKPGEKERSLFES AWKKEKDIVSKEIEKLRTSIQTL CKSALPLGKIMDYIQEDVDAM QNELQM\YHSENRQHAEALQQ EQRITDCAVEP\LKAELA\ELEQ LIKD\Q\QDKICAVKANILKNEE KIQKMVYSINLTSRR
9688	40056	A	9748	93	800	RANLPTQPYCHCGLAPAALTRI VGGSAAGRGEWPWQVDLWLR RREHRCGAVLVAERWLLSAAH CFDVYGDPK/QWAAFLGT/HVP ERRGGAVERVARIYKHPFYNL YT/FDYDVALLELAGPVRRT/SL VRPICLPEPA/HATPDGTRCVIT GWG/YGS/TGAQLQKAAVRLLS EQTCRA/LYPVQISSRMLCAGF/ LQGGVDSCSGDAGGPLACREPS GAPVPGQPRTCTAPARWPRRSA LSPAPL
9689	40057	A	9749	107	378	NLVP*LRSGD/SPLGDQSPVLLIF TP*ERSTYNLKSSD*PAQETS/PP ISNPDPTEN/PDCSTHLAATPRA PGTLAQGSLTDSFPDLLSLAAE D
9690	40058	A	9750	2	286	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9691	40059	A	9751	215	631	GTQSCNQKVLNSANNLQELGIG PKFQMRLKPQLAPMQPNRGTS LGRSIPCPPVLCSMRKIHLRPQV LRPTSPRNISPILNRVSEVSDHA GTPALVLHP*RQVPLFWGRGK YPNPFSLCLYPFSAFLGGKKHP TPSPSP
9692	40060	B	9752	1	933	
9693	40061	A	9753	1	2283	MLPNRLGSSETITDAELRVTLT VEELNGLRAVQDMFVKQILKA ARSLRVITIPNLKYPGTQTLRKA AAPDPNTTGLIFLEKLCEIAAAI ASYVAVPSLEINHRKKANPNLL LRRSGSGSVSLQLLAEKIWEGV REPWARVLVLWEWLPDQNPLS GLTKSNSTSRHELPHGRAIQLH LSGWELWSEPSNLLDLVVTGDI ENTSLAPEDPTFLTMPSGSHCPE SPSDGPGLSSLVALVWFLVED WLSRKRLESEPAELPLGKAGEV VFDTLPLPSRRTHFSGFLGHFCY SFSDGYSTNRAAPDGSSTKAEK HGSCRKQPPYTLQCRDKAGLR VHGNSPVSAYGWLFSEERPGKP TRTPFSWEGDPPGLLTADETSL VVHLELPVFPSFLKRAGNSRHS GMGSPLEAEEAYSTVVMADVS QYPVNEPLVAAVVCQEPERAQ PDVHFFQ/CLRLGGHAGGVAAR PLPAAETPPLQRRPSVRA*SAP* SGARAADDPRRTHS\QAEEAQR PEPDILNHVFDDVESF/VSRLQK SAEAARVLEHR/KRGRRSRRRA AGEGLLTLR/AKPPSEAEYTDV LQKIK/HAFSLLARLRGNIADPS/ SSELLHFLFGPLQMIV/QPSGGP EFASSVRRPHLT/RDAVALLRD NVTPRE/RRLWTSLGDSWTRPG LELSPEEGPPY/IPEFFSGWEPPV TDPQSAPGRTQLRNSYSTSGGA
9694	40062	B	9754	1	930	
9695	40063	A	9755	76	247	QLKTDTAQLPRKLFVESHNYH CSWPGLQSGLPHYSGYHTSSS* LYLSDPADIHPISP
9696	40064	C	9756	95	301	
9697	40065	A	9757	352	545	DILNHVFDDVESFVSRLQKSAE RPGCWRRRTRPQKPAPGVAG* RGTWRGI*TPPDLFQMSPLSP
9698	40066	B	9758	406	602	
9699	40067	A	9759	1	543	

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9700	40068	A	9760	2	138	LDDFVGRMLTLMGCPIPEC/PR VPSPLREGRKTQAALSVRRGRS HRR
9701	40069	A	9761	1	417	
9702	40070	A	9762	830	1029	YLPHLSLRLLPCPPPLPLSKPNS LP*LRPSLLQRDYLSIFILILNMP SISSTTMLLYGQKEISSLH
9703	40071	B	9763	40	980	
9704	40072	C	9764	419	700	
9705	40073	A	9765	271	1185	
9706	40074	A	9766	2	1655	RGRRSRRRAAGEGLLTLRAKPP SEAEYTDVLQKIKYAFSLLARL RGNIADPSSPELLHFLFGPLQMI VNTSGGPEFASSVRRP\LVTSD\ AVALL\GNNVTPRENELWTSLG DSWTR/LRA/EELSPEEGPPYRP EFFSGWEPPVTDPQSRAWEDPV EKQLQHERRRQQSAPSGRCQ WVTGDLEPESEPQLESETAGK WVLCNYDFQA\RNSSEAVRSSS GDVL\EVL\DDSR\KWWKVRDP AGQEGYVPYNILTPYPGPRLHH SQSPARSH\DSTPPPPPAPAP/VP/ LPPALARPRWDRPRWDSCDSL NGLDPSEKEKFSQMLIVNEELQ ARLAQGRSGPSRAVPGPRAPEP QLSPGSDASEVRAWLQAKGFSS GTVDALGVLTGAQLFSLQKEEL RAVSPEGG\ARVYSPVTVQRSL LEDKRES\SELEAVMEKQKEEG GRRGGNGGHLTCQAPFAKSDE APWENGPPQTLPNSGSRSSEGW PICSGPGLPPLPVDRLNDPCCSP SGEDLDWLGVGRAWRQSTESA SRPPRGCSGALSIVILRPSPINMP PCLAKKKKK
9707	40075	C	9767	565	762	
9708	40076	A	9768	1	401	SPLRPLLLALALASEPCAQGAC PASADLKHSDGTRTCAKLYD\C SDPYYENCCGGAELSLESGADL PYLPSNWANTASSLVVAPRCEL TVWSRQGKAGKTHKFSAGTYP RLEEYRRGILGDWSNAISALYC RCS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9709	40077	A	9769	1	1489	MPQLLQNINGIIEAFRRYARTEGNCTALTRGELKRLLEQEFADVIVKPHDPATVDEVLRLLDEDHTGTVEFKEFLVLVFKVAQACFKTLSESAEGACGSQESGSLHSGASQELGEGQRSGTEVGRAGKGQHYEGSSHRQSQQGSRGQNRPGVQTQGQATGSAWVSSYDRQAESQSQERISPQIQLSGQTEQTQKAGEGKRNQTTEMRPERQPQTREQDRAHQTGETVTGSGTQTQAGATQTVEQDSSHQTGRTSKQTQEATNDQNRGTETHGQGRSQTSQAVTGGHAQIQAGTHTQTPTQTVEQDSSHQTGSTSTQTQESTNGQNRGTEIHGQGRSQTSQAVTGGHTQIQAGSHTETVEQDRSQTVSHGGAREQGQTQTQPGSGQRWMQVSNPEAGETVPGGQAQTGASTESGRQEWSSTHPRRCVTEGQGDRQPTVVGEEWVDDHSRETVILRLDQGNLHT\SVSSAQGQDAAQSEEKRGITARELYSYLRSTKP
9710	40078	A	9770	2	3031	
9711	40079	A	9771	6288	6584	TAVSLPAPLFSDLQIPPRKRSLKETVMAPENLTN*RAPPQSSARVFQ*EALYVPGP*ALDPPEVCSSYSSVCGLHQLSHSSSESSSTLGSLLGSFQML
9712	40080	A	9772	884	1032	ESRPNTTTRLRKTSSWSFQS*TATQTKGPRDPGASMTKPGATSERSASG

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9713	40081	A	9773	1	1457	RSAQKEKTAAKEQQGEKTEVL SSDDDAPDSPVILEIPSLPPSTPP STPTYKKSLRLSSDQIRRLNLQE GANDVVFSVTTQYQGTCRCKA TIYLWKWDDKVVISDIDGTITK S\DALGHILPQLGKDWTHQGITS LYHKIQLGQLVMPLDARPERP MDGMKVRAFMERLLFVRRGT DKRWSVRMYVTCSQSSNLNEE IYINQVVIQANMKLQLWAMRT DDARGLSSLGDTEPSPCPSVVP GLQPKPAPVCAGDALLQAQIPG VLLGTLFSGAAFYSGLYGGSEQ FLDHLLHPARAAPPPPLVGPGP APRVPGSPSAPELAGPAVWRFA AAASRGVVVAASGWGRGGEA SQTFQTGKEPGGTRHPTRMPLG STGCIFPGTLEKSQGYERYNAM RADPALCFLEKVGMPDEKSLSA EQGVTDGTSDIPERARQNEEQL TSFGLLWPTPQGSTDHIDNHPR ERYPEMRWELDVPLPDIDYMEI PVDWWDA
9714	40082	A	9774	3	4804	KRLENIQKTLEVAFSEAVWMQ PSVVLLDDLDLIAGLPAVPEHE HSPDAVQSQRLAHALNDMIKE FISMGSLVALIATSQSQQSLHPL LVSAQGVHIFQCVQHIQPPNQE QRCEILCNVIKNKLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSISTREKLVL TTLDFQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
9715	40083	A	9775	1	897	
9716	40084	A	9776	486	800	CLQLSWLSLGQAQVHWLGRA VHTAFCMD*VLLFGESFGFLVR LTPGILLGLL*P*KQGHCHSVSL GEVRI/CGIIS*TFITSWAFSVLQ GKASAQPVKVSTQNSRY
9717	40085	C	9777	332	497	

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9718	40086	A	9778	1	6504	MWGSDRLAGAGGGGAAVTVA FTNARDCFLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSDQGENVAEINRQVGQKL GLSNGGQELHAVSLEQHLLDQI RIVFPKAIFPVWVDQQTYIFIQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADAEYKKLHS YGRDQKGMMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSIFSFQSEKKQETSWG LTEINAFKNMQSKVVPL
9719	40087	A	9779	1	5421	
9720	40088	B	9780	124	273	
9721	40089	A	9781	84	493	IHANNCS*L*KAALNFVLLLLQ KRL*GEKHLTLSETGREGNKVG GVGS*VTGTGQETELGSLGRCH SPLSVLHLLPFFS/ILLGRTHLNA LLIRDYFASSCKYL*EVLLSLSD GSG*NLMSVWMAGNSSAEYVR
9722	40090	A	9782	1	5954	MDGMTEACIKGGIEACYAAVS CVCTLLGALDELSQGKGLSEGQ VQLLLLRLEELKDGAEWSRDS MEINEADFRWQRRVLSSEHTP WESGNERSLDISISVTTDTGQTT LEGELGQTTPEDHSGNHKNSLK SPAIPEGKETLSKVLETEAVDQP DVVQRSHT\VPYPDITNFLSVDC RTRSYGSRYSESNFSVDDQDLS RTEF\DSCDQYSM\AAEKDSGRS DVSDIGSDNCSLADEEQTPRDC LGHRSLRTAALS
9723	40091	A	9783	1	2217	
9724	40092	A	9784	1	1360	
9725	40093	A	9785	1	777	MNIKNPIAAQHLDNLPIVKASSI GMTWGLVRNGVSAPTQKSCIRI HILARCTGAVAFEKLYFKSPAN QAHARKVGKQVQDCYIGRDIV AKAGAIIHLNVGKGTPVCCPLL EEGINSEVWTTEGQYGRAK\NA RPVQVKLKDSTSFPYQRQYPLR PKA/LTKGFQKIVKDLKAQGLV KPCSNPCSTPILGVQKPNRQWRI EALKLQIVLQMEPQMQSMTKI YHGPLGRPASPCSDVNDIEGNP TKEISTAPPLLCPNSAGSS
9726	40094	A	9786	1	415	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9727	40095	A	9787	1	451	MVHFISRLLYSDGLDVPGDPIQ DSDDAALSVSPHCSPDSRVSTT KHLWVSPRLLRVAVRVKNIDIT NFSSSW\NDGLAFCALLHTYLP AHIPYQELNSQDKRRNFMLAFQ AAESVGIKSTLDINEMVRTERP DWQNVMLFVI\AIYKYFET
9728	40096	A	9788	3	605	DEWPPERIIQYNEPTTWH/EDGL WGYRTRFYMINQIIW/LQAILEII TNKTDRALTILAQQETQMRNAI NQNRLALDYLPAAEGGICGKF NLTNCCLHVDDQGQVVEDIVR DMIKLSHVPMQVWHGFDPGA MFGKWFPVLGGFKTLIIGVILVI GTCLLLPCLLPVLLQMIKSFIAT LVHQNASEQLYYMNHYRSVLQ EYMGS
9729	40097	A	9789	3	876	GAGGGFGSPMDIFDMFF\GGGG RMHRERRGKNVVHQLSVTLED LYNSATRKLALQKNAICDKCE DRGGKKGGVEYCPNCRGTGM QIRIHQIGPGKVQQIQSVCVECQ GHGEQISPKDRCESCNGRKILR EKKILEFHIDKGMKYGQKITFH GEGYQEPGLEGEDIIIVLDQKD DAVFTRQGEDLFMCQIVKHGDI KCVINEGMPIYPRPYEKGRLIIE FKVNLPENDFLSPDKLSLLEKL LPKRKEVEETDEMDQVELVDF DPNQERWHHYNGEAYEDDEH
9730	40098	A	9790	199	410	
9731	40099	A	9791	134	1369	KMVKETTYYDVLGVKPNATQE ELKKAYRKLAL\KY\HPDKNPN EGEKFKQISQAYEVLSDAKKRE LYDKGGEQAIKEGGAGGGFGS PMDI\FDMFFGGGGRMQRERRG KNVVHQLSVTLEDLYNGATRK LALQKNVICDKCEGR/SGRFKE QGAVRSACPNCRGTGMQIRIHQ IGPGM\VQQIQSVCMECQGHGE RIRPKDRCKSCNGRKIVREKKIL EVHIDKGMKDGQKITFHGEGD QEPGLEPGDIIIVLDQKDHAVFT RRGEDLFMCMDIQLVEALCGF QKPISTLDNRTI\VITSHPG\QIVK HGDIKCVLNEGMP\IYRRPYE\K GRL\IIEFKVNFPENGFLSPDKLS LLEKLLPE\RKEVEETDEMDQV EL\VDFDPN\QERRRHYNGEAY EDDEHHPRGGVQCSDLLMGPV

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9732	40100	A	9792	3	337	GYSQAPRKR/GGECSSLSQPFSK AQPDAASLEPPSLETPAGRTPA TLTQGSPPAAVREPLSPGHNAK ARLRSRPARPPWIPDPDPPGHFV TDFCAPESLQGETRTSRSFQLL
9733	40101	A	9793	1	346	SGS*QLQMCSGLPAHTQDETHI SSCGQLDLALPPLLPPLPPSPLN TLPPQGLCTC
9734	40102	A	9794	1	1110	MEGEEAAGAAGPDPVGHRKKC GFHPVCEREAPSTFAAVMIHLV VQYIGEICRYLLKQPVREAERR HRVRLAVGNGLRPAIWEEFTER FGVRQIGEFYGATECNCSIANM DGKVGSCGFNSRILPHVYPIRL VKVNEDTMELLRDAQGLCIPC QAGEPGLLVGQINQQDPLRRF\ NGYVSESATSTKIAHSVFSKGD SAYLSRDALMMDELGYMYYR DRSGDTFRWRGENVSTTDVEG ELSRL\LGQTDVAVYGVAVPGK LGLQGVVLRHGVEGKAGMAA VADPHSLLDPNAIYQELQKVLA PYARPIFLRLLPQVDTTGTFKIQ KTRLQREGFDPRQTSDRLFFLD LKQGHYLPLNEAVYTRICSGAF
9735	40103	B	9795	28	376	
9736	40104	A	9796	3	461	VRQCRGIRDPYRFKKRTELFIA AEGIHTGQFVYCGKKAQLNIGN VLPVGTMPEGTIVCCLEEKPGD RGKLARASGNYATVISHNPETK KTRVKLPSGSKKVISSANRAVV G/VVSGSS*MLRAVGEHAVSAG GQPVARLGPWNSITCCSKTWV
9737	40105	A	9797	1	701	MQEVPGMFERNYPHPAITFKPS VPVSRSLDYAPLPGGVFRDPYW FKKRTELFIAAEGIHTGQFVYC GKKAQLNIGSVLPVGTMPEGMI VCCLEEKPGGRSKLSWASGNY ATAISHNPETKKTRVKLPSGSK KVVSSANRAVVGVVAGGGRT DKPILKACQAYHKYKAKRNW WPRVWDVAMNPMEHPFGGGN HQHIGIPSAI/SRDDPAGCKMGL IAARQTGRLWGTKTVQEKEN

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9738	40106	A	9798	1	910	QCGGIRRTGPVAMGRVIRGQR KGAFSVFRAHVKHRRGAARLR AVDFAERHGYIKGIVK/DAERW PGREGKGRPAGTPHSRRLCPQD IIHDRGR\GAPLA\RVVFRDPYRF KKRTELF\IAAEG\IHTGQF\VYC GKK\AQ\LNIGNVLPVGT\MP*\G TIVCCLEEKPGD\RGK\LARASG NYATVIS\HNPETKKT\RVKLPS GSKKVISSANRAVVGVVAGG\G \RIDKPIFEGWPGRYHKYKAKR NC*PRIRGV\AMNPVEHPF\GGG NHQHIGK\PST\IRRDAP\AGRKV GLIA\ARRTGRLRGTKTVQEKE
9739	40107	A	9799	1	405	LEISIMAASISGYTFSAVCFHSA NSNADHEGFLLGEVRQEETFSIS DSQISNTEFLQVI\KVIGWYRFR RNTQQQMSYREQVLHKQLTRI LGVPDLVFLLFSFISTANNSTHA LEYVLFRPNRRYNQRISLAIPN
9740	40108	A	9800	1	232	
9741	40109	A	9801	1	420	
9742	40110	A	9802	3	1272	EISIMAASISGYTFSAVCFHSAN SNADHEGFLLGEVRQEETFSISD SQ\ISNTEFLQVIEIHNHQPCSKL FSFYDYASKVNEESLDRILKDR RKKVIG\WYRFRRNTQQQ\MSY K\EQVLHKQLT\RILGVPDLVFL LFSFISTANNSTHALEYVLFRPN RRYNQRISLAIPNLGNTSQQEY KVSSVPNTSQSYAKVIKEHGTD FFDKDGVMKDIRAIYQVYNAL QEKVQAVCADVEKSERVVESC QAEVNKLRRQITQRKNEKEQE RRLQQAVLSRQMPSESLDPAFS PRMPSSGFAAEGRSTLGDAEAS DPPPPYSDFHPNNQESTLSHSR M\ERSVFMPRPQAVG\SSNY\AS TSAGFEVFLGSGADLPPPQRAA GDSGEDSDDSDYENLIDPTEPS NSEYSHSKDSRPMAHPDEDPRN
9743	40111	A	9803	3	513	GAYGGGYGACDNYNGYGYGF GSDRFGRDLNYCFSGMSDHKY GDGGSTFQSTTGHCIY\VHIEIGP DGRVTGEADVEFATHEDAVAA MSKDKANMQHSYVEPFLNCAA GASGTAYGSQMMGGMGLSIQS SYGGPASPQLSGGYGGGYGGH SSMSGFDQVLQENSCDFQSDIA
9744	40112	B	9804	73	1127	

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9745	40113	A	9805	1	3647	MRVRHVGQAALELLTSVRESR ATSAFQVSPYEDEPCRPCNCDP VGSLSSVCIKDDLHSDLHNGKQ PGQCPCKEGYTGEKCDRCQLG YKDYPTCVSCGCNPVGSASDEP CTGPCVCKENVEGKACDRCKP GFYNLKEKNPRGCSECFCFGVS DVCSSLSWPVGQVNSMSGWLV TDLISPRKIPSQQDALGGRHQVS INNTAVMQRLAPKYYWAAPEA YLGNKLTAFGGFLKYTVSYDIP VETVDSNLMSHADVIIK
9746	40114	B	9806	141	236	
9747	40115	B	9807	66	266	
9748	40116	A	9808	1	330	
9749	40117	A	9809	1	792	
9750	40118	A	9810	129	311	
9751	40119	A	9811	3	538	
9752	40120	B	9812	96	536	
9753	40121	A	9813	1	2090	MSSNQKSPTKTSKSPGTANVLD VNNSTLMFVGGLGGQIKKSPA VKVTHFKGCLGEAFLNGKSIGL WNYIEREGKCRGCFGSSQNEDP SFHFDGSGYSVVEKSLPATVTQ IIMLFNTFSPNGLL\LYLGSYGT KDFLSIELFRGRVKVMTDLGSG PITLLTDRRYNNGTWYKIAFQR NRKQGVLAVIDAYNTSNKETK QGETPGASSDLNRLDKDPIYVG GLPRSRVVRRGVTTKSFVGCIK NLEISRSTFDLLRNSYGVRKGC LLEPIRSVSFLKGGYIELPPKSLS PESEWLVTFATTNSSGIILAALG GDVEKRGDREEAHVPFFSVMLI GGNIEVHVNPGDGTGLRKALL HAPTGTCSDGQAHSISLVRNRR IITVQLDENNPVEMKLGALVES RTINVSNLYVGGIPEGEGTSLLT MRRSFHGCIKNLIFNLDHGFVD SVEQKRFCGVPSCARESARGRA QAQDTAQELQSESACDKRSPQP PGKGKHMYGGVLQPQSLFQKN LLLFYDEVLDLQPNGKEKEFSV GANHNAFMVVHWGVCGFCLF PSGEWLASPFCVHPQITIHPPDR FQASVTDEGYLFLAKPTQPAPA CPLDPIRPLLLGHAQQPLLTDQ HTDAAVTPSSAVTARAANYCA GGRNERKKTGREKRHLTGGPC VALRTFTVLHISSHHQVDGIRA GYVQRDGLQPTNRQIVM

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9754	40122	A	9814	1	8705	MRGGVLLVLLLCVAAQCRQRG LFPAILNLASNAHISTNATCGEK GPEMFCKLVEHVPGRPVRNPQ CRICDGNSANPRERHPISHAIDG TNNWWQSPSIQNGREYHWVTI TLDLRQVFQVAYVIIKAANAPR PGNWILERSLDGTTFSPWQYYA VSDSECLSRYNITPRRGPPTYRA DDEVICTSYYSRLVPLEHGEIHT SLINGRPSADDLSPKLLEFTSAR YIRLRFERIRTLNADLMTLSHRE PKELDPMLPR
9755	40123	A	9815	1	564	MGDLEDKLVPFIGELPRHLDQN SEQLKQVVQRELKELHETCQQ HQLCQASTSGEPKERDKEEGK DSKPRSLRFTWSMKTTSSMDPN DMMREIRKVLDANNCDYEQKE RFLLFCVHGDARQDS/LPCQWG DGKSCQVGPRLS\LNGV\RFKRI S\GTSYCPLKNIA\SKIA\NELKP VKKSQIYQVQGRYIHI
9756	40124	A	9816	2	451	ANAHGFIMELQDGYSTETGEK GAQLSGGQKQRVAMARALVR NPPVLILDEATSALDAESEYLIQ QAIHGNL\QKHTVLIIAHRLSTV EHAHLIVVLDKGRVVQQGTHQ QLACPRAGFYGKLVQRQMLGL QPAADFTAGHNEPVANGSHKA
9757	40125	A	9817	1	498	MVKY/YLGQGVLRSSW/DQVV PA/FWQRYRNPVQRYLTEDIVH RENQTMTTFTWNINHARPMVV EERCVYCVNSDNSGWTEIRREA WVSSSLCGVSRAVWEFGLAQF KSNVTKTLKGFEYILAKLQGEA ASKTLIKTAREAKEKAKETALA ATEKAKDLASKAATKKQQQ
9758	40126	A	9818	3	231	
9759	40127	B	9820	94	375	
9760	40128	A	9821	45	439	

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9761	40129	A	9822	304	1557	DRQNVMEQFNPGLRNLINLGK NYEKAVNAMILAGKAYYDGV AKIGEIATGSPVST\ELGHVLIEI SSTHKKLQRESLMENF\KKFHK EIIHELEKKIEL\DVKYMNATLK RYQTEHKNKLESLEKSQAELK KIRRKSQGSRNALKYEHKEIEY VETVTSRQSEI\QKSIADGCKEA LLERERGASCFPGLNKHCGFA/ NTHIHYYHLQSAELLNS\KLPR WQETCVDAIKVP\EKIMNMIEEI KTPASTPVSGTPQASPMIERSNV VRKDYDTLSKCSPKMPPAPSGR AYTSPLIDMFNNPATAAPNSQR VNNSTGTSEDPSLQRSVSVATG LNMMKKQKVKTIFPHTAGSNK TLLSFAQGDVITLLIPEEKDGWL YGEHDVSKARGWFPSSYTKLL EENETEAVTVPTPSPTPVRSFSG
9762	40130	B	9823	1	1128	
9763	40131	A	9824	1	434	
9764	40132	A	9825	92	319	SIPPYPIPPPVDRKEID*LEGMQT SGLFQQTSG*EEGVGSIMASGR PPHPEPLKADFICKREVRLAFSI ACIWMR
9765	40133	A	9826	1	851	
9766	40134	A	9827	227	305	LVIFSIFNLVG*NISDCIILICQLK
9767	40135	A	9828	66	808	YCWQSQGAKPRDLLGPDLIPLN HSPRVSHLLCHRHIRKAGGVFV ADEIQVGFGRVGKHFWAFQLQ GKDFVPDIVTMGKSIGNGHPVA CVAATQPVARAFEATGVEYFN TFGG\SPVSCAVGLAVLNVLEK EQLQDHATSVGSFLMQLLGQQ KIKHPIVGDVRGVGLFIGVDLIK DEATRTP\ELKRHVYLVSRLKE NYVLLSTDGPGRNILKFKPPMC FSLDNARQVVAKLDAILTDME EKVRSCENR
9768	40136	A	9829	3	597	

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9769	40137	A	9830	1	3281	MGFHHVGQAGLKLLTSGTPQL LALVQHWVPGARLVEELPHEL VLVLPYTGAHDGSFATLFRELD TRLAELRLTGYGISDTSLEEIFL KVVEECAADTDMEDG/TLRAA PMHRHCWPRRNPTAQDAATGD SAG\DGEPAGSAPETDQGSGPD AVGRVQGWALTRQQLQALLL KRFLLARRSRRGLFAQIVLPALF VGLALVFSLIVPPFGHYPALRLS PTMYGAQVSFFSEDAPGDPGR ARLLEALLQEAGLEEPP
9770	40138	A	9831	1	684	RTRGPPPQSRSGGRRRRIPLYLP TSCIKELVAGGVAVESWPGRD AAQLLLCSCLLSPPPVMTETRE PAETGGYASLEEDDEDLSPGPE HSSDSEYTLSEPDSEEEEDEEEE EEETTDDPEYDPGYKVK*RLGG GRGGPSRRAPR\AAQPPAQPCQ LCGRSPLGEAPPGTPRCTGTSCC MPGVRCRQSPHTGSLAEGVGW EEGAEEIGVVTVVMGDGVLPV CVVLEVDV
9771	40139	A	9832	1	670	MESDIGRKGGKDPEAGPEHSSD SEYTLSEPDSEEEEDEEEEEEET TDDPEYDPGYKVKQRLGGGRG GPSRRAPRAAQPPAQPCQLCGR SPLGEAPPGTPPCRLCCPATAPQ EAPAPEGRALGEEEEEPPRAGE GRPAGREKEEEEEEEGTYHCTE CEDSFDNLGEL\TGTSCCMPGV RCRQSPHTGSLAEGVGWEEGA EEIGVVTVVMGDGVLPVCVVL
9772	40140	A	9833	3	512	
9773	40141	A	9834	3	815	MLYSRGPQPMGHGPVLVCGLL GTGCTAGAQELREAYTSISSQID QAEERISEIEDKLNEIKREDKITE KRMKRNEQSLQEIWDYVKRPN LRLIGVPKSDVENGTKLENTLQ DIIQENFPNLARQANVQIQEIQR TPQRYSSRRATPRHIIVRFTKVE MREK\MLRAAREKGRVTHKGK PVRLTADLSAETVQARREWGPI FNILKGKNFQPRISYPAKLSFISE GEIKYFTDKQMLKDFVTT/RPA LKELLKEALNMERNNWYQPLQ KHAKL

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9774	40142	A	9835	1	561	MVNGRJPQAPSQFSHLARLHPA PSPNSDPSPFLAELLLMPSVIGL TPSYPSRFSSESTFLQEAFPDLC QAEDPVYANGGLNYSYRGYGA LSSNLQPPASLQTGNHSNGPTD L\SMKGGAFTTSTTPTPTPSSTST SRPVPTAQLSPTEISAVRQLIAG YRESAAFLLRSADELENLILQQ NRPRRHL
9775	40143	A	9836	2	226	KGVQFQFSSYG*PVFPTPFIK*G VLSPLFVFLRFLKDQMVVDV*H YF*GLCSVPLVYISVLVLVPCCF FFTVAL
9776	40144	A	9837	2	350	YKVSKPKAQLCSQQVKYLWLK LSKGTRALSEERIQPILAYPHPK TLKQLRGILGITGFCRIWIP\R*S SPTGQE/FSLYVTEETGIALGILT QVQGTSLQPMEYLNKEIDELDQ GRTH
9777	40145	C	9838	213	365	
9778	40146	A	9839	1	1923	

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9779	40147	A	9840	1	2091	MVLVVVAVVVVVLVVAVIVV VVVVVAAVVVGAVVVVVVVV MVVVVVVVVVEEDNQHKTGA INNNNTAKNPQQSPFHSPATST GAEATQMRRNQKTNPHNMTK QVSLTPPKITLAHQQWIQTKKK YLIYLKKHSGVNKIPRNPTYEG CEGPFQGELQTTAQQNKGGHK QTEDHSMLMDRKNQYCENGH TAQAVPNPYTLLSQIPEDAEWF TVLDPKHAVFCIPVHPDSQFLF AFEDPSNPMSQLIWTVLPQGFR NSPHLFGQALAQDLSQFSYLDT LVLRYMDDLLLATHSETLCHQ ATQALLNFLATCGYKVSKPKA QLCSQQVKYLGLKLSKGTRTLS EERIQPILGYPHPKTLKQLTAFL GITGFCQIWIPRYSKIARPLNTRI KETQKANTHLVRWTPEAEVAF QALKKALTHAPVLSLPVGQNFS LYVTEK\TGIALGVLT/PGTSAQ LAELIALTRAPELGEGKRVNIY ANSIGREREFLTSKGTLVKHQE AIKRLLLAVQKPKEVAVLHCW GHQKGKEREIEENRQADIEARR AARQDPPLEMLTEGPLAFELA MATARAELSLAIHHCCLPPPQ TRCWLPSLRIRQGVCCIPDPAR AITLTAWPKIPFLGIRKAKNPQV REHEACHHLGSGLPPFWKWPT TILGALGARTPGNTGSTYTFIGY TYTSPVIFILSWQYVYFHGLYY
9780	40148	A	9841	1	1284	

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9781	40149	A	9842	1	1522	MVAPGSVTSRLGSVFPFLLVLV DLQYEGAECGVNADVEKHLEL GKKLLAAGQLADALSQFHAAV DGDPDNYIAYYRRATVFLAMG KSKAALPDLTKVIQLKMDFTA ARLQRGHLLLKQGKLDEAEDD FKKVLKSNPSENEEKEAQSQLI KSDEMQRLRSQALNAFGSGDY TAAIAFLDKILEVCVWDAELRE LRAECFIKEGEPRKAISDLKAAS KLKNDNTEAFYKISTLYYQLGD HDCSFSEFRDVLNLDQDHKR\C FAHYKQVKKLNKLIESAEELIR DGRYTDATSKYESVMKTEPSIA EYTVRSKERIC\HCF\SKDEK\PV EAI\RVCSEVLQMEPDNVNALK DRAEAYLIEEMYDEAIQDYETA QEHN\ENDQQIREGLEKAQRLL\ KQSQKRDYY\KILGVKRNAKK QEIIKAYRKLALQWHPDNFQNE EEKKKAEKKFIDIAAAKEVLSD PEMRKKFDDGEDPLDAESQQG GGGNPFHRSWNSWQGFNPFSS GGPFRFKFHFN
9782	40150	A	9843	5	519	LTCQEEHKKKHPDSSVNFVEFS KKCLERWKTTSAKEK/SKFEEK AKSDKARCDREIKNYIPPKCKK GRPPSAFFLFCSEHRPKIKSGHP GLFVVETAKKLGEMWSGQSAK DKQPYEQKAVKLQERYEKGIA AYRAKGKSEAGKKGSKKNKPE DEEEEEKEDEDEEEEGEDEE
9783	40151	A	9844	1	3140	YSIATVLAAEEKLDPRRDEAKR LRPQRNFNITFTHGTVFRPLTLE STFFNSALLFTTIKQDLPPLPKTI ITNAFHRFRNHHQTGFKLSAAN QRGPLAATLSGPGGEGQSAVA RLTGEKKNHPGAQYANRLSPR VGRFINAAGTTGFPTGKRARSD SSLAKENNQKAYKETYGVSHIT RHDMLQIPKQQQNEKYQVPQF DQSTIKNIESAKGLDVWDSWPL QNADGTVAEYNGYHVVFALA GSPKDADDTSIYMFY

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9784	40152	A	9845	2	604	FLELPPAAAAAVLSASPGALER EARSPRSPQTADTSPRPRAPAC APSRARAMPSDRPFKQRRSFAD \RCKEVQQIR\DQHPSKIPV\IIER YKGEKQLPVLDKTKFLVPDHV NMSELVKIIRRRLQLNPTQAFFL LVNQHSMVSV\STPIADIYEQEK DEDGFLYMVYASQETFGF*ASS PCLSAHLPLTHPRLCPPPGPAHP
9785	40153	A	9846	3	303	RDQHPSKIPVIIERYKGEKQLPV LDKTKFLVPDHVNMSELVKIIR RRLQLNPTQAFFLLVNQHSMVS VSTPIADIYEQEKD\EDGFL\YM VYGLPGKPFGF
9786	40154	A	9847	254	2110	
9787	40155	A	9848	234	1904	
9788	40156	A	9849	5	189	
9789	40157	A	9850	1	1546	MASASSQPSLAVGFSSFDPGAP SCTASSASGILSPTASEVPYASG MPIKKTGHRGVDSSGETTYKKT TSTALKGAIQLGITYTVGSLSTK PERDVLMQDFYVVESIFFPSEGS NLTPAHHYNAFRFKTYAPVAF RYFRELFGIPPDDYLCSLCSEPLI ELCSSGASGSLFYVSSDDELIIK TLQHKEAEFLQKLLPGYYLNLS QNPRTLLPKFFGLYCVQTGGKN IRIVVMNNLLPRSVKMHIKYDL KGSTYKRRASQKEREKPLPTFK DLDFLQDIPDGLFLDADTYNAL CKTLQRDCLVLQSFKIMDYSL WLSIHNIDHAQREPLSSDTLQV SIDTQRLAPQKALYSTAMEFIQ GEARLGDTMEADDHMGGIPAQ NSKGERLLLYIGIIDILQSYTFLK KLEHSWKAVVHDGDAVSVHR PGFYAERFQHFMCNAVFKKIPL KPSPSKKFRSGLSFSLHTGSSGN SCITYQPLVSEEHKSQVIKVQVE PGVHLGRSDVLPQTSE\PPLEEIT

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9790	40158	A	9851	233	2051	AGPGAGSTCLREARRGRGGGP QNAGSVKRRWEDSIPRRGRTGL KESQAAEGEGAAKMASASSGP SSSVGFSSFDPAVPSCTLSSASGI KRPMASEVPYASGMPIKKJGHR SVDSSGETTYKKTTSSALKGAI QLGITHTVGSLSTKPERDVLMQ DFYVVESIFFPSEGSNLTPAHHY NDFRFKTYAPVAFRYFRELFGI RPDDYLYSLCSEPLIELCSSGAS GSLFYVSSDDEFIIKTVQHKEAE FLQKLLPGYYMNLNQNPRTLLP KFYGLYCVQAGGKNIRIVVMN NLLPRSVKMHIKYDLKGSTYK RRASQKEREKPLPTFKDLDFLQ DIPDGLFLDADMYNALCKTLQ RDCLVLQSFKIMDYSLLMSIHNI DHAQREPLSSETQYSVDTRRPA PQK\ALYSTAMESIQGEARRGG TMETDDHMGGIPARNSKGERL LLYIGIIDILQSYRFVKKLEHSW KALVHDGDTVSVHRPGFYAER FQRFMCNTVFKKIPLKPSPSKKF RSGSSFSRRAGSSGNSCITYQPS VSGEHKAQVTTKAEVEPGVHL GRPDVLPQTPPLEEISEGSPIPDP SFSPLVGETLQMLTTSTTLEKLE
9791	40159	A	9852	30	298	EPFIFLFIYLFIYLFFETESRPVIQ AGVQWCNLSSLQPLPTGFKQFS \CLSPLTSWDYRHPPPCPANFCS FSRDGVSPCWPGWSQTPDLR
9792	40160	A	9853	3	938	
9793	40161	A	9854	208	870	LGMAGRLFTVNLQSPLNPSTLL AEVCVEQCTLMDSKMKPLWIM YSNEEAGSGGRVSVSLKRDDD LWQDMLTMQTIRLMDVPDTIA NIQLNNRNMDGGNEEFTLSCA GYCVATYVLGIGDRHSDNIMIR ASGQLFHIDFCHFRQRVPFILTY DFVHVIEQGKTNN/SEKFERFRG YCERA\YTILRRHGLLFLHLFAL MQAAGLPELSCSKDIRYLKDSL VHPL

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9794	40162	A	9855	1	790	VEELSKKLADSDQASKVQQQK LKVGQLGEWVWPLDKGGKLFS KLWGRGGLVYKWFLLIYKISY ATGIVGYMAVMFTLFGLNLLF KIKPEDAMDFGISLLFYGLYYG VLERDFAEMCADYMASTIGFY SESGMPTKHLSDSVCAVCGQQI FVDVSEE/EDH*EHRCS/CFHEF CIRGWCIVGKKQTCPYCKEKV DLKRMFSNPYPLLGSLLGVGCG KKVLASVTCIWVLLGPSLLPPT RTCQTMNNKKIMKVMMRIKR MMTDTMAS
9795	40163	A	9856	1	1005	FRGRAVKMAAVVEVEVVGGA AGERELDEVDMSDLSPEEQWR VEHARMHAKHRGHEAMHAEM VLILIATLVVAQLLLVQWKQRH PRSYNMVTLFQMWVVPLYFTV KLHWWRFLVIWILFSAVTAFVT FRATRKPLVQTTPRLVYKWFLL IYKISYATGIVGYMAVMFTLFG LNLLFKIKPEDAMDFGISLLFYG LYYGVLERDFAEMCADYMAST IGFYSESGMPTKHLSDSVCAVC GQQIFVDVSEEGDH\ETTYRLSC NHVSHEFCIRGWCIVGKKQTCP YCKEKVDLKRMFSNPWERPHV MYGQLLDWLRYLVAWQPVIIG VVQGINYILGLE
9796	40164	A	9857	28	267	LNIGKGDSKKPRGKMSSYAFFV QTCREEHKKQHPDASVNFSEFS YKKDIAAY*AKGKPDAAKKGFI KAEKSKKKKEEEED
9797	40165	A	9858	1	194	MGKGDPKKLRGKMSSYAFFVQ TCQEEHKKQQPDASVNFSEF/S KKCSERWKTMSAKEKSEDMA KL
9798	40166	A	9859	241	958	HQIFILFFRKITKHGQRRSLRSPR GKMSS\FAFF\VQTCREEHKKRH PDASVN\FSEFSKKC/SQRGWKT MS\SKEKGKF*RYGQKRDKAR YER\EMKTYYPS\KGGDQKRSF KDPNAPQGGPPFGPSFLF\CSEY RPKIKREDHPGLSIGDVAKKLG EMWELTLLQ/SDKQPYEKKAA KLKEKYEKDIAAYRAKGKPDA AKKGVVKAEKSKKKKEEEEDE EDEEDEEEEEDEEDEEDEEEDD

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9799	40167	A	9860	2536	2909	KSGVPGSRFSSSDKSDTGVTGL FSTYFLKSDFQLQLIDISASTAS KSLFSAVLFQEYILSFGLSEIISIL SSAVCWREAPKLSMVGCLAAG GKLTGC*AAGCLATDGRTETL DAAPAAAALSAV
9800	40168	A	9861	5	1752	KCTICLRNS/IAVCCGCGQGLSG YLNGEGADGAERGGGGSGVEC LRAPVCGQAASSLAASQLAAG GQAANHAQLRCLSPADCALML FIQVEVLTNSIAMVSVHLEKQP LKLVLGELGFRSPAGEEQATPV VGGEGLGCIEDSAAVAEGGIAI GGIVGINTALQEVLKPHTIKMQ RNNAQLSRRKEPKEGLCGERG QDRMSRAKGSSSKGKELPPGCR RVTMKPLLVRETQEGQAAERG AEEQLQTLGPFAVYRDSPSKNF YKRDKMLKGLEEAKVNFVWR TNEGFLEEDAGQEFGIQKAVTP ALCPSRKAEVPLSCLTLKLSED GKAKKAPYNTGPLGLLHLSMC SHSRKGFEQLWQLNSGKLLQG PRDSVEGSARRAETAVHCPAVL HFAPALLLAALRCQRDLESAAA PSHTRSCQHPRLLSGAVQTAGF SNPPKVVIQIKWNFLVMLLNFP GSTKLIARLKQQMNYKEMASQ RLTQSMLPHRSRLIGAGPCNRC VHPEPVIVTLFGQKVFARIIKKN QTCLLCSQIWCAHYQQGWICA WLAGFGKIYIFSTIGVIDTLSSG HIHLQPNCTARDSASWESPA
9801	40169	A	9862	1	668	MWRLVIQDAKDENGVLVGNR VLAHSSLAVLSCLALNNRRISG WTP/CGPSGSPPGFMGRRGTST/ RLPTG**CPEGQPPRCPCG*ASG CASSPAECRMPATHLPGNSGRV PFPPGPVNYSPLRLQAPEQVTG S/SPWPFS/RPVLGPLPLEGS\PPP F/RLPPRPRPAGVAAGSSWGHS AASVRRSPGRRPEGESIHPRPPA SRLPWLRATREEEAGAPKLGED SYPNF

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9802	40170	A	9863	2	624	FMGRRGTSTPFPLADNAPRGSP PGAHVVGGWDPDLRRAPVTGF SCSGSCSQRGAADWESFPRSPP CRASGCASSPAECRMPATHLPG NSGRVPFPPGPVNYSPLRLQAP EQVTGS/SPWPFS/RPVLGPLPLE GS\PPPF/RLPPRPRPAGVAAGSS WGHSAASVRRSPGRRPEGESIH PRPPASRLPWLRATREEEAGAP KLGEDSYPNF
9803	40171	A	9864	51	225	
9804	40172	A	9865	1	276	AFAAIPTNTLLLEQKALDEPAE TESVSKDNTL*PPVETPTTLPRA AGRETKYANLSSPTSTVSESQ/P D*AWSNSPSTCKIQNITEKRGGS L
9805	40173	A	9866	3	441	QTNFKGCSKVTSSKLNMSLLW TPTGR*GCDRKVEQGPPGDLGT AAVRPKSLAISSSLVS/ACSASK TQGTDLKTSSHPEMLHGMAPQ QKHGQQYKTKSSYKAFASIPYK HIAFGTEDS/STTLPRAAGRETK YANLSSPTSTVSESQAD
9806	40174	A	9867	123	417	SLDLDLFTVSGLLSLDSSGILTR NLEVSAN*VWVGSLLTVGTNV KIRGLASEPPAETVSFSSKFLFN KLLFSRFSSSILKENEKERKNER HRGSNSV
9807	40175	A	9868	153	1624	TTRRKSMNPTLSGKYLEDNSDL FSEQALDEPAKTESVSKDNTLE PPVELYFPAQLRQQTEELCATID KVLQDSLSMAPSLSPTKQASSS LAYMNVERTPSPTLKSNTMLSL LQTSTSSSVGLPPVPPSSSLSSLK SKQDGDLRGPENPRNIHTYPST LASSALSSLSPPINQRATFSSSEK CFHPSPALSSLINRSKRASSQLS GQELNPSALPSLPVSSADFASLP NLRSSS/APSCQSAHPGAPAQSL SSAPT\CGSGTLPSRLGKSESTTP NHRSPVSTPSLSISLTRTEELISP CALSMSTGPKNKKSKTPTTLPR AAGRETKYSKSNDYLTLNAGS QQERDQAKLTCPSEVSGTILQE REFEANKLQGMQQSDLFKAEY VLIVDSEGEDEAASRKVEQGPP GGIGTAAVRPKSLAISSSLVSDV VRPKTQGTDLKTSSHPEMLHG MAPQQKHGQASAYKGEESNEE DWTILKSSRMTNPRKLSDNKI
9808	40176	A	9869	1	762	

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9809	40177	A	9870	1	537	
9810	40178	A	9871	490	681	MGLVLLHVGKLGSSWLRNGSQ ETAGQIISPLSSWHDTGAGAAL DFSPGLSCLPVR*GSRRAAPH
9811	40179	C	9872	258	527	
9812	40180	A	9873	1	2865	MLPAFEHQTPSSSAFGLLNLQQ WFVRGSRAFGHRLKAALSGSL LLKFSDSDWLPCSSACRGPIVG LHLVIVYVKSHQNAYRHKNIQL KQTLLSCNTTKVRSFIIEVSETR NPPAGTNSGHILGTCPGYRYAK GKETGKEIIKGPQNPPGYRLCPL QAVGGGEFGPTQVHVPFSLSDL KQIRVDLGKFSDDPDRQYPLRP EAHEGLQDILRYLKVQGLVRK CSSPCNTRILGVQKPKGQWRLV QDLRFINEAVIPL
9813	40181	A	9874	3	177	
9814	40182	A	9875	255	1299	AAVFPLWCWRTRGKCHSLEWR PCTVCSWPDSPPKVSAGQALCG SETLPLTQTPDIQVPATLESGHP ANLL\VSAAWKSRKSLIFSWTW GTVISLGPRTPHFSEITIIPLPWS HGSSITFQVTFPRFHVTTEMTIQ LNVSSPVALENATSLSVLKNQS LRFVYVTDSNPPARLSWTWEG QALNLSQSSESAVLELPPVESC DGGEFVCQAQHPLGSQHVSISL SVQSDSVISIEEGVLQTLGFTLIR GILMGTSCTFICGFTWICCTSPVI PKPGTQSCFSTRDSATLPDACG SPGPKRVWMCSESHQPLCAVP DEDEQELHYAVLHFHKVQPQE PKVTDTEYSEIKIHK
9815	40183	A	9876	27	385	ASTTTGSGTSTAAARCTAWSPG PLVTAVEKFEAEAAALGQRIST LQKGSPDPLQVRMLNDQLMLL ERTFLNPRAFPEERYYSHVLWA /PSHGLRSHIPG\LSNACSRARDT ASGSEAWAEG
9816	40184	A	9877	160	480	
9817	40185	A	9878	19	433	GLDHGWAGDRWRTRPVVGAG EGRAPRLNSPSGQIRSPGPGDLS IYDNWIRYFNRSSPVYGLVP\GF SSHQAVARTAGSVILRLSDSFFL PLKVSDYSETLRSFLQAAQQDL GALLEQHSISLGPLVTAVEKFE AKAAAL

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9818	40186	A	9879	1	996	MALSKERSTVTRTQWARKTML QGETIQISESVSTYLRPYSVSGT VLGTNMSKTSARIYPTYHTAFD TFDYVDKFLDPGFSSHQAVART AGSVILRLSDSFFLPLKVSDYSE TLRSFLQAAQQDLGALLEQHSI SLGPLVTAVEKFEAEAAALGQR ISTLQKGSPDHVLWA/PSHGLRS HIPG\LSNACSRARDTASGSEA WAEVQRQLSIVVTALEGSVEAL HEVLQLPAALRACPPLRKALAV DAAFREGNAARLFRLLQTLPYL PSCAVQCHVGHARREALARFA RAFSTPKGQTLPLGFMVNLLA WMDSGKHGTCARPTGCPWTER RELCS
9819	40187	A	9880	66	744	RAHEDRERSGVQIRTQSWNGG KREKDFLHQSG\LETLLMKGC WRKSKTSARIYPTYHTAFDTFD YVDKFLDPGFSSHQAVARTAG SVILRLSDSFFLPLKVSDYSETL RSFLQAAQQDLGALLEQHSISL GMHSPDPEVRMLNDQLMLLER TFLNPRAFPEERYYSHVLWA/PS HGLRSHIPG\LSNACSRARDTAS GSEAWAEVQRQLSIVVTALEG AAATLRPVADL

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9820	40188	A	9881	2	2241	PRVRRMQWTKVLGLGLGAAA LLGLGIILGHFAIPKKANSLAPQ DLDLEILETVMGQLDAHRIREN LRELSREPHLASSPRDEDLVQL LLQRWKDPESGLDSAEASTYE VLLSFPSQEQPNVVDIVGPTGGI IHSCHRTEENVTGEQGGPDVVQ PYAAYAPSGTPQGLLVYANRG AEEDFKELQTQGIKLEGTIALTR YGGVGRGAKAVNAAKHGVAG VLVYTDPADINDGLSSPDETFP NSWYLPPSGVERGSYYEYFGDP LTPYLPAVPSSFRVDLANVSGF PPIPTQPIGFQDARDLLCNLNGT LAPATWQGALGCHYRLGPGFR PDGDFPADSQVNVSVYNRLEL RNSSNVLGIIRGAVEPDRYVLY GNHRDSWVHGAVDPSSGTAVL LELSRVLGTLLKKGTWRPRRSI VFASWGAEEFGLIGSTEFTEEFF NKLQERTVAYINVDISVFANAT LRVQGTPPVQSVVFSATKEIRSP GPGDLSIYDNWIRYFNRSSPVY GLVPSLGSLGAGSDYAPFVHFL GISSMDIAYTYDRSKTSARIYPT YHTAFDTFDYVDKFLDPGFSSH QAVARTAGSVILRLSDSFFLPLK VSDYSETLRSFLQAAQQDLGAL LEQHSISLGPLVTAVEKFEAEA AALGQRISTLQKGSPDPLQVRM LNDQLMLLERTFLNPRAFPEER YYSHVLWAPSHGLRSHIPG\LS
9821	40189	A	9882	1	1962	
9822	40190	A	9883	1	166	MEYYAALKKDEFMSFVGTWM KLETIILSKV\CQGQKVKHHMFS LTGALLVRGPWA
9823	40191	A	9884	1	378	
9824	40192	A	9885	1	681	
9825	40193	A	9886	1	3174	MEYYAAIKNDEFMSFVGTWM KLETIILSKLLQGQKTKHRMFSL IGSIIVKVPSSLQAHLQLSGKEV DVNSEVHVQEMAEARKDDVV TVTDAEKALDKIQHLFMVKTLS KIGIQGTYLNVIKAIYDKPTANII LNGEKLKAFPLRNETRQGCPLS PLLFNTVLKVLARAVRQEKEIK GIQIGKEEVILSLFADDMIVHLE NPIVSAQNLLKLIDNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASER
9826	40194	B	9887	1	352	

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9827	40195	A	9888	3	430	FFFFLPVAGLRRPRPRLGPVPPR PRVPPPQDRAATMKKFFQEFKA DIKFKSAGPGQKLKESVGEKAH KEKPNQPAPRPPRQGPTNEGTD GSRCCPQP/WLEQKQSRAWGPH IAGHHPKPGEKGTSSRSHRQRE PRGPRDQRGI
9828	40196	A	9889	1	1062	MKKFFQEFKADIKFKSAGPGQK LKESVGVWGRPNGLMSVKGN CECGNLWLLYPEVAALAAEAE GPEVGSVEDQRRQQGYFVRLG SLSARIRHLAYEHSVGKLRQSK HRAQDTLAQLQETLELVDHMP CGVTPTAPARPGKVHELWGEW RQRPP/REPPPE\QAELETLVLAR SLTHELQGTVEALEFSVWGLPA GAQEKVAEVRRSVDALQTAFA DARCFRDVPAAALAEGRGRVA HAHACVDELLELVVQAVPLPW LVGPFAPILVERPEPLPDLADLV DEVIGGPDPRWAHLDWPAQQR AWEAEHRDGSGNGDGDRMGV AGDICEQEPETPSCPVKHNPDA RAGLLTHGPVEAG
9829	40197	A	9890	11	285	
9830	40198	A	9891	2	138	FFFLGFHVFYSIPLIPRDNSF*GV FSSLDLITAVFVTLAELRSVT

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9831	40199	A	9892	121	2320	EMAFQKAVKGTILVGGGALAT VLGLSQFAHYRRKQMNLAYVK AADCISEPVNREPPSREAQLLTL QNTSEFDILVIGGGATGSGCAL DAVTRGLKTALVERDDFSSGTS SRSTKLIHGGVRYLQKAIMKLD IEQYRMVKEALHERANLLEIAP HLSAPLPIMLPVYKWWQLPYY WVGIKL\YDLVARKANCLKSSY VLSKSRALEHFPMLQKDKLVG AIVYYDGQHNDA\RMNLAIALT AA\RYGAATANYMEVVSL\LKK TDP\QTGK\VHVSGARCKGCPST GQEFDVRAKCVINATGPFTDSV RKMDDKDAAAI\CQPSAGVHIV MPGYYSPESMGLLDPATSDGR VIFFLPWQKMTIAGTTDTPTDV THHPIPSEEDINFILNEV\RNYLS CDVEVRRGDVLAAWSGIRPLV TDPKSADTQSISRNHVVDISESG LITIAGGKWTTYRSMAEDTINA AVKTHNLKAGPSRTVGLFLQG GKDWSPTLYIRLVQDYGLESEV AQHLAATYGDKAFEVAKMAS VTGKRWPIVGVHLVSEFPYIEA EVKYGIKEYACTAVDMISRRTR LAFLNVQAAEEALPRIVELMGR ELNWDDYKKQEQLETARK\FL YYEMGYKSRSEQLTDRSEISLL PSDIDRYKKRFHKFDADQKGFI TIVDVQRVLESINVQMDENTLH EILNEVDLNKNGQVELNEFLQL

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9832	40200	A	9893	1	2020	MLKPLMGGGAHRRAAAGARK WDGTAIIASTSGLEVLWVTTSR SKTVESVGLAKPGQHNDARMN LAIALTAARYGAATANYMEVV SLLKKTDPQTGKVRVSGARCK DVLTGQEFDVRAKCVINATGPF TDSVRKMDDKDAAAI\CQA\SA GVHIVMPGYYSPESMGLLDPAT SDGRVIFFLPWQKMTIAGTTDT PTDVTHHPIPSEEDINFILNEVR NYLSCDVEVRRGDVLAAWSGI RPLVTDPKSADTQSISRNHVVDI SESGLITIAGGKWTTYRSMAED TINAAVKTHNLKAGPSRTVGLF LQGGKDWSPTLYIRLVQDYGL ESEVAQHLAATYGDKAFEVAK MASVTGKRV/WPIVGVRLVSDF PYIEAEVKYGIKEYACTAVDMT SRRTRLAFLNLQAAEEALPRLL ELMGRELNWDDYKKQEQLET ARKFLYYEMGYKSRSEQLTDR SEISLLPSDIDRYKRRCHKFDAD QRGFMTVVEVQRVLESINVQM DENTLHEILNEVDLNKNGQVEL NEFLQLMSAIQKGRVSGSRLAI LMKTAEENLDRRVPIPVDRSCG GLYFCVRNWWVLGLTDFKNE AADPSGVKLQTFTVSVTALKV ARLELFVSPGGLVVLLGSGVKL QIFAPNMAMHNKAAPPQIPDTR RELAELVKRKQELAATLAKFG
9833	40201	A	9894	2	593	ISSAVEFETSQLSGLWTEQSAA RSRGENIVCGPQGPRG/GPWVP AEPTGSPVVSEEPLDLLPTLDLR QEMPPPRVFKSFLSLLFQGLSVL LSLAGDVLVSMYREVCSIRFLF TVVSLL\NLFLSAFWLGLLYLVS PLENEPKEMLTLSEYHERVRSQ GQQLQQLQAELDKLHKEVSTV RAANSERGAKLVFQRLNEGFV

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9834	40202	A	9895	1	1105	MRRSSRPGSASSSRKHTPNFFSE NSSMSITSEDSKGLRSAEPGPGE PEGRRARGPSCGLLFQGLSVLL SLAGDVLVSMYREVCSIRFLFT AVSLLSLFLSAFWLGLLYLVSP LENEPKEMLTLSEYHERVRSQG QQLQQLQAELDKLHKEVSTVR AANSERVAKLVFQRLNEDFVR KPDYALSSVGASIDLQKTSHDY ADRNTAYFWNRFSFWNYARPP TVILEPHVFPGNCWAFEGVQGQ VVIQLPG/HECTLSDITLQHPPPS VEHTGGANSAPRDFAVFFLLSF FTHQGLQVYDETEVSLGKFTFD VEKSEIQTFHLQNDPPAAFPKV KIQILSNWGHPRFTCLYRVRAH GVRTSEGAEGSAQGPH
9835	40203	A	9896	10	395	VEPGKRLIDRIVETICSCFQGPQ TDEGVQLQIIKALLTAVTSPHIEI HEGTILQTVRTCYNIYLASKNLI NQTTAKATLTQML/NHARSDSG KVSTENGDAPRERGSSLSGTN\ DGAQEVVKDILEDVVT

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9836	40204	A	9897	1	1698	MLGTSVEDIAQFLHQEERLDST QVGDFLGDSARFNKEVMYAYV DQLDFCEKEFVSALRTFLEGFR LPGEAQKIDRLMEKFAARYIEC NQGQTLFASADTAYVLAYSIIM LTTDLHSP/PDLEMHQPAGARS ADRNRCEDALPVWIWA*KRRE PEGPHIGRRRVHGPWPR*FGEW RSG*KTDGQLPRIGW*DQLAEC GCSCGQDFYWVYQTGWKCNS* LCPLAVCCVHG*TGFPPPSSHV QLAEDCGDIILQHESDPTTVVS NMACDWRSLQ*DKL*MLGTSV EDIAQFLHQEERLDSTQVGDFL GDSARFNKEVMYAYVDQLDFC EKEFVSALRTFLEGFRLPGEAQ KIDRLMEKFAARYIECNQGQTL FASADTAYVLAYSIIMLTTDLH SPQILKCISQLELAQLIGTGVKT RYLSGSGREREGSLKGHTLAGE EFMGLGLGNLVSGGVDKRQM ASFQESVGETSSQSVVVAVDRI FTGSTRLDGNAIVDFVRWLCA VSMDELASPHHPRMFSLQKIVE ISYYNMNRIRLQWSRIWHVIGD HFNKTSCDRLRELHVSEVFTVI TETRETKGPRDTPIFIETLVKVK DAEDQLGARVGYIELDLNSGKI LESFRPEERFPMMSTFKVLLCG AVLSRIDAGQEQLGRRIHYSQN DLVEYSPVTEKHLTDGMTVRE LCSAAITMSDNTAANLLLTTIG
9837	40205	A	9898	1	492	
9838	40206	A	9899	1	3555	
9839	40207	A	9900	1	4145	MFVLKVGCPSLLLRDPRRSLLH YTCFTSVPVLVQVGCNPNEDV AIFAVDSLRQLSMKFLEKGELA NFRFQKDFLRPFEHIMKKNRSP TIRDMAIRCIAQMVNSQAANIR SATIFQHHFPAAIDSFQDAVKCL SEFACNAAFP\DTSMEAIRLIRF CGNYL\SERPRVLLEYTSDDMN VAPGDRVWVRGWFPILFELSCII NRCKLDVRTRGLTVMFEIMKS YGHTFEKHWWQDLFRIVFRIFD NMKLPEQLSEKS

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9840	40208	A	9901	1	5477	MQESQTKSMFVSRALEKILADK EVKRPQHSQLRRACQVALAWK LLLIAPLAVGKATPVKMWSNK VEQLTVMNMHSAEQETDEIKA EIEKQRLGTAAPPKANFIEADK YFLPFELACQSKSPRVVSTSLDC LQKLIAYGHITGNAPDSGAPGK RLIDRIVETICSCFQGPQTDEGV QLQIIKALLTAVTSPHIEIHEGTI LQTVRTCYNIYLASKNLINQTT AKATLTQMLNVIFTRMENQVL QEARELEKPIQSK
9841	40209	A	9902	2	740	TGWEGRAEAEVPQDDRREPRH S/IEVEEEDQKLVSASLEPIGG/P PDCPQKPQ\PQCPLSPSKKWGC DLCL*QHKLAQKWRREISTSVP SQPGLGPGRTADTGPSLPT\TPA GQEAGRTPAPPAWSAFDLDST VVKMEKGWICS*KYTRSQASC SELPRRLGRAGPTEELGMPTQE VAPLPARG*GPESLPL/ASRQEF LSGRTVRVKLGLPLPLTEGKIV LPGGEGGSPHVCPSPWIIERRTA DQGVVAE
9842	40210	A	9903	1	1376	MPSSSVGPARPSLRGSSEQLAW LRGIFSYRSSPPPSPQQSSPNQTR SRQHYAPSVFEKYTASVTVGSK EVTLNLYDTAALAGPWPALHS WRPLRGAGCGALEAKPYTKQ WAALGPPMVPGLLRYLLWSLQ TLATPGQRPREGPHAHTPRAEA TAGQEPARDPKGSARNPEPQRP RGKGVRAAPKQGVRGMSIPAQ PHASTRAGSERRSE\QRRLLSSF TGSCDSDLLKFNQLKFRKKKLK FCKSHIHDWGLFAMEPSGDPLE SAWIHARNAPTTTPSQTPHPPPR EAGNPNPPPRAPEARGPGHDKA AQKACVHGGPNTQHPRPQPEP AVPPAALAPPPKHQLSSQASSPS RLGRAAERPHKTQQRQTPTHT GPRAAATAEHAPQALPPPAPAP HYNRTRPAQLRNPPTPKKGSEE PAQPTKHTPATPAKRDPKGGG ARRRPARPLQPHSGGEEDEKES

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9843	40211	A	9904	724	2076	KLCPCLYHFFHTNVQRHAPFVA NPFLLTHIQISTKHPAIVGTTELL LCVGGVQRVLQLAPQRLQLLA QVPALLLRLGPGHTLRLQVLLG LGQGCLSLPQGFQQLGPGPTLV FCPLPELLEEDAVGEALATDAD ALQDPVAAKLVQHQPWLQLPG LGKQPPPLPVSQLEVGRAVPLH HPQGALLLLALLEGLQSLLPRV HSPFLHDTFRRHRPVPASLQLN SFEQLCITTPQKLQQLFNHTMF VSPPAVNVQANPAGLLALLDEE CWFPKATDKSFVEKVAQEQGG HPKFQ\RPRHLRDQADFSVLHY AGKVDYKANEWLMKNMDPLN DNVAALLHQSTDRLTAEIWKD VEGIVGLEQVSSLGDGPPGGRP RRGMFRTVGQLYKESLSRLMA TLSNTNPSFVRCIVPNHEKRAG KLEPRLVLDQLRCNGVLEGIRI CRQGFPNRILFQEFRQ
9844	40212	A	9905	2	480	VGCMGCSKGPWRQAFQVDVH VSDLALPQCRLQTGMRGAFGK PQGTVARVHIGQVIMSIRTKLQ NKEHVIEALRRAKFKFPGRQKV CSAAAPFSHLCPRPPDSVLSIAP *IHISKKWGFTKFNADEFEDMV AEKRLIPDGCGVKYIPSRGPLD KWRALHS
9845	40213	A	9906	1	485	SDEYDQLCSEALVGAQICAKK YIVKCCGKNGFHIRVRLHPFHV ICINRMLACAGTDRLQTGMGG AIGKP\QGTVARILIGQVIMSIRT KLQNKEHVIEALRRAKFKFPGR QKIHISKKWGFTKFNADEFEDM VAEKRLIPDGCGVKYIPSRGPL DKWRALHS
9846	40214	A	9907	198	452	DYYLEGLINHIVHHDHFLNLQN HSSNLPVAEICYR*RYRKKVQQ RIIIAKDYTTELFSNR*LFN

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9847	40215	A	9908	2	1968	SYLHCKWATMEELEKDPRIAQ KIKRFRNKQAQMKHIFTEPDED LFNPDYVEVDRILEVAHTKDAE TGEEVTHYLVKWCSLPYEEST WELEEDVDPAKVKEFESLQVLP EIKHVERPASDSWQKLEKSREY KNSNQLREYQLEGMNWLLFN WYNRKNCILADEMGLGKTIQSI TFLSEIFLRGIHGPFLIIAPLSTIT NWEREFRTWTEMNAIVYHGSQ ISRQMIQQYEMVYRDAQGNPL SGVFKFHVVITTFEMILADCPEL KKIHWSCVIIDEAHRLKNRNCK LLEGLKLMALEHKVLLTGTPLQ NSVEELFSLLNFLEPSQFPSETA FLEEFGDLKTEEQVKKLQSILKP MMLRRLKDDVEKNLAPKQETII EVELTNIQKKYYRAILEKNFSFL TKGANQHNMPNLINTMMELRK CCNHPYLINGAEEKILEDFRKT HSPDAPDFQLQG\MIQA\AGKL VLIDKLLPKLIAGGHKVLIFSQM VRCLDILEDYLIQRRYTYERIDG RVRGNLRQAAIDRFCKPDSDRF VFLLCTRAGGLGINLTAADTCII FDSDWNPQNDLQVPEGRIQKV WEQMSWPRAQPQDNAAAACL QDFGSQLGVQSEETGPFHNRQK QDSGNSHTAPRGRESFIKPPSSR DLLPLKIQKEGPATNYNS
9848	40216	C	9909	223	402	

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9849	40217	A	9910	1	1710	MFEKAARQEWIQVAKSVTRVA MSSYTFQKNPDLISVGEDVEKK LELSYAAVTMAWGQYGDYGY PYQQYHDYSDDGWVNLNRQG FSYQCPQGQVIVAVRSIFSKKE ADSVSRASATGPDSGQFFLLER VGTCKTTAEAQPQRDDPYLVT RTVEGLSRTVEGVGRGLTQAA AGEGAGAVEAAW/NSLCGPFSS TPMASDEETEAIRGHETRPDDT AKNSGAIQQHSQCSWPLYY/RA PHSVKRYQTCSNNGLVAGFQS RYFESVLDREWQFYCCRYSKR CPYSCW/LSLAADQTLMTPGVG EAPRKCSSFRKGNRTIEPALTGP KSPTYSVGMPSLKLRPNDSHPS AVLLLPNFWLTTEYPGHYGEE MDMISYNYDYYIRGATTTFSAV ERKEERRERKGIGDKKHTEPTV LVWAAIPHYLRLGNLRTIEIYFH SSGSWKVQDQVDPEEEPARQN HRDRVPCHTPPLGGQEGDSQPV VMRAKDHYELEKQKALGQVE DEEDLCQQQRLPEQTYGSEEAP QEAKKNLGSPEPNSQAGAQKPI SMATNRAVFDVTCNFSPHWLQ CLQSRSLSPEDPGL
9850	40218	B	9911	101	1237	
9851	40219	A	9912	1	622	NLSDRHRGSHLESQHFQRLKQE DLLSPRIQDQPGQHWETLSHINI VVIGHVDSGKSTTTGHLIYKCG GIDKRTIEKFEKEAAEMGKGSF KYAWVLDKLKAER\ERGITIDIS LWKFETSKYYVTIIDAPGHRDFI KNMITG\TSQADCAVLIVAAGV GEF\EAGISK\NGQT\REHALPG/ YSQKRYEEIVKEVSTYIKKIGYT PDTVACVP
9852	40220	A	9913	1	762	VVQTQISKTADELISYWGTSFPP PFAASLTLYELEYCITIDISLWK FETSKYYATVIDAPGHRDFIKN MITGTSQADCAVLIFAAGVGEF EAVTFAPVNVTTEVKSVEMHH EVLSEALPGDNVDFDVKNVSV KEVHHGNVAGQISAGCAPVLD CHMAHIACKFAKLKKKTGSTS GKKLEDGPTFLKSGDAAIVDM VPGKPMCVESFSVYPPLSRFAV CDMRQTVAVGVIEAMDKMAA\ GAGKVTMSAQKAHNAK

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9853	40221	A	9914	1	618	MVQARPGAHPTLLPGPTAAWV SGFSGGGSDLTGAREAQERGR WSPTESSSASVSPVAKVSKFTLS SELEGGDYPKERERTGGGPGRP PDWTPHGTGA\LQSPHPRTAPA PHPTPCPGRPRDAGQRSPGAPA WSPRVHRPTPSLLPPRRWTAAA LWAAWQRPLPASQPGRGTSPG NPGPGRTPPSPQEVGSPGHIHIS LRTGFPPTL
9854	40222	C	9915	3	406	
9855	40223	A	9916	1379	2096	NGGGCGAARGGAAPGEGTRRG ACWATRGLPGTGRSAAAPARR GERQQLAMDVFLMIRRHKTTIF TDAKESSTVFR/ELKRIRRGQSS KRPPDEQRL\YK\DDQLLD\DG\ KTLGECGF\TSQNRHRPQAPAT VGSGLPASSAASSTDDTFEALCI EPFSS\PPEL\PDVDGRPQGFGEG SAQLNKAVQVETPQEGPIFPQL KGDLGSLPGCCLFFPPLPGMGP TPCGLLLGLVLGSSCAVLSPRS
9856	40224	A	9917	1	695	MAHAGRTGYDNREIVMKYIHY KLSQRGYEWDAGDVGAAPPG AAPAPGIFSSQPGHTPHPAASRD PVARTSPLQTPAAPGAAAGPAL SPVPPVVHLALRQAGDDFSRRY RGDFAEMSSQLHLTPFTARGRF ATVVEELFRDGSVNREMSPL\V DNIALWMTEYLNRDLHTWIQD NGGWPWDFLIGATTPVTIPYLP YHSTEECQLINVKGTAEFKIPFA KPDEMIQAKIIDGC
9857	40225	A	9918	3	422	CSLKNWREVLALLLTYSGTEKF PELC\DLMEKVMVLNRSLEQLR GPH/GGSAVLGQQSPPFPFPRIV VGATLHSKETSSYRLGSQPSHQ VPTPSPRPRVFTPQSSPAMPLAP SHPSPYQGPRTQNISDYRAPGP QAIQPLPL
9858	40226	A	9919	1	849	

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9859	40227	A	9920	3	868	NSSPPFPFPRIVVGATLHSKETS SYRLGSQPSHQVPTPSPRPRVFT PQSSPAMPLAPSHPSPYQGPRT QNISDYRAPGPQAIQPLPLSPGV RPGPQDSWKEAPAPRGNLQRN KLPETFMPPAPITGPS/IM/RPHP* ATRDSSLTAPLSPV*VMLPQEF QENS\PAGDKDNVFPSLGKPPSP PCVQVMVDGPHSSR/PCAEGD WVQVPGVLTAEKGRLLISPTLL *WEQCDCESLGTSP*GSHEKDS LPLWPFSLLLYQQLQHLPPEKM ERKELPPEHQSLKSSFEALLQRC
9860	40228	A	9921	1	307	MKLKELERPAVQAWSPASQYP LYLATGTSAQQLDSSFSTNGTL EIFEVDFRDPSLDLKHRGVLSA LSRFHKLVWGSFGSGLLESSGV IVGGGDNGMLILYNVTHILSSG KEPVIAQKQKHTGAVRALDLN PFQPPEDIKALSWNRQAQHILSS AHPSGKAVVWDLRKNEPIIKVS DHSNRMHCSGLAWHPDIATQL VLCSEDDRLPVIQLWDLRFASS PLKVLESHSRGILSVSWSQADA ELLLTSAKDSQILCRNLGSSEPC PRLVFISQVTTESEFLMRSAELQ EALGSGNLLNYCQNKSQQALL QSEKMLWQFLKVTLEQDSRMK FLKLLGYSKDELQKKVATWLK SDVGLGESPQPKGNDLNSDRQ QAFCSQASKHTTKEASASSAFF DELVPQNMTPWEIPITKDIDGLL SQALLLGELGPAVELCLKEERF ADAIILAQAGGTDLLKQTQERY LAKKKTKISSLLACVVQKNWK DVVCTCSLKNWREALALLLTY SGTEKFPELCDMLGTRMEQEGS RALTSEARLCYVCSGSVERLVE CWAKCHQALSPMALQDLMEK VMVLNRSLEQLRGPHGVSPGP ATTYRVTQYANLLAAQGSLAT AMSFLPRDCA/PAARDIYAPSTN YCSSYEPHP*ATRDSSLTAPCLQ SASAPAT*EDGKEGAAPRASVL EEQL*GASPTLLPVCN*LKDKK

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9861	40229	A	9922	3	2751	SVSWSQADAELLLTSAKDSQIL CRNLGSSEVVYKLPTQSSWCFD VQWCPRDPSVFSAASFNGWISL YSVMGRSWEVQHMRQADKISS SFSKGQPLPPLQVPEQVAQAPLI PPLKKPPKWIRRPTGVSFAFGG KLVTFGLPSTPAHLVPQPCPRL VFISQVTTESEFLMRSAELQEAL GSGNLLNYCQNKSQQALLQSE KMLWQFLKVTLEQDSRMKFLK LLGYSKDELQKKVATWLKSDV GLGESPQPKGNDLNS
9862	40230	A	9923	363	543	
9863	40231	A	9924	2	737	EAETEYFVRCIKHMFTNHIVFQ LFHLLTFQFDCTNTLNDQLLEK VTVQMEPSESYEVLSCIPAPSLP YNQPGICYTLVRLPDDDPTAVA GSFSCTMKFTVRDCDPNTGVPD EDGNDDEYVLEDLEVTVSDHIQ KVLKPNF\AAAWEE\VGDT\FEK EETFALSSTKTLEEAVN\NIITFL GMQPCERS\DKVPENQD\SHSL YLAGIFRGGYDL\LVRARLALA DGVTMQVTVRCKHRTPVDIILA
9864	40232	A	9925	327	464	GSPTTRPAKPLTLSSGHLRSRPR WAEGPQYHLP*ISAPRAKLGV MM
9865	40233	A	9926	2	1179	WQPDIGPYGGLLNVVVDGLFII GWMYLPPHDPHVDDPMRFKPL FRIHLMERKAATVECMYGHKG PHHGHIQIVKKDEFSTKCNQTD HHRMSGGRQEEFRTWLREEWG RTLEDIFHEHMQELILMKFIYTS QYDNCLTYRRIYLPPSRPDDLIK PGLFKGTYGSHGLEIVMLSFHG RRARGTKITGDPNIPAGQQTVEI DLRHRIQLPDLENQRNFNELSRI VLEVRERVRQEQQEGGHEAGE GRGRQGPRESQPSPAQPRAEAP SKGPDGTPGEDGGEPGDAVAA AEQPAQCGQGQPFVLPVGVSSR NEDYPRTCRMCFYGTGLIAGH GFTSPERTPGVFILFDEDRFGFV WLELKSFSLYSRVQATFRNAD APSPQAFDEMLKNI\QSLTS
9866	40234	A	9927	287	537	TGKFPSC/CLLSFYGTGLIAGHG FTSPERTPGVFILFDEDRFGFVW LELKSFSLYSRVQATFRNADAP SPQAFDEMLKNIQSLTS
9867	40235	A	9928	1	3651	

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9868	40236	A	9929	1	3720	MEEMFGGGAADDYGKAGPPE DEGDPKAGAGPPPGPPAYDPY GPYCPGRASGAGPETPGLGLDP NKPPELPSTVNAEPLGLIQSGPH QAAPPPPPPPPPPPAPASEPKGG LTSPIFCSTKPKKLLKTSSFHLL RRRDPPFQTPKKLYAQEYEFEA DEDKADVPADIRLNPRRLPDLV SSCRSRPALSPLGDIDFCPPNPG PDGPRRRGRKPTKAKRDGPPRP RGRPRIRPLEVPTTAGPASASTP TDGAKKPRGRG
9869	40237	A	9930	503	739	QGWRRRRPISKISESRNMQNFL HALSNCLPEGGA*DRCSSRLEE GRQLPPLLLGSLQVAKKSGGTG WMVRCSQCLFLG
9870	40238	A	9931	1	1148	MGGKGDDSWVISATPLGKCCA AVPLGGNPTLRVDQLWRKQRP PLQQCTASAPGGWVTSLMGAG THAANTGFQLVWSSKRPMYKV LQAFFGVQRSDRSAMNGQGFS KCVGMPITHTRQQADLGRGPE ETEDKKQQSRGSDELRSEGEEP EPYLLRTSK\VKDKERILKAARE MKQIIYNGAPIHLAADFSVETL QAKKEWCDIFKVLKKKTFYPK MVLTAGPSHPQSVISVSFTGLA NAASLTMSPDLHGQPGFAGLSS VAAVDWQWALLRPSPPQGRM GLLPICQATQGPQLCVASPSDK EGFLLLFGKEIARLTNKGGARL YKCDIVQGVCCEDPLATLDWE LRPDLEQGERPTPERHKPFLLG KSFSAPLIKICRYEWQMF
9871	40239	A	9932	333	689	NSFLTCILPPVSI*TDLLQPSAQ WKQLSLARRNVHSTRLAGARR CAASGPSPVAAHCYHPVSGHSR LLHGCQHGHWGSWQVPEVPPG SPFSLAPVWKRRQTALPAILHL PVEHYYPEL

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9872	40240	A	9933	84	933	PLTSPEAFSNRCGLRGPP\PCVP VGRLQF\NDVSSLGICLPDSSCC SSWHGPHSLHH/HVQACKASIR ASGTAASANCAFSRYHVHCSIA FQIKVLHNLIVLTVIIPAAEHMA WGPGIAQPNPPHRASGHSSWGP EVGPKLSTTAILVGTYPQVPPV GLETGPPSLFQPLPISTHTAWNT ENCPANATVIAHPTLAAQGTKN PPTLLVHHCHYQHLSLKDDGT RRENSLKLGEGKVILQTEGIQK GMDPTMEYATNYWKKLQLWK RRQTALPAILHLPVEHYYPEL
9873	40241	A	9934	1	627	MESLDTETSTWGECHRKIRGM VPQVKELAEEEEAPPDGAVAE YRREKQKYEALRKQQSKKGTS REDQQIIIKNLPCTNHCIWQSTH EHIPALSDLSGKRAKQVIPVKG GEHYERTLALLNQFKSKLTQAI AETPENDIP\ETEV\EDDEGWMS HVL\QFEGKSRKSGKVPSMQDS DTFEIYDPRNP/LVNKRREGKK AKSLMREKKERRLK
9874	40242	A	9935	1	371	PMRPAFTRVEMARVLMERNQY KERLMELQEAVRWTEMIRASR EHPSVQEKKKSTIWQFFSRLFSS SSSPLRPKRPYPSVNIHYKSPTE GCSV\AAGFSPPPCHLHCDVCPL PRLFPQDLEVTPG
9875	40243	A	9936	2	186	
9876	40244	C	9937	109	408	
9877	40245	C	9938	161	341	
9878	40246	C	9939	303	439	
9879	40247	C	9940	201	419	
9880	40248	C	9941	122	307	
9881	40249	A	9942	3	80	YNPAPYKEKTITL/PCPRKLGPP QGS/S*NGPPSSSSSSQCSVSFND PHLPEGQVQAAR*WAPPGIL
9882	40250	C	9943	249	427	
9883	40251	A	9944	90	244	TVVPHDPCGTDAHVCETHMD MCPSHSVMLCGWLTFAEFRGA MGEGGRESFLLNQASFCY*CSQ AGFSSNLWRCSRAGRGNTADE LWCHMTLVAQMPTYVKHTWT CVPATVLCSVAGSPLLSSGVQW GREGGKASS
9884	40252	C	9945	4	204	
9885	40253	C	9946	340	497	
9886	40254	C	9947	158	184	

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9887	40255	A	9948	200	386	LFYTME*IMAFLLSSSSSPGRPF* RILGGAKVYAGMQRYSFFLIGS RIITYLGIFGRELYFC
9888	40256	B	9949	47	622	
9889	40257	A	9950	1	630	
9890	40258	A	9951	1	782	
9891	40259	A	9952	1	677	MHGLGRWDACPQDEMSESGQ SSAAATPSTTGTKSNTPTSSVPS AAVTPLNESLQPLGDYGVGSK NSKRAREKRDSRNMEVQVTQE MRNVSIGMGSSDEWSDVQDIID STPELDMCPETRLDRTGSSPTQ GIVNKAFGINTDSLYHELSTAG\ S*VIGDVDEGADLLGNNDRKK VYTSVQTRPPQACTFSVRLVES THAELVGIEGRLYHKIHPLRVH GAVGYSVLT
9892	40260	C	9953	202	366	
9893	40261	A	9954	1	2429	MKEGGWGCDPVGRGVTSGHV LQMKLLPFRQKKAHIMEIQLNG GTVAEKVAWAQARLEKQVPV HSVFSQSEVIDVIAVTKGRGVK GVTSRWHTKKLPRKTHKGLRK VACIGAWHPARVGCSIARAGQ KGYHHRTELNKKIFRIGRGPHM EDGKLVKNNASTSYDVTAKSIT PLGGFPHYGEVNNDFVMLKGC IAGTKKRVITLRKSLLVHHSRQ AVENIELKFIDTTSKFGHGRFQT AQEKRAFMADGLSLSPAASDS DYPPGEMFLDSDVNPEDPGAD GVLAGITLVGCATRCNVPRSNC SSRGDTPVLDKGQGEVATIANG KVNPSQSTEEATEATEVPDPGP SEPETATLRPGPLTEHVFTDPAP TPSSGPQPGSENGPEPDSSSTRP EPEPSGDPTGAGSSAAPTMWLG AQNGWLYVHSAVANWKKCLH SIKLKDSVLSLVHVKGRVLVAL ADGTLAIFHRGEDGQWDLSNY HLMDLGHPHHSIRCMAVVYDR VWCGYKNKVHVIQPKTMQIEA SAGQGPGEGKRLLLASSSPASSI RKSTRPTHDST\KSFDAHPRRES QVRQLAWIGDGVWVSIRLDST LRLYHAHTHQHLQDVDIEPYVS KMLGTGKLGFSFVRITALLVAG SRLWVGTGNGVVISIPLTETVV LHRGQLLGLRANKTSPTSGEGA RPGGIIHVYGDDSSDRAASSFIP

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9894	40262	A	9955	9	452	KIKVLSKNSQVTDFPVPTLLND GQCLGYNSTPYKEKAITL/PCPR KLGPPQGSFKTA/APSSSSPSFNF FNGSQNSVTNFWSSCFH*KVLI LKTNNLKLPHAKKKTKVV/LQ NILLSF*RFYDALLSLTSLLLLN LNGQLKQTVMRPFFHH
9895	40263	A	9956	1	3223	ATATPSTTGTKSNTPTSSVPSAA VTPLNESLQPLGDYGVVSKNSK RAREKRDSR\NMEVQVTQEMR NVSIGMGSSDEWSDVQDIIDST PELDMCPETRLDRTGSSPTQGI VNKAFGINTDSLY\HELSTAGS\ EVIGDVDEGADLLGEFSGMGK EVGNLLLENSQLLETKNALNV VKNDLIAKVDQLSGEQEVLRG ELEAAKQAKVKLENRIKELEEE LKRVKSEAIIARREPKEEAEDVS SYLCTESDKIPMAQ
9896	40264	B	9957	176	658	
9897	40265	A	9958	2	5671	AGGPCVRSSRELWTILLGRSAL RELSQIEAELNKHWRRLLEGLS YYKPPSPSSAEKVKANKDVASP LKELGLRISKFLGLDEEQSVQLL QCYLQEDYRGTRDSVKTVLQD ERQSQALILKIADYYYEERTCIL RCVLHLLTYFQDERHPYRVEY ADCVDKLEKELVSKYRQQFEE LYKTEAPTWETHGNLMTERQV SRWFVQCLREQSMLLEIIFLYY AYFEMAPSDLLVLTKMFKEQG FGSRQTNRHLVDETMD
9898	40266	A	9959	1	404	MVDQEAIFGCKNRNNCSHLEPP VSRLEGGAFVRDLLSPTQYLLA SCPYQYDGSFVIQQIPSSNLFMV VVDSSCLCESVAPITMAPIEIRYI LLC\EVHSLPRKPENARECGGA PSL\QAQTVLLLLPLLLMLFSR
9899	40267	A	9960	1	1374	
9900	40268	A	9961	102	205	

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9901	40269	A	9962	1	1527	MVPDAAVLAQLAIRARVNRRW PTGLSAPHLCGAACSRCRHAAI AKYFGDALPACAKGCDHCQNP TAVRRRLEALERSSSWSKTCIG PSQGNGFDPELYEGGRKGYGG FSRYDEGSGGSGDEGRDEAHK REWNLFYQKQMQLRKGKDPKI EEFVPPDENCPLKEASSRRIPRL TVKAREHCLRLLEEALSSNRQS TRTADEAD\FRAKAVELEHETF RNAKVANLYKASVLKKVADIH RASKDGQPYDMGGSAKSCSAQ AEPPEPNEYDIPPASHVYSLKPK RVGAGFPKGSCPFQTATELMET TRIREQAPQPERGGEHEPPSRPC GLLDEDGSEPLPGPRGEVPGGS AHYGGPSPEKKAKSSSGGSSLA KGRASKKQQLLATAAHKDSQS IARFFCRRVESPALLASAPEAEG ACPSCEGVSGTPDWPQRSTQGR KMEPGDIRLPLPRLRSASGRGQ APARPETRAPLKSSPPLQRTHG KGKRPRFPARRTQRASLRRGHA PQPIPPS
9902	40270	A	9963	2	99	
9903	40271	A	9964	115	1360	ENGQLHMVNLALDGVRSSLQK PRPFRLFPKGFSVELCMNREDD TARKEKTDHFIFTYTREGNLRY SAKSLFSLVLGFISDNVDHIDSLI GFPEQIAEKLFSAAEARQKFTEP G\AGL\RALQKFTGGLWEVWVL CSLCFLLWKLPDICCKLGDEHE LLEHLTNEALSRY*PVTTCR*IV SVLF*RLIQQDYRVMKRGLENL TLLDLSCKFSSKL*IILMLEEWP *RSCSSFSGTGLKVRLLVPSLIFL DSTI*YFACANWEFDHSNCKTE GWADQVLQIFLPCG*CSFSS*FQ VSYPTSRETAESCFRSTLSLVQN MHDEAAQRFCEKFPFL*SFLPFI CILKAVRLF*KLQFYKEKAPDC HGPVLKHEAISSQESKKSKKRP FEESETEQNNSSQPSKQKYVCL AVEDWDLLNSY

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9904	40272	A	9965	3	1026	DNVDHIDSLIGFPEQIAEKLFFA AEARQKFTEPGAGLRALQKFTE AYGSLVLCSLCLRNRYLVISEK LEEIKSFRELTCLDLSCCKLGDE HELLEHLTNEALSSVTQLHLKD NCLSDAGVRKMTAPVRVMKR GLE\NLTLL\DLSCNP\EITGGRA LGYPLFLFRGNLN\CFRDISGDR GSRDIKTL\KHKLQTHIGLVHSK VPLKEFDHSNCKTEGWADQIV LQWERVTAEAVKPRETSEPIAA AQRFYGKRSRAEAPLK\CPLAD TH\MNSS\EKLQ\FYKEKAP\DCH GP\VLKHEAISKPRSPKKSKKRP FEESETEQNNSSQPSKQKYVCL AVEDWDL\LNSY
9905	40273	A	9966	1	289	VKHCLHRPILWDPWKTSGIQQ VLTPL*KAMEKLEAILLIICSLE AIGLITLPSLSMTQFLQLHVECC YVSPDQTPYFIDVETEAMKDEV TVHNPHG
9906	40274	A	9967	1	1413	MVVPPNIAELKNLEVLNFLNNQ IEKLPTQISRLQKLKHLNLGFLS PCNSMNRLNISPQGFGSLPALE VLDLTYNNLNENYLPGNFFYLT TLCALYLSDNDFEILPPDIGKLT KLQILSNRDNNLISLPKEIRVLT QLKELHIQGNRLTVLPPELGSR GGSGSRFSAETATGGAQNAPPS VLGSAGTIFK\QRRNPSPAALRG GSVAA*PSPAAAKYGKDQREH LPTAAGDGVGWEPTRDIQVGS ATAQALSQANAARGRLSTAQA AGSLHVECCYVSPGQTLYFTDV EIEAMKDESRGISILYKHRHLK VPLDQKLPKSKGHQPDGYGQH DHKPQMTSLTRNIATLR
9907	40275	A	9968	1	619	MNRLNISPQGFGSLPALEVLDL TYNNLNENYLPGNFFYLTTLCA LYLSDNDFEILPPDIGKLTKLQI LSNRDNNLISLPKEIRVLTQLKE LHIQGNRLTVLPPELASSSRCGP LSHPYAGKRIPRNAVFKFEQNT\ PWHTPPKKAGREMLLDVTGFP EAATSKPPAFLHRRRGRGSWNP RSRSSSLQRTPWPPGSREAEYPP ASGA

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9908	40276	A	9969	810	1672	GLPSVTMSKSLKKLVEESREKN QPEVDMSDRGISNMLDVNGLF TLSHITQLVLSHNKLTMVPPNIA ELKNLEVLNFFNNQIEELPTQIS SLQKLKHLNLGMNRLNTLPRG FGSLPALEVLDLTYNNLSENSL PG\NFFYL\TTL\RALYLSDN\DF EILPPDIG\KL\TKLQILSLRDNDL ISLPKEIGELTQLKELHIQGNRL\ TVVPPEL\GNLGF*LGQKQVFK AENNPWVTPIADQFQLGVSHVF EYIRSETYKYLYGRHMQANPEP PKKNNDKSKKISRKPLAANNR
9909	40277	C	9970	120	347	
9910	40278	A	9971	2	10018	LCVSPVTAGRPARSLREMEVEQ EQRRRKVEAGRTKLAHFRQRK TKGDSSHSEKKTAKRKGSAVD ASVQEESPVTKEDSALCGGGDI CKSTSCDDTPDGAGGAFAAQP EDCDGEKREDLEQLQQKQVND HPPEQCGMFTVSDHPPEQHGM FTVGDHPPEQRGMFTVSDHPPE QHGMFTVSDHPPEQRGMFTISD HQPEQRGMFTVSDHTPEQRGIF TISDHPAEQRGMFTKECEQECE LAITDLESGREDEAGLHQ
9911	40279	A	9972	2	5196	APLDGEVELLQQKLREKLDEFN ELAIQKESADRQVLMQEEEIKR LEEMNINIRKKVAQLQEEVEKQ KNIVKGLEQDKEVLKKQQMSS LLLASTLQSTLDAGRCPEPPSGS PPEGPEIQLEVTQRALLRRESEV LDLKEQLEKMKGDLESKNEEIL HLNLKLDMQNSQTAVSLRELE EENTSLKVIYTRSSEIEELKATIE NLQENQKRLQKEKAEEIEQLHE VIEKLQHELSLMGPVVHEVSDS QAGSLQSELLC
9912	40280	A	9973	1	8277	GEFGSEKKTALHEKEETLRLQS AQAQPFHQEEKESLSLQLQKKN HQVQQLKDQVLSLSHEIEECRS ELEVLQQRRERENREGANLLS MLKADVNLSHSERGALQDALR RLLGLFGETLRAAVTLRSRIGE RVGLCLDDAGAGLALSTAPAL EETWSDVALPELDRTLSECAEM SSVAEISSHMRESFLMSPESVRE CEQPIRRVFQSLSLAVDGLMEM ALDSSRQLEEARQIHSRFEKEFS FKNEETAQVVRKHQ
9913	40281	A	9974	1	393	

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9914	40282	A	9975	2	153	
9915	40283	A	9976	184	790	KFTKHISMNQEDLDPDSTTDVG DVTNTEEELIRECEEMWKDME ECQNKLSLIGTETLTDSNAQLSL LIMQVKCLTAELSQWQKKTPE TIPLTEDVLITLGKEEFQK\RGQ DLEMVLSTKESKNEKLKEDLER EQRWLDEQQQIMESLNVLHSE LKNKVETFSESRJFNELKTKML NIKEYKEKLLSTLGEFLEDHFPL
9916	40284	C	9977	23	217	
9917	40285	A	9978	25	100	
9918	40286	A	9979	1	2850	
9919	40287	A	9980	108	1132	HPHQVETSRDVAGEQSHAVAF MSTGISQADVCRLEWFSAPNLK GRPRKKKPCPQRRDSFSGVKDS NNNSDGKAVAKVKCEARSALT KPKNNHNCKKVSNEEKPKVAI GEECRADEQAFLVALYKY\MK ERKTRIERIPYLGFNQINLWTMF QAAQKLGGYETITARRQWKHI YDELGGNPGSTSAATCTRRHYE RLILPYERFIKGEEDK\PLPPIKP RKQENSSQENENKTKVFGTKRI KHEIPKSKKEKENAPKPQDAAE VSSEQEKEQETLISQKSIPEPLPA ADMKKKIEGYQEFSAKPLASR VDPEKDNETDQGSNSEKVAEE AGEKGPTPPLPSAPL
9920	40288	B	9981	177	3543	
9921	40289	B	9982	63	374	

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9922	40290	A	9983	1	2023	MGGGSWAPTGLCPLQSLLAMS PEKRKLAAQEGQFTEPRPEEPP KEKLHTLEEFSYEFFRAPEKDM VSMAVLPLARARGHLWAYSCE PLRQPLLKRVHANVDLWDIAC QIFVDILPHQPACTSAVVGVSV YPQSVSAWSCPSTVLLDSHT\IL RYMGDYPSRQAWPTLELTDQIF TLALQHPALQDEVYCQILKHLT HNSDRHSEERGWQLLWLCTGL FPPSKGLLPHAQKFIDTRRGKLL APDCSRRIQKVLRTGPRKQPPH HVEVEAAEQNVSRICHKIYFPN DTSEMLEVVANTRVRDVCDSI ATRLQLASWEGCSLFIKISDKVI SQKEGDFFFDSLREVSDWVKK NKPQKEGEEASVELGEGVAGW VEGALAASVRPMPIHPSIRSRVS LGCGNNQALGPGGAPVTLPYQ VYFMRKLWLNISPGKDVNADT ILHYHQELPKYLRGFHKCSRED AIHLAGLIYKAQFNNDRSQLAS VPKILRELVPENLTRLMSSEEW KKSILLAYDKHKDKTVEEAKV AFLKWICRWPT\FGSAFF/EGEG KPCPTPGPPTQAASAQPSPSRPS VNQHTSWQTSEPSYPDVILIAIN RHGVLLIHP\KTKDLLTTYPFTK ISSWSSGSTYFHMALGSLGRGS RLLSET\SLGYKMDDLLTSYVQ QLLSAMNKQRGSKAPALAST

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9923	40291	A	9984	428	2502	VSKEIVYNKLLPYAERLDAESD LQLAQIKCNLGRAVQLQELWP GGLFWTRKLS/TRAGPLALSSLE LSPSGDPRVVTEPVKYSSRPPCH FPTGLPGSLPSLYVLRICFSRSV RVVVFPPGGPWVAQGPRPRGR ETWGFTMLLRYIRLYGRKFSKE DHVLFIKLLYELVSIPKLEISMM QGFARLLINLLKYFPADATAEM LEEWRPLMCPFDVTMQKAITY FEIFLPTSLPPELHHKGFKLWFD ELIGLWVSVQNLPQWEGQLVN LFARLATDNIGYIDWDPYVPKG GPSKLVQKHLAGLFNSITSFYH PSNNGRWLNKLMKLLQRLPNS VVRRLHRERYKKPSWLTPVPDS HKLTDQDVTDFVQCIIQPVLLA MFSKTGSLEAAQALQNLALMR PELVIPPVLERTYPALETLTEPH QLTATLSCVIGVARSLVSGGRW FPEGPTHMLPLLMRALPGVDPN DFSKCMITFQFIATFSTLVPLVD CSSVLQERNDLTEVERELCSAT AEFEDFVLQFMDRCFGLIESSTL EQTREETETEKMTHLESLVELG LSSTFSTILTQCSKEIFMVALQK VFNFSTSHIFETRVAGRMVADM CRAAVKDWGKPGDLWNLGIQ WHVPSSEEVSFAFYLLDSFLQP ELVKLQHCGDGKLEMSRDDIL QSLTIVHNCLIGSGNLLPPLKGE
9924	40292	A	9985	2	5396	AESDLQLAQIKCNLGRAVQLQE LWPGGLFWTRKLSTYIRLYGR KFSKEDHVLFIKLLYELVSIPKL EISMMQGFARLLINLLKKKELL SRADLELPWRPLYDMVERILYS KTEHLGLNWFPNSVENILKTLV KSCRPYFPADATAEMLEEWRP LMCPFDVTMQKAITYFEIFLPTS LPPELHHKGFKLWFDELIGLWV SVQNLPQWEGQLVNLFARLAT DNIGYIDWDPYVPKIFTRILRSL NLPVGSSQVLVPR
9925	40293	A	9986	1	477	VREFPGRRFRGCCGALRPRYKR LVDNIFPEDP\GYVCIAMEALDQ LLMACHCQSINLFVESFLKMVA KLLESEKSNLQILGTNSFVKFA NIEEDTPSYHRSYDFFVSRFSEM CHSSHDDLEIKTKIRMSGIKSLQ GVVRKTVNDELQANIWDPQH

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9926	40294	A	9987	1	2371	AGGARLRPARGRPPRLLPPRPG PCRPPPVPAPTVNERRAPPRAG WERRSDAGLSRGARPAEMYGV CGCCGALRPRYKRLVDNIFPED PEDGLVKTNMEKLTFYALSAPE KLDRIGAYLSERLIRDVGRHRY GYVCIAMEALDQLLMACHCQS INLFVESFLKMVAKLLESEKPN LQILGTNSFVKFANIEEDTPSYH RSYDFFVSRFSEMCHSSHDDLEI KTKIRMSGIKGLQGVVRKTVN DELQANIWDPQHMDKIVPSLLF NLQHVEEAESRSPSPLQAPEKE KESPAELAERCLRELLGRAAFG NIKNAIKPVLIHLDNHSLWEPK VFAIRCFKIIMYSIQPQHSHLVIQ QLLGHLDANSRSAATVRAGIVE VLSEAAVIAATGSVGPTVLEMF N\TLLRQLRLSIDYALTGSYDGA VSLGTKIIKEHEERMFQEAVIKT VGSFASTLPTYQRSEVILFIMSK VPRPSLHQAVDTGRTGENRNR LTQIMLLKSLLQVSTGFQCNNM MSALPSNFLDRLLSTALMEDAE IRLFVLEILISFIDRHGNRHKFSTI STLSDISVLKLKVDKCSRQDTV FMKKHSQQLYRHIYLSCKEETN VQKHYEALYGLLALISIELANE EVVVDLIRLVLAVQDVAQVNE ENLPVYNRCALYALGAAYLNLI SQLTTVPAFCQHIHEVIETRKKE APYMLPEDVFVERPRLSQNLDG
9927	40295	A	9988	1	662	IPGSTISWSPAAARGLSVCRCCR LHPASAMDLFGDLPEPERSPRP AAGKEAQKGPLLFDDLPPASST DSG/SSLQALPGSGGPLLFDDLP PASSGDSGSLATSISQMVKTEG KGAKRKTSEEEKNGSEELVEK KVCKASSVIFGLKGYVAERKGE REEMQDAHVILNDITEECRPPSS LITRVSYFAVFDGHGGIRASKF AAQNLHQNLIRKFPKGDVISVE

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9928	40296	A	9989	3	1145	KEAQKGPLLFDDLPPASSTDSA VAALGTTPSPVTLWFLQTRRGS KIWRNSLDYQSKVGAEPWCHE RQQKADRFLGKRGRVPASSVIF GL\KGYVAERKGEREEMQDAH VILNDITEECRPPSSLITRVSYFA VFDGHGGIRASKFAAQNLHQN LVRKFPKGDVIS\VEKTVKRCLL DTFKHTDEEFLKQASSQKPAW KDGSTATCVLAVDNILYIANLG DSRAILCRYNEESQKHAALSLS KEHNPTQYEERMRIQKAGGNV RDGRVLGVLEVSRSIGDGQYK RCGCHLCAPTSRRC\QLTP\NDR FI/LVWPCDGLF\KVFTPEEAVN FIL\SCLEDEKIQTREGKSAADV RLRSSPATRLANKAVAAGARP DNVTV\MVVR\IGH
9929	40297	A	9990	2	419	
9930	40298	A	9991	2	1842	CLRLIAAAPPI/AIEPATTSSLALF LLLQRDQSSRTRGLPEEKEEVT MDTSENRPENDVPEPPMPIADQ VSNDDRPEGSVEDEEKKESSLP KSFKRKISVVSATKGVPAGNSD TEGGQPGRKRRWGASTATTQK KPSISITTESLKSLIPDIKPLAGQE AVVDLHADDSRISEDETERNGD DGTHDKGLKICRTVTQVVPAE GQENGQREEEEEKEPEAEPPV PPQVSVEVALPPPAEHEVKKVT LGDTLTRRSISQQKSGVSITIDD PVRTAQVPSPPRGKISNIVHISN LVRPFTLGQLKELLGRTGTLVE EAFWIDKIKSHCFVTYSTVEEA VATRTALHGVKWPQSNPKFLC ADYAEQDELDYHRGLLVDRPS ETKTEEQGIPRPLHPPPPPPVQPP QHPRAEQREQERAVREQWAER EREMERRERTRSEREWDRDKV REGPRSRSRSRDRRRKERAKSK EKKSEKKEKAQEEPPAKLLDDL FRKTKAAPCIYWLPLTDSQIVQ KEAERAERAKEREKRRKEQEE EEQKEREKEAERERNRQLEREK RREHSRERDRERERERERDRGD RDRDRERDRERGRERDRRDTK RHSRSRSRSTPVRDRGGRR
9931	40299	A	9992	1400	2959	
9932	40300	C	9993	169	430	

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9933	40301	A	9994	2	199	STSR/KMTELEEVTLNGKPLQA LRVTDLKAALEQRGLAKSGQK SALVKRLKGVRSRRCWGVGGE RTR
9934	40302	A	9995	1	4033	MWRRKHPRTSGGTRGVLSGNR GVEYGSGRGHLGTFEGRWRKL PKMPEAVGTDPSTSRKMAELEE VTLDGKPLQALRVTDLKAALE QRGLAKSGQKSALVKRLKGAL MLENLQKHSTPHAAFQPNSQIG EEMSQNSFIKQYLEKQQELLRQ RLEREAREAAELEEASAESEDE MIHPEGVASLLPPDFQSSLERPE LELSRHSPRKSSSISEEKGDSDD EKPRKGERRSSRVRQARAAKLS EGSQPAEEEEDQETP
9935	40303	A	9996	3	6305	ELEEVTLDGKPLQALRVT\DLK AALEQRGLAKSGQKSALVKRL KGALMLENLQKHSA\PHAAFQP NSQIGEEMSQNSFIKQYLEKQQ ELL\SSRLEREAREAAELEGKSS SISEEKGDSDDDKPRKGERRSS RVRQARAAKLAEGSQPAEEEE DQETPSRNLRVRADRNLKTEEE EEEEEEEEEDDEEEEGDDEGQK SREAPILKEFKEEGEEIPRVKPE EMMDERPKTRSQEQEVLERGG RFTRSQEEARKSHL
9936	40304	B	9997	99	332	
9937	40305	A	9998	3	236	YIFTILNTLQGVFILLFGCLMDR KIQEALRKRFCRAQAPS/SHHLP GELLPSDPQLCIQEHVRRHSMA LLRGHGHSQKL
9938	40306	B	9999	1	3099	
9939	40307	A	10000	355	858	RASSAAWGPSRKTSASSSAFSSS CWSSS*QS*SYSSSSLS\HGQGE RERQEGPEGRPAAVPHREQRG AEERLEHHPG*DAMLWCH*LH RLVPSAGGEHGSRPLLHGELPG LRAQRHHAFVENGLL*KGEDV VR*Q*ARAGHGGDVHPHHADP GHGLLHDPLPAHPPDW

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9940	40308	A	10001	3	1478	GRALTSRRRACQGASEAAGSPA QVTTSTGHHQHRSHQHRSPPA QVTTSTGHHQHRSPAQATTSTG HHQHRPPPAQVTTSTGHHQHR SPAQATTSTGHHQHRSH\HTGH HQHRS/HTSTGHHQHRSPAQAT TSTGHHQHRPPPAQVTTSTGHH QH\GHQHRPPPA/HGHHQHSSPP A/HGHHQHRPPPA/HGHHQH\G HHQHSSPPA/HGHHQHR\HHQ\P GHHQHRSP/HSTAHHQH\GHHQ HSSPPA/HGHHQHHQH\GHHQH SSPYQH\GHHQHRPPPA/HGHH QHRSH\HTAHHQHRSHQH\GHH Q\PGHHQHRSPAQATTSTGHTS TGHHQHRP/HTSTGHH\HTGHH QHRSHQHRSPPAQATTSTAHH QHSS/HTSTGHHQHRSP/HSTGH HQHSSPPA/HGHHQHSSPPAQA TTSTGHHQHRESPAVAAAADPS ALSAARRGSPGPAAAPQSRGTR GGGAPAKWWGSALGLGWAGR ARARLGRPLRPILGAMPPAPRT PRERREHGEVE
9941	40309	A	10002	5	341	PPRRRGQKRRQK/REEGERERG ERKRPRDRKEERKG/RRTKRQG GTETRESRPNGDGPQAKRKKQ TAGQREREEGEQRSSRQRGAA ERERGRETTHITCLLVPCWWEP NGRLCL
9942	40310	A	10003	1	582	MLAQRGGRSVVQCIAVSKLSV TQRSFVTLIMDEEALGNCGGSS GSQTCEKAVCIHNLPFLTSHAF QSGFPPHQSPEASLPKMVSDAQ TARLSLESMRELGFHISESAGFP APVSGYEHSNPSRPGVMPSGTS HWKQRSQKVEDNRTEMVKGIQ GDT\VKHQQHLPRINGN*LAYM TAKSRTWLPVQQDPGPQTI
9943	40311	A	10004	1	332	MEYYAAIKNDEFMSFVGTWM KLETIILSKLSQGQKTKHHIFSLI EAQAQVSPPPPYPAPQELTQPL LQQPRAPEAPAQQ/PPGSLLTAT VRLSASPGPGLIFDQLLPRCGF

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9944	40312	A	10005	1	1108	MLAQRGGRSVVQCIAVSKLSV TQRSFVTLIMDEEALGNCGGSS GSQTCEKAVCIHNLPFLTSHAF QSGFPPHQSPEASLPKMVSDAQ TARLSLESMRELGFHISESAGFP APVSGYEHSNPSLSTTNLSGPSR RRQPPVSPLTLSPGPEAHQGFSR QLSSTSPLAPYPTSQMVSSDRS QLSFLPTEAQAQVSPPPPYPAPQ ELTQPLLQQPRAPEAPAQQPQA ASSLPQSDFQLLPAQGSSLTNFF PDVGFDQQSMRPGPCLSSTGAS GAT\GSRELQDSFHLRPSPYSNC GSLPNTILPEDSSTSLFKDLNSA LAGLPEVSLDVDTPFPLEEELQI EPLSLDGR\HMLSDSSMGLLDP SVEETFRADRL
9945	40313	A	10006	1	691	MRERARPPRGCLAPPLPPG/E/S GADGQPAPRGRGTAGG/ELAA AGCGARAAMHRGAVPSAEPVP ASP/DGRWQWAGEGRPCNAAG GSRT/GAGCGWPAPAGWGPAP SSAASCPASGGATHRGASAAPG GGGGGRAP/GPDALEQRRAGAP PNAPGTPGSPEESSLRMRRESA AGAPAVGMAAATSLGQALGPR VPRSPYRTAVVLSSRSAFGYFSL ITLARYTLGCLSHSDITLFEC
9946	40314	A	10007	1	1065	MADKRAGTPEAAARPPPGLAR EGDARTVPAARAREAGGRGSL HPAAGPGTAFPSPGRGEAASTA TTPSLENGRVRDEAPETCGAEG LGTRAGASEKAEDANKEEGAIF KKEPAEEVEKQQEGEEKQEVA AEAQEGPR/PPEPWCPN/C/MDP LEAIQWEAEAVSAQADRAYLP LERRFGRMHRLYLARRSFIIQNI PGFWVTAFLNHPQLSAMISPRD EDMLCYLMNLEVRELRHSRTG CKFKFRFWSNPYFQNKVIVKEY ECRASGRVVSIATRIRWHWGQE PPALVHRNRDTVRSFFSWFSQH SLPEADRVAQIIKDDLWPNPLQ YYLLGDRPCRARGGLARWPTE TPSRPYGFQSG
9947	40315	A	10008	2	433	
9948	40316	A	10009	125	289	TRKSGCLKIRFHVFLFLYRNPG MDVADAYVTFVRHSQDVLRD KVNE\EMYI\ERLF
9949	40317	A	10010	1	774	
9950	40318	A	10011	1	1749	

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9951	40319	A	10012	1	1175	MFASCYMRNIPKRVIEFGTCLWRTCKNCLSSLEFKMPFPPHPRSVTYNLKQERCRLSLDASLSCMLSIEDSQIPNTRLECCKGLSRCTSVASTCPLVTFSFCLFSPKMEQYSKDDSEKTLKGWFSPGQVFVLDEYCARNGVRGCHRHLCYLRDLLERAENGAMIDPTLLHYSFAFCASHVHGNSQQMHVYLSGLPPNTDPEGSKTPSPPEPEAKKDTKKESKKRKDSKTQANQELKRSLTSNLP/ICEPTQ/W*TFPKYQIYQLTSL*ASHKCLLFRHRHGWLLY/IDADNGSGTSEDLFWKLDALQTFIRDLHWPEEEFGKHLEQRLKLMASDMIESCVKRTR\IAFEVKLQKTSSIQQIFRVPQFNMAPCFNVMGLMAKGSIQPKL\CSMEMGQE
9952	40320	A	10013	1	3951	MLDPSSSEEESDEIVEEESGKEVLGSAPSGARLSPSRTSEGSAGSAGLGGGGAGAGAGVGAGGGGGSGASSGGGAGGLQPSSRAGGGRPSSPSPSVVSEKEKEELERLQKEEEERKKRLQLYVFVMRCIAYPFNAKQPTDMARRQQKISKQQLQTVKDRFQAFLNGETQIMADEAFMNAVQSYYEVFLKSDRVARMVQSGGCSANDSREVFKKHIEKRVRSLPEIDGLSKETVLSSWMAKFDAIYRGEEDPRKQQ
9953	40321	A	10014	1	457	VAAVAATALKGGGARNARVLRGIFAGATA\NKAS\HNRTRALQN/HTASPEGKEEP\EPLIPGTGKYIPQKRGAKNPHENCGNLPWAIGFPCGILLFDPSPKR/RKLDKDRV\KQMKARQNMRVSNTG\EYES\QRFRASSQS\APSP\DVGSGVSGVQT
9954	40322	A	10015	464	863	TPAAVESSPSIPLAPRLLYTG*PLQP/GPRGQGCVPRIVPCCPKP/VCAPRPPWPRRSQRLRSAGLSPLCAAAAPPVPAGSHGTPGRVWAPLSNSACCTCCRHPS*LHPGTLDPGRWQAR*GPALPRGPLPGSPP
9955	40323	A	10016	1	300	PKILVGASKVVLL\SAHKLGFIGDTLSRQAK\AVDVASRVTHYSNLL\CDFL\QGIVATTKAAALQYPIAFPGPKDMVERVKELGHS\TQQFRRVLGQLAAA

1326

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9956	40324	A	10017	3	291	ARI/VFAIISFYFMPCCPLTA/SSF YLLSGLLDAFDGHALALLIKFC VRGSESHKMIDLSGNP/VLRIYY TS/RVGSVGLFR/MGLWVTAPIA LLKSLISVIT
9957	40325	A	10018	1	344	VLIRARLSDNPAVRGSESHKMI DLFCYPVLRIYYTSRPALFTLCA GNELFYCLLYLFHFSEGPLVGS VGLFRMGLWVTAPI\ALLKSLIS VIHLITAARNMA\ALGRQQDRA KKK
9958	40326	A	10019	1	469	MVRSCFVDDRRKRCNFNRQAS EVLNEYFYSHVSNPYHSEEAKE ELAKKCGITVSQVSNRFGNKKI RYKKNIGEFQEEANIYAVKTAV SVTQGGHSSTS\SPTPPSCAGCG GSFNISGSGDMFLGMPGLNGDS YSASQALESGDASPAQSEMPK MGT
9959	40327	A	10020	232	1728	PGGGRGGAGRGPQGPPPAMDE RLLGPPPPGGGRGGLGLVSGEP GGPGEPPGGGDPGGGSGGVPG GRGKQDIGDILQQIMTITDQSLD EAQGQKTPPLNCP\RKKPVLFS GRGEIKEKTG\LSIRSSQEEEPVD PQLMRLDNMLLAEGVAGPEKG GGSAAAAAAAAASGGGVSPDN SIEHSDYRSKLAQIRHIYHSELE KYEQACNEFTTHVMNLLREQS RTRPVAPKEMERMVSIIHRKFS AIQMQLKQSTCEAMMMLRSRF LDARRKRRNFSRQATEVLNEYF YSHLSNPYPSEEAKEELAKKCG ITVSQVSNRFGNKKIRYKKNIG KFQEEANIYAVKTAVSVTQGG HSSTSSPTPPSSAGSGGSFNISGS GDMFLGMPG\LNGDSYSASQ/V WESLRHSMGARGVIGG*TFGG RARCYSPR\EMRANGSWQEAV TPSSVTSPTEGPGSVHSDTSNLI LPLRVTGVGALTRRLEEDAGFQ RTNPNTGEAQDREGPMGSSPP
9960	40328	A	10021	337	830	IPRLPGSIQLSFVGAFGQTSKSLF FLCVFILLLFQFFLCSVYVPMCT E/RRINIPIGPCGGMCLSVKGRC EPVLKEFGFAWPESLNCSKFPP QNDHNHMCMEGPGDEEVPLPH KTPIQPGEECHSVGTNSDQYIW VKRSLNCVLKC/GYDACLYSRS AQEVT\DIWMA

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9961	40329	A	10022	1	1561	MAWRGAGPSVPGAPGGVGLSL GLLLQLLLLLGPARGFGDEEER RCDPIRISMCQNLGYNVTKMPN LVGHELQTDAELQLTTFTPLIQ YGCSSQLQFFLCSGYVPMGTEK INIPIGPCGGMCLSVKRRCETPS LK\EFGFA\WP\ESLNCSK/YPHP QND\HNPHVPWKGPGDEEVPLP HKTPIQP\GEECHSVGTNSDQYI WVKRSLNCVLKCGYDAGLYSR SAKEFTDIWMAVWASLCFISTA FTVLTFLIDSCRFSYPERPIIFLS MCYNIYSIAYIVRLTVGRERISC DFEEAAEPVLIQEGLKNTGCAII FLLMYFFGMASSIWWVILTLT WFLAAGLKWGHEAIEMHSSYF HIAAWAIPPVKTIVILIMRLVDA DELTGLCYVGNQNLDALTGFV VAPLFTYLVIGTLFIAAGLVALF KIRSNLQKDGTKTDKLERLMV KIGVFSVLYTVPATCVIACYFY EISNWALFRYSADDSNMAVEM LKIFMSLLVGITSGMWIWSAKT LHTWQKCSNRLVNYT
9962	40330	A	10023	496	664	FYKAVPSIHQLDVPQTHQP*ST GLVQKVYSRSKHVSL*PKYYY VQLVPKLDHLIFY
9963	40331	A	10024	1	954	
9964	40332	A	10025	127	481	GRTREATWRVYSVAVGVSRSQ IIRIAREFADNADKTHGRSMIIV GAGLNHWYHLDMNYRGLINM LIFCGCVGQSGG/GWAHYVGQ EKLRPQTGWQPGVCLDWQRPA RHMNSTSYFLLVP
9965	40333	B	10026	161	234	
9966	40334	A	10027	3	199	DDFLDLAESPNASDTESSDEIPL KAGPGTLIMATGVQDFNRTEFD RLNAIKGHLEI\ALLEKHFFT
9967	40335	A	10028	37	455	LRTHLLPRLSQSSPVSSLPRALL RPPGQLELWAVPAGPGPLL\AA DASQNLTQHMEALASQSRGRV DMSDGHLAVLSPIEEELRKLRE ETNAEMLRQELDRERQRRMEL EQKVQEVLKARTEEQMAQQPP KGQAQASNGA

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9968	40336	A	10029	1	1721	DKIRFRGHKRDDFLDLAESPNA SDTECSDEIPLKVPRTSPRDSEE LRDPAGPGTLIMATGVQDFNRT EFDRLNEIKGHLEIALLEKHFLQ EELRKLREETNAEMLRQELDRE RQRRMELEQKVQEVLKARTEE QMAQQPPKGQAQASNGAERRS QGLSSRLQKWFYERFGEYVED FRFQPEENTVETEEPLSARRLTE NMRRLKRGAKPVTNFVKNLSA LSDWYSVYTSAIAFTVYMNAV WHGWAIPLFLFLAILRLSLNYLI ARGWRIQWSIVPEVSEPVEPPK EDLTVSEKFQLVLDVAQKAQN LFGKMADILEKIKNLFMWVQP EITQKLYVALWAAFLASCFFPY RLVGLAVGLYAGIKFFLIDFIFK RCPRLRAKYDTPYIIWRSLPTDP QLKERSSAAVSRRLQTTSSRSY VPSAPAGLGKEEDAGRFHSTKK GNFHEIFNLTENERPLAVCENG WRCCLINRDRKMPTDYIRNGV LYVT\ENYLCFESSKSGSSKRNK VIKLVDITDIQKYKVLSVLPGSG MGIAVSTPSTQKPLVFGAMVH RDEAFETILSQYIKITSAAASGG
9969	40337	A	10030	18	573	
9970	40338	C	10031	71	205	
9971	40339	C	10032	190	243	
9972	40340	A	10033	18	283	
9973	40341	A	10034	1	190	
9974	40342	A	10035	1	135	
9975	40343	C	10036	90	137	
9976	40344	B	10037	272	560	
9977	40345	A	10038	3	422	
9978	40346	A	10039	205	1090	
9979	40347	A	10040	1	2142	

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9980	40348	A	10041	15	1524	FPGRRFRAEGERTECAEPPRDEP PADGALKRAEELKTQANDYFK AKDYENAIKFYSQAIELNPSNAI YYGNRSLVYLRTECYGYSL*D ATRAIELDKKYIMGYYRRA\AS NMALGKFRAALRDYETVVKV KPHDKDAKMKYQECNK\IVKP KAFERAIAGDEHKRSVVDSLDI ESMTIEDEYS*PKLEDGKVTISF MKELMQWYKDQKKLHRKCAY QILVQVKEVLSKLSTLVETTLK ETEKITVCGDTHGQFYDLLNIFE LNGLPSETNPYIFNGDFVDRGSF SVEVILTLFGFKLLYPDHFHLLR GNH\ETDNMNQIYGFEGEVKA KYTAQMYELFSEVFEWLPLAQ CINGKVLIMHGGLFSEDGVTLD DIRKIERNRQPPDSGPMC\DLLW SDPQPQNGRSISKRGVTCQFGP DVTKAFLEENNLDYIIRSHEVK AEGYEVAHGGRCVTVFSAPNY CDQMGNKAS\YIHLQG\SDLRP\ QFHQF\TAVP\HPNVK\PMAYAN
9981	40349	A	10042	94	188	VIEHLVSQDGLDFL/NLVICPPR PPKVLGLQA
9982	40350	A	10043	419	495	EPTNENSPIALSR*VNSQKISMK AV
9983	40351	A	10044	1	265	EMESRSIA\RMECSGSISAHCKL RLPGSHHSPASVSRVAGTTGTC HHARLIFLYF/LLETGFHCVSHD GLHLL/NLVICPPRPPKVLGLQA
9984	40352	A	10045	3	706	ADAWAWPHC/CTVLL*CLGFA GVLFGWPSLVFVFKNEDYFKD LCGPDAGPIGNATGQADCKAQ DERFSLIFTLGSFMNNFMTFPTG YIFDRFKTTVARLIAIFFYTTAT LIIAFTSAGSAVLLFLAMPMLTI GGILFLITNLQIGNLFGQHRSTII TLYNGAFDSSSAVFLIIKLLYEK GISLR/VLLHLHLCLQYLACSTH FPPDAPGAHPIPTAPQLQLWPV PWEWHHKGREGNS

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9985	40353	A	10046	1	1413	MKRGNGSRRRRRLLSENNGVF HIESFAQHPKDEKSRKLLGPIEH WTFVVEKGKGKPEETGTVSMV LEDGEVEADIKQGSVVGCCNV PPDAARERAEKAYMDGEQPTLI LLLWDLKKQIPVHKGTHSVGR HQTELLPNNGGGVVRFFYTTAT LIIAFTSAGSAVLLFLAMPMLTI GGILFLITNLQIGNLFGQHRSTII TLYNGAFDSSSAVFLIIKLLYEK GISLRASFIFISVCSTWHVARTF LLMPRGHIPYPLPPNYSYGLCP GNGTTKEEKETAEHENRELQSK EFLSAKEVSTYTNAFAFTQFGV LCAPWNGLLMDRLKQKYQKE ARKTGSSTLAVALCSTVPSLAL TSLLCLGFALCASVPILPLQYLT FILQVISRSFLYGSN\GRFLTLAF PSEHFGKLFGLVMALSA\VVSL LQFPIFTLIKGSLQNDPF\YVNV MFMLAILLTFLPPLSGISGMPYL
9986	40354	B	10047	316	395	
9987	40355	A	10048	1	1614	RMQQQAVMHYMQQQQQQQQ QQLGGPPTPAINTPVHFQSPPPV PGEVLKVGPVLACPPPCPH*SQ PPLEPLPYLSETYGNKFAAHISP AQ\ALRNPHQPPPQGCELDTCC PPPLATVLP/ISPMAMLHIGSNPE REVSEELASGHAACRARAHCC ASETMPNTVLLARVGWVCKGS REGGTHCGSEPGESGVTSSSCP ADLTQKRELTGTASLYPCAFEY PTPPSFSPSLPAAPLPASLFLVLT WAG*KANDL*/VRFLRGRVMG LGGQQLT\RLSALLQKSRELEN HSRRLEMTNKQLWLRIQVWS* TWTSLVTLTLNLAPGPKGQYFR MFCFGNKQSSASLSNTYQLEVL FCETLILAPTLLAPSSLMAHLEL ALKAIVTLKVPHVTSVQWAWP MQAHSTSTLTSLAQQVVKQEL PSEEGPGEALMLGAEVPDPEPL PALPPQAPLPLPTQPPSPFHHLD FSHSLSFGGREDEGPPGYPEPLA PGHGSPFPSLSKKDLDLMLLDD SLLPLASDPLLSTMSPEASKASS RRSSFSMEEGDVL

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9988	40356	A	10049	1	1651	GGVTAGARAPARGSVTAEAAA RAGRGSGRGADGGREGRTGRA SLVARGRSRPGAGGGHSLRAR HPNLRQVAGA/GGARAADRLT FRAREPAPAATMASRIGLRMQL MREQAQQEEQRERMQQQAVM HYMQQQQQQQQQQLGGPPTP AINTPVHFQSPPPVPGEVLKVQS YLENPTSYHLQQSQHQKVREY LSETYGNKFAAAHISPAQ\ALR NPHQPPPQGCELDTCCPPPLAT VLPISPMAMLHIGSNPERELDD VIDNIMRL\TMSLGYINPEMQM PNTVLLARLPLSSSHLNVYSSDP QVTASLVGVTSSSCPADLTQKR ELTDAESRALAKERQKKDNHN LIERRRFNINDRIKELGMLIPK ANDLDVRWNKGTILKASVDYI RRMQKDLQKSRELENHSRRLE MTNKQLWLRIQELEMQARVHG LPTTSPSGMNMAELAQQVV\KQ ELPSEEGPGEALMLGA\EGP\DP EPLPALHRQAPLPLPTQAPSPFH S/HWDFSHSL\SFGG\RVDDWSP GLPRTPGAGAWLPIPQPVQEGS GPHAPGRLTATAGL
9989	40357	A	10050	2	76	TPLAPPPKPVRRRLKSRR*IKAR S
9990	40358	A	10051	3	206	
9991	40359	A	10052	1	492	

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9992	40360	A	10053	2	2395	KQTELRRSGSRDVTGALLVAA AVASEAVGSLRVAEGGPNTLLL QVLR\SW\PWCNKATQTMEERK VKRRSPKSFSAHCTQVVNVQK KMSIPV\SKS\TGFSNPASQVNFT SRPKVKKEVMK\EKTKPQGLEE GQRHSSQLPIQHSFLT\DVSRCS RKMERGLLSL\LNDFHSWKTFK HFGN\ECSI\EQMEHVSGELQEK LARLNLELYGELEELPEDKRKT ASDS\NLDRLLSDCREMIPAFRT FLKRHDKTIVTKMLSLPELLLY PSRRFEEYLNLLYAVRLHTPAE HVDRGDLTTAIDQIKKYKGYID QTLSEVNRYLIRVQDVAQLHCC DEEISFSLSVACRSVDSASPESL PEMQNSQATLALLNQNLHFNKI TRLYEHIHDLSLFLFNDALLVSS RGTSHTPFERTSKTTYQFIASVA LHRLLIENIPDSKYVKNAFILQG PKYKWICATEIEDDKFLWLSVL RNAIKSSMEKACGLVFTGQFMF DTMGMTNILNNQDTAQALADG LMELSKEDSKCGKKIKDVEGN VIPTKCDPKTTFSLFMKERNVV EDNSWDTKSRLSKNDLNFEALI NLERILQKDSAEKRARVVRELL QSERKYVQILEIVRDVYVAPLK AALSSNRAILSAANIQIIFCDILQ ILSLNRQFLDNLRDRLQEWGPA HCVGEIVTKFGSQLNTYTNFFN NYPVILKTIEKQWETFSERSSSS
9993	40361	A	10054	2	296	
9994	40362	A	10055	2	369	
9995	40363	B	10056	82	2483	
9996	40364	A	10057	2	3343	YDVVLDAIDTMQRVAWHIND MKRKHEHAVRLQEIQSLLTNW KGPDLTSYGELVLEGTFRIQRA KNERTLFLFDKLLLITKKRDDT FTYKAHILCGNLMLVEVIPKEP LSFSVFHYKNPKLQHTVQAKSQ QDKRLWVLHLKRLILENHAAKI PAKAKQAILEMDAIHHPGFCYS PEGGTKALFGSKEGSAPYRLRR KSEPSSRSHKVLKTSETAQDIQ KVSREEGSPQLSSARPSPAQRNS QPSSSTMISVLRAGG

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9997	40365	A	10058	32	483	LKGHADAVLAAGTEAVKCHLL LGRHLLRLMASSGIHHKIVN*R QYAKFSHG*IQKF**WQHRQQF RGKETEMASAVDLPVTLTETEA NFPPEYEKFWKTVENNPQDFTG WVYLLQYVEQENHLMAARKA FDRFFIHYPYCYGYWKKYADL
9998	40366	A	10059	1	1090	MRQKRKEEKELFHNKDCEKKE KNSWERMRHTGTEKMASESET PTGAISQYKERMPSVTHSPEIM DLSELRPFSKPEIALTEALRLLA DED/WDKQLHALEQLLASCYS GTRHTTSSFHCGHQGMWWHPE AWRC/LATAEPQREPGKSTISSH SSLWN*Q/LHSHKLQSVPGLKV KNLRSGVSRAAVVCLSDLFTYL KKSMDQELDTTVKVLLHKAGE SNTFIREDVDKALRAMVNNVT PARAVVSLINGGQSHLHIAVRR CTAQHLSDVLEFMEPERILSAA KDMAERILPAAAKFAQDSSQET RYYGRKMLFFMMCHPNFEKM LEKYVPSKDLPYIKDSVRNLQQ KVCGKSLFYKQLYKQSLFLHP
9999	40367	A	10060	36	203	
10000	40368	A	10061	1	798	MKFQYKEDHPFEYRKKEGEKI RKKYPDRVPVIVEKAPKAR/RA *SGQEEVPSAL*PYCCLP/DGAG LGTCS/HAMPEPPTHSMGTCAA RASPTSTTPCSTAPSPIDRE\EQT TQGLRNASARRGTGRQLHLQ/S PVWDPLGEASWAPESSGNVESI SSSGIVNIPISTLCLAQGFSRFVN APIDTLYLAALVGPWRTFMSSS GIVNTPIGTLYLAQGMVHYHKS PFPTCLVQMSKIESLPKEKGAQ GVAAGLPSSLAPTCPPPDPSMK LHNN
10001	40369	A	10062	164	605	ALLKQHLRTVHRSAPPIRGHCC VSSSWT*G/AGKLSLEHTEEPSD VPSHLLYRWSISSAITEVFQALA SS\IPPRSQ*MSTPRR\NESTRHSP GPSIEEVKECMQDDN*YLQGTS YAPAGSQSYSAKLCFQVLKRN TCPPEKPNPASER

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10002	40370	A	10063	3	2480	RPITGAEIVAIINSLPTKKSPGLD GFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIILIPKPG RDTTKKENFRPISLMNIDAKILN KILANRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHINRT KDKNHMIISIDAEKAFDKIQQ/R LHAKNS/RIN*VLM/ETYFKIIRA IYDKPIANIILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLYTN NRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLK EIKEDTNKWKNIPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMT FFTELEKTTLKFIWNQKRAHIA KSILSQKNKAGGITLPDFKLYY KATITKTAWYWYQNRDIDQW NRTEPSEITPHTYNCLIFDKPEK NKKWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLEENLGITIQNI GMGKDFMSKTPKAMATKDKID KWDLIKLKSFCTAKETTIRVNR QPTKWEKIFATYSSDKGLISRIY NELNQIYKKKTNNPIKKWAKD MNRHFSKEDIYAAKKHMKKCS SSLAIREMQIKTTMRYHLTPVR MAIIKKSGNNRCWRGCGEIGTL LHCWWDCKLVQPLWKSVWRF
10003	40371	A	10064	317	582	STVCCFLLRFIGGGFRHIPLSVD LWIHYIKILKETLDPGDPETNNT IRGYVEH*Y*NVFYDINNYSDV DNRAHES*AGSLTSIPLLKK
10004	40372	A	10065	41	434	GDLQPTAALWEPLSGLAKAGA RSLSLQGGVGGEARARTRAAR GACGPAAAPGGHGLGGHALGA AGR/RLLALGRLGTCSLPCLSLP PSPWAPVPPEPPR*VPPHAPGRP VPSATQRLRSAGAQRRTGRQL
10005	40373	A	10066	67	459	LRDCKYTHRHCVSSSRFINTPIN TLCLAQGL*VHQSTLCI*LLWV GGLGGNFCVQYSVSN*SDGDV ENLCI*LRDCKCTNQHPVKTGH FGSTNQQDVGWGQIKRIKAGLP EPASGNSLGSPSTLWELCSLQ

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10006	40374	A	10067	2481	2882	IPQGNYRVIARNAKTQRGGNLT LTKPS/GIGRRGENSSISSWQRQ QKGKKETGSQRKRQRGRDKKL ERKRDRHRSQREGKKERKRQR RSQRERWK**RKNSVPIPLKAR VNFSLPTQGNSLLDLNPYLPLK QLKK
10007	40375	B	10068	52	5199	
10008	40376	A	10069	1510	2454	
10009	40377	B	10070	97	3414	
10010	40378	A	10071	164	620	PPTGCGTGPIGCSGPGTGPVPVP VAP\PFPQEGARTQPGSAGA\PG ARGLRRAETLVALGAVGPGLP TPPPPPPPAPQSQAPGGPEAQPF GSRVCVLASCCAHRPRPAPSAP PAPPAPPESTVRPAPPTRPGFSS YSSISHAFTATNFPFGTA
10011	40379	A	10072	1	513	MATLAGEGRPAGWVPWISLLA VGVLIIWKLWPAPPIGGELQFA FVCFLLGNVYEAFEHWKRLLN LLCRSEAAMKK/HATRLWINLI SILHHQLGEIPADFFVDIVSQHN FLTSTLQVFFSSACSIAVDATLR KKAEKFQAHLTKKFRWDFAEE PEDCAPVVEELPEGIEMG
10012	40380	A	10073	1	1642	MDYIRTDLTTAAPSPPRRLGPPP PGEQPPSGSGHVRPPGARPPHR GGGRGGGGGDPAAPPARGGGG GGKARPPGGGAAPCEPGCQCR APMVSVSSERHPLYNRVKTGQI ANCALPCHNPFFSQDERAFTVF WIGLWSVLCFVSTFATVSTFLID MERFKYPERPIIFLSACYLFVSV GYLVRLVAGHEKVACSGGAPG AGGAGGAGGAAAGAGAAGAG AGGPGGRGEYEELGAVEQHVR YETTGPALCTVVFLLVYFFGMA SSIWWVILSLTWFLAAGMKWG NEAIAGYSQYFHLAAWLVPSV KSIAVLALSSVDGDPVAGICYV GNQSLDNLRGFVLAPLVIYLFIG TMFLLAGFVSLFRIRSVIKQQD GPTKTHKLEKLMIRLGLFTVLY TVPAAVVVACLFYEQHNRPRW EATHNCPCLRDLQPDQARRPD YAVFMLKYFMCLVVGITSGVW VWSGKTLESWRSLCTRCCWAS KGAAVGGGAGATAAGGGGGP GGGGGGGPGGGGGPGGGGGSL YSDVS\TGLTWRSGTASSVSYP

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10013	40381	A	10074	3	475	HSSLNSVDKARALEADNGELE VNIRDWYQKQGPGASRDYSHY YTTIQDLRDKILGATIENSRIVL QIDNARLAADDFRTKFETEHAL RMSVEADINGLRRVLDELTLAR TDLEMHIEGLKEELAYLKKNHE EEISTLRGQVGGQVTV*VDSAP GTDL
10014	40382	A	10075	39	1323	NGMWSNWNPLIPQRWEEKFQS PSRHRGSSSRGVSLSS\SGGYSGI LSGSNGLLAGNEKLTMHNLNN CLASYLDKVHALEAANSKLEF GLSVWVLDEVTLARTDLEAQI KGLKEELAYLKKKHEEEINALR GQVGDQVHILSDRQSQYEIMA KQNWKDAEAWFTSWTEELNQ EVTGHIEQLQISRSEVTDLQCTL QGLEIELHSQLSVKAPLEGTLA ETEACFGAQLVQIQALISSIEAQ LGDVRADGEWQNQEYQRLLE QEIATYRSLLEGQEDHYNNLST SKVQIPECTVSNVPVASVCLQT LEPHSLASNPGSSTYSVTFGQYI NLSVSPFLLLEATIAGAKKAAT GNNSTQFSPPAERQLCIFTCPRT IPLTTASHAGSYGPKLVKYTSL RPLPMAAPTESNPALPSSRATA HRLLPAPGHFPSGL
10015	40383	B	10076	133	180	

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10016	40384	A	10077	1	2182	MSVDKAELCGSLLTWLQTFHV PSPCASPQDLSSGLAVAYVLNQ IDPSWFNEAWLQGISEDPGPNW KLKVSNLKMVLRSLVEYSQDV LAHPVSEEHLPDVSLIGEFSDPA ELGKLLQLVLGCAISCEKKQDH IQRIMTLEESVQHVVMEAIQEL MTKDT\P\DSLSPETYGNFDSQS RRYYFLSEEAEEGDELQQRCLD LERQLMLLSEEKQSLAQENAGL RERMGRPEGEGTPGLTAKKLLL LQSQLEQLQEENFRLESGREDE RLRCAELEREVAEL\QHRNQAL TSLAQEAQALKDEMDELRQSS ERAGQLEATLTSCRRRLGELRE LRRQVRQLEERNAGHAERTRQ LEDELRRAGSLRAQLEAQRRQ VQELLGQRQEEAMKAEKWLFE CRNLEEKYESVTKEKERLLAER DSLREANEELRCAQLQPRGLTQ ADPSLDPTSTPVDNLAAEILPAE LRETLLRLS/LLENKRLCRQEAA DRERQE/EKLQRHLEDAN\RAR HG\LETQ\HRLNQQAAYSELRA QVEDLQKALQEQGGKTEDAISI LLKRKLEEHLQKLHEADLELQR KREYIEELEPPTDSSTA\RRIEEL QHNLQKKDADLRAMEERYRR YVDKARMVMQTMEPKQRPAA GAPPELHSLRTQLRERDVRIRH LEMDFEKSRSQREQEEKLLISA W\YNMGMALQ\QRAGE\EPAPA
10017	40385	A	10078	1	687	
10018	40386	A	10079	1	1104	
10019	40387	A	10080	1	677	MAAAGGGGGGAAAAGRAYSF KVVLLGEGCVGKTSLVLRYCE NKFNDKHITTLQASFLTKKLNI GGKRVNLAIWDTAGQERFHAL GPIYYRDSNGAILVYDITDEDSF QKVKNWVKELRKMLGN\ETCL CIVGNKIDLEKERHVSIQEAESY AESVGAKHYHTSAKQNKGIEE LFLDLCKRMIETAQVDERAKG NGSSQPGTARRGVQIIDDEPQA QTSGGGCCSSG
10020	40388	A	10081	1	1467	
10021	40389	A	10082	2	244	
10022	40390	A	10083	1	257	
10023	40391	A	10084	1	558	
10024	40392	B	10085	41	618	
10025	40393	A	10086	1	591	

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10026	40394	A	10087	128	851	KMEKEKGNDDGIPDQENSLDFS EHFNQLELLETHGHLIPTGTQSL WVGNSDEDEEQDDKNEEWYR LQEKKMEKDPSRLLLWAAEKN RLTTVRRLLSEKATHVNT\RDE DEYTPLHRAAYSGHLDIVQELI AQGADVHAVTVDGWTPLHSA CKWNNTRVASFLLQHDADINA QTKGLLTPLHLAAGNRDSKDT LELLLMNRYVKPGLKNNLEET AFDIARRTSIYHYLFEIVEGCTN
10027	40395	A	10088	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEEDP NCHEQHLSNTATHLGTDQEAVI DGRRKPEESRTTSHICRCRS
10028	40396	A	10089	2	461	
10029	40397	A	10090	2	749	
10030	40398	B	10091	1	1077	
10031	40399	A	10092	1	1114	MPQNSLEECALELGKKSLQEN VNNFPKTKLFQFLKLTNWILPKI TKFKPIEGAENVFTDGSSNGKA SYFGLKGKVFQTPYTAAQKVE LVAVIEVLTAFDMPVSMISDST YVVHSTQLTENAQLRLHTDEQ LMTLFSQLQTAVR\CFAVMGIP ASRKTDNVPGYTIQTLATFFSM WNIKHITGIPYNSQGQAIVGRIN LSLKQRLQKQKEGNREYRTPQ MQLNLALLALIFLSLSKGQMLS AAEQHLQKPPAKTEAEQLIWW RDTKTRSWEIGKIITCGRGYAC VSPGQNQQPIWTPSRHLKPYHE PDAK\KRFREDPEDPPSCSHVKT DAEEDPNCHEQHPSNTAIHLRS DQEAVTDGRRKPEESGTTSHNE
10032	40400	A	10093	239	783	RRAPGTAPDAGPELRS\LHNLL GPACIFLRKGFAENRQPVQLRE AFREFDKDKDGYINCRDLGNC MRTMGYMPTEMELIELSQQIN MNLGGHVDFDDFVELMGPKLL AETADMIGVKELR\DAFREFDT NGDGEISTSELREAMRKLLGHQ VGHRDIEEIIRDVDLNGDGRVD FEAPFPGSSN
10033	40401	A	10094	1	304	
10034	40402	A	10095	3	154	
10035	40403	B	10096	126	251	
10036	40404	B	10097	122	2916	

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10037	40405	A	10098	3	2433	LAELSSLSVLRLSHNSISHIAEG AFKGLRSLRVLDLDHNEISGTIE DTSGAFSGLDSLSKLTLFGNKIK SVAKRAFSGLEGLEHLNLGGN AIRSVQFDAFVKMKNLKELHIS SDSFLCDCQLKWLPPWLIGRML QAFVTATCAHPESLKGQSIFSVP PESFVCDDFLKPQIITQPETTMA MVGKDIRFTCSAASSSSSPMTF AWKKDNEVLTNADMENFVHV HAQDGEVMEYTTILHLRQVTF GHEGRYQCVITNHFGSTYSHKA RLTVNVLPSFTKTPHDITIRTTT MARLECAATGHPNPQIAWQKD GGTDFPAARERRMHVMPDDD VFFITDVKIDDAGVYSCTAQNS AGSISANATLTVLETPSLVVPLE DRVVSVGETVALQCKATGNPP PRITWFKGDRPLSLTERHHLTP DNQLLVVQNVVAEDAGRYTCE MSNTLGTERAHSQLSVLPAAG CRKDGTTVGIFTIAVVSSIVLTS LVWVCIIYQTRKKSEEYSVTNT DETVVPPDVPSYLSSQGTLSDR QETVVRTEGGPQANGHIESNGK ASVTVKQSSAVTVSLGAGGGL QVFTGQVPGIRWGKLGEVEGG VCPRDASHFPEPDTHSVACRQP KLCAGSAYHKEPWKAMEKAE GTPGPHKMEHGGRVVCSDCNT EVDCYSRGQAFHPQPVSRDSAQ PSAPNGPEPGGSDQEHSPHHQC
10038	40406	A	10099	1	164	
10039	40407	A	10100	368	566	

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10040	40408	A	10101	3	1160	RDQRGYRDDRSPAREPGDVSA RTRSGGGGGRSATTAMPPPVPN GNLHQHDPQDLRHNGNVVVA GRPSCSRGPRRAIQKPQPAGGR RSGRGPAAGGLCLQPPDGGTC VPEEPPVPPMDWEALEKHLAG LQFREQEVRNQG\QARTNSTSA QKNERESIRQKLALGSFFDDGP GIYTSCSKSGKPSLSSRLQSGM NLQICFVNDSG\SDKDSDADDS KTETSLDTPLSPMSKQSSSYS\D RDTT\EEESESLGWTWDFLYKG KRNLQAEAKMALAMAKPMAK MQVEVEKQNRKKSPVADLLPH MPHISECLMKRSLKPTDLRD\LI MGQLQVIVNDFISQ\IKSLNEEW VQLLLI\QDELHTEQDAMLVDIE DLTRHAESQQKHMAEKMPAK
10041	40409	A	10102	1	506	RGPRTEPQDPCCPRAAAGARPS GPG/QDLPRLRLPGSPGAPGAG GGAGTAAGRKGPGLPEEAAAD GAWRLGEGWAAASEEPAPPGP HTSQRGASPPQPGWARAAGLS NQPTKDRIFGGSHKAAPQASAD SPTSLQCGAAGHCPKASRRALG DNPETEATSSLSPTEWLQ
10042	40410	A	10103	1	429	MGSRLNWMEVIPEQCTYLHVLI KCMFFWNRQHRGGIQEKAALK QRTPRIFHEKNTPCYLLVQE*H RSNAFGEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEETLFSNM
10043	40411	A	10104	4	122	
10044	40412	A	10105	53	619	ILVWSIVPEGKILWGTKQQRRD SRTQRLLKKSPWRAKQSVWEE/ ERKKKNKEEKEEKEKKEKEKK EKEKEKKRKKKRKKKKKKKK KKKKKKKKKKKKKEEEEEEE EDEEEEEEEEEKKKKEKEEKVK EKKKEEKK/QEEKEEEN/EEEEK EEEEKEEKSSSSKYSLLDSVPTL LISLWVILNTLPELLQPA
10045	40413	A	10106	2821	4680	
10046	40414	A	10107	18	1535	
10047	40415	A	10108	3	1494	
10048	40416	A	10109	3	617	
10049	40417	A	10110	3	1142	
10050	40418	B	10111	1	2151	
10051	40419	B	10112	1	1461	
10052	40420	A	10113	1	1248	
10053	40421	A	10114	2	1624	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10054	40422	A	10115	1	1416	
10055	40423	A	10116	1	2262	
10056	40424	A	10117	1	1791	
10057	40425	B	10118	1	1497	
10058	40426	B	10119	1	1599	
10059	40427	A	10120	1	1722	
10060	40428	A	10121	1	3168	
10061	40429	A	10122	1	1083	
10062	40430	A	10123	1	589	MGAIYDKPTANIILNGQKLEAF PLKTGIRQGCPLSLLLFNIVLEV LARAIRQEKEIKVIQVGKEEVK LSLFADDMIVYLEDPIISAPNLL KLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKE\KEDTNKWKNIPCSWVG RINIVKMAILPKPYVES
10063	40431	A	10124	1	1566	
10064	40432	B	10125	1	2406	
10065	40433	A	10126	1	2478	
10066	40434	B	10127	69	1259	
10067	40435	B	10128	225	997	
10068	40436	A	10129	2	1124	
10069	40437	A	10130	1	2058	
10070	40438	A	10131	258	823	TLMQKSSAKYWQTESSSTSKSL STMIKWASSLGCKAGSIYANQ* M*SSI/YTNNRQTESQIMSELPFT IASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTFFTELEKTTLKFIRNQ KRACIAKSILSQTKLEASRYLTS NYTTRLQ
10071	40439	A	10132	1	1512	
10072	40440	A	10133	1	992	
10073	40441	B	10134	1	2019	
10074	40442	A	10135	1	1203	
10075	40443	A	10136	1	1578	
10076	40444	A	10137	1	2956	
10077	40445	A	10138	1	1983	
10078	40446	A	10139	1	3156	
10079	40447	A	10140	1	3325	
10080	40448	A	10141	1	1870	
10081	40449	A	10142	1	1446	
10082	40450	A	10143	1	2310	
10083	40451	A	10144	1	1293	
10084	40452	A	10145	1	1038	
10085	40453	A	10146	1	1713	
10086	40454	A	10147	1	2271	
10087	40455	A	10148	1	3654	
10088	40456	A	10149	1090	1647	

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10089	40457	B	10150	1	1248	
10090	40458	A	10151	1	1884	
10091	40459	A	10152	1	1140	
10092	40460	B	10153	1	1545	
10093	40461	A	10154	1	3300	
10094	40462	A	10155	1	1824	
10095	40463	A	10156	1	1023	
10096	40464	A	10157	1	2169	
10097	40465	A	10158	1	2661	
10098	40466	A	10159	1	1104	
10099	40467	A	10160	1	1668	
10100	40468	A	10161	1	1945	
10101	40469	A	10162	1	3303	
10102	40470	A	10163	1	1382	
10103	40471	A	10164	1	399	MPPVDASRDLRELNPLSSYKAK PNEYLLLVQVLFLNRNTKEGLI RLLARYPDDLQQTESQIMSELP FTIASKRIKYPGIQLTKDVEDLF KENYKPLLSK\KEDANKWKNIP CSWIGRINIVKMAVLPKKKIWV
10104	40472	A	10165	1	2218	
10105	40473	B	10166	1	2562	
10106	40474	A	10167	1	3169	

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10107	40475	A	10168	1	2105	MKAEIKMFFETNENKDTTYQN LWDAFKAVCRGKFIALNAHKR KQERSKIDNLTSQLKELEKQEQ THSKASRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK WDITTDPTEIQTTIREYYKHLYA NKLENLEEMDKFLDTYTLPRLN QEEVESLNRPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL VPFLLKLFQSIGKEGILPNSFYE ASIILIPKPGRDTTKKANFRPISL MNIDAKILNKILAKRIQQHIKKL IHHDQHINKAKDKNHMIISIDAE KAFDKIQQPFMLKTLNKLGIDG TYFKIIRAIYDKPTANIILNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIVSAQ NLLKLISNFSKVSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFK\E NYKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKGFCRFRN HHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHP GAQYANRLSPRVGRFINAAGTT GFPTGKRAVSATQLMDFADFG TTIKQDFRLLGQTSVDRLLQLS QGQAVKGNQLLPVSLVKRKTT LAPNTQTASPRALADSLMQLA RQVSRLESGQ
10108	40476	A	10169	1	1689	
10109	40477	A	10170	425	1333	
10110	40478	A	10171	1	2274	
10111	40479	A	10172	1	3828	
10112	40480	A	10173	3	3130	
10113	40481	A	10174	1	960	

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10114	40482	A	10175	746	2470	TLMQKSSIKYWQNESSSTSKSL STMIKWASSLGCKAWFNIRKSI KVIQHINRAKDKNHMIISIDAEK AFDKIQQPFMLKTLNKLGIDGT YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLIRNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLLKEN YKP\LLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKNWKKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHTYNYLIFDKPEKNKQWGKD SLFNKWCWENWLAICRKLKLD PFLTPYTKINSKWIKDLNVRPK TIKTLEENLGITIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKL KSFCTAKEATIRVNRQPTKWEK IFATYSSDKGLISRIYNELKQIY KKKTNNPIKKWVKDMNRHFA KEDIYAAKKHMKKCSPSLAIRE MQIKTTMRYHLTPVRMAIIKKS
10115	40483	A	10176	1	3492	
10116	40484	A	10177	1	3139	
10117	40485	A	10178	637	2760	
10118	40486	A	10179	2	3932	
10119	40487	A	10180	1	1865	
10120	40488	A	10181	1	5754	
10121	40489	A	10182	959	1615	
10122	40490	A	10183	701	6973	
10123	40491	A	10184	3	3319	
10124	40492	A	10185	1	3296	
10125	40493	A	10186	1	2296	

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10126	40494	A	10187	1614	2615	TLMQKSSIKYWQTESSSTSKSL STMIKWASSLGMQGWFNICKSI NVIQHINRTKGKNHMIISIDAEK AFDKIQQPFLLKTLNKLGIDGT YLKIIRAIYDKPIANIILNGQKLT FEKFPLKIGTRQGCPLSPLLFNI VLEVLARAIRQEKEIKGIQLAKE EVKLSLFADDMIVYLENPIVSV QNLLKLISNFSKVSGYKIYKIDV QKSQAFLYTNNRQTESQIMSEL P\FTIASKRIKYLGIQLTRDVKDL FK\ENHKPLLKE\IKEDTNKWKN IP\CSWVGGRINLVKMAIL\PKVI YRFNAIPIKL\PMTFFTELEKNYF KVHMEPKKEPVLPSQS
10127	40495	A	10188	141	401	
10128	40496	A	10189	1	156	MQFPKTKTKKKEEEEEEEEEEE EEEEEEEEE\EEEEEEEEEEEGEE EKEEII
10129	40497	A	10190	1	1446	

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10130	40498	A	10191	272	2722	ETSCPLVRVHYAEAITGRCTAP EDEGSLGQKPPARRSNNRTEGA WGKRQLMSSP/STEPRVCLTIEG QEIDFLLDTGAAFSVLISCPGRL SSTSVTIQGILGQPVTRYFSHLL SCNWETLLFSHAFLLMPERPTG LLGRDILAKAGAIIYMNMGNKL PICCPLLEEGINPEVWALEGQFG RAKNAHPVQIRLKDPTTFPYQR QY/PLRPEAHKGLQNIVKHLKA QGLVRKCSSPCNTPILEVQRPRL VQDLRLINEAVISLYPVVPNPYT LLSQIPEEAEWFTVLDLKDAFF CVPLHSDSQFLFAFEDPTNHTS QLTWMVLPQGFRDSPHLFGQA LAKDLGHFSSPGTLVLQYVDDL LLATS*EALCQQATLDLLNFLA NQGYKVSMSKAQLCLQQVKY LGLILAKGTRALSKE*IQPILAY PRPKTLKQLREFLGITSFCRLWI PGYSETARPLYTLIKDTQRANT HLVEWESEAETAFKTLKQALV QAPGLSLPTGQNFSLYVTERAG IALGVLTQTRGTTPQPVAHLSK ETDVVAKGWPHCLRVVAAVA VLVSEAIKIIQGKDLIVWTTHEV NGILGAKGSLWLSDNCLLRYQ ALLLEGPVLQICTCMALNPATF LPEDGEPIKHDCQQIIVQTYAAR DDLLEVPLTNPDLNLYTDGSSF VENGI/RKVSDVTILESKPLPPGT SAQLAELVALTWALELGKGKR

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10131	40499	A	10192	1	2529	MTQEPSAIMREVPEMVNILKGT GDIHNTEIQNDNGKVGMTKCM AKPKDELRNLKLILSESLESAQR QGVSKQEKVLQCRRAQDLQPT MPEPPIPSMGSCAARASPTSATP CSRAPSPTDHPTAAKCRRMAR YWQAAPPAALVLDQLGEASW APESANLVGKWRTFVSSSGTA NAPISTLSKQTTGLYQSAGCGW GQNLGAKYRAPVGQLKATSTA ARLKTRVSGFLGKGSLTTPDSS ELGPLDPTDHTSQLTWTVLPQG FRDSPHLFGQALAQDLGHFSSP GTLILQYVDDLLLATSLEALCQ KATLDLLNFLANQGYKVSRLK AQLCLQ\SEIARPLYTLIKETQR ANTHLVVSEPEAVI/AFETLKQA LVHAPALSLPIGQNFSLYITERA GIALGDLTQTCGTTPQPVAYLS KEIDVVAKGWPHCLRVVAAVA ILVSEAIKIMQGKDLTVWTTHD VNGILGAKGSLWLSDNHLLRY QALLLEGLVLQICTCVALNTAT FLPEDGEPIEHDCQQIIVQTYAT RDDLLEVPLTNPDLNLYTDGSS VVENGIRRAGYAIVSDVTILESK PLVPGTSAQLAELVALTRALEL GKGKIINVYTDSKYAYLILHAH AAIWKEWEFLTSGNPHGCHRE VMELLHMVQETKEVGVLHYQS HQNGKERGEQQRKQLAEASAA FLWGRALDLQPTMPEPPIPSMG
10132	40500	A	10193	1	197	
10133	40501	A	10194	1	259	
10134	40502	A	10195	1	295	
10135	40503	A	10196	1	439	
10136	40504	A	10197	1268	1420	
10137	40505	A	10198	1	389	
10138	40506	C	10199	1	298	
10139	40507	A	10200	2	90	
10140	40508	A	10201	3	1252	
10141	40509	A	10202	2	82	WMKLETSKLT*EQKTKHCMFS LISGS
10142	40510	A	10203	149	244	
10143	40511	A	10204	485	668	
10144	40512	B	10205	1	598	
10145	40513	C	10206	422	784	

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10146	40514	A	10207	3	899	IYNHLIFDKPDKNKQWGK\DSL FNKWCWENWLAICRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEENLGNTIQDIGMGKDFMTK TPEAMATKAKIDKWDLIQLKSF CTANETVIRVNRQPTEWEKIFAI IYPSDKGLISKIYKELYEKKTNN LIKKWAKDMNRHFSKEDFYEA KKHEKSSSLLGQGVTKGGCCLP MNLLGTYRSEENPSEYQRRQLI KTLRVCKPSSSYFLTSDFLDTPS FSCEPTQTNELQGCSLRFRVAT AAGPVQVRGARLPSFAAPERGL AQIPRQMDSKI
10147	40515	A	10208	3	352	APGRRRRLCQPAGGPGAWPGS AVPGSVSPAPDARSPISGPSRAL RRHLRPSAAGGPGLEIPTHDPH LPGVDYKEGRP\PSGKAGRGGP\ PGKGSPSASGARALGVPAAAA TPRASTL
10148	40516	A	10209	1	510	
10149	40517	A	10210	73	327	
10150	40518	A	10211	1	957	MWSTCKLHGQGAKYILCAAEL SWGAASCLHGSTMSLTVVSMA CVG\AWPLMGGQDKP/FLSARP STVVPRGGHVAF/RCHYRRGFN NFMLYK/EDRSHVPIFHGRIFQE S/FIMGPVTPAHAGTYRC/RGSR PHSLTGWSAPSNP/LVIMVTGN HRKP/SLLAHPGPLLKSGETVI/L QC/WLSA/PSDPLDIVIT/GWENP CLSHVL*S*SHS*ELPADDGEKH GQMQREPKTG*NPSSSWPSPTE/ PSSKSGICR/HLHVLIGTSVVIFL FI/LLLFFLLYRWCSNKK\DSDE QDPQEVTYAQL/NHCVFIQRKIS RPSQR/PKTPLTDTSVYTELPNA
10151	40519	A	10212	351	637	AWIGDMGLDWRYGLRVEISA WSGDMGLEWRYGL\REGMFN DTLRLIGEHHDGVSKANFSISR MKQDLAGTYRCYGSVTHSPYQ LSAPSDPLDIVII
10152	40520	A	10213	1	1314	
10153	40521	A	10214	1	1008	

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10154	40522	A	10215	3	1080	GQDKPLLSAWPSLVVPLGHVIL RCHSYLGFNNFSLYKEGVHRKP SLLAHPGRLVKSEETVILQCWS DVRFEHFLLHREGKFKDTLHLI GEHHDGVSKANFSIGPMMQDL AGTYRCYGSVTHSPYQLSAPSD PLDIVITGLYEKPSLSAQPGPTV LAGESVTLSCSSRSSYDMYHLS REGEAHERRFSAGPKVNGTFQ ADFPLGPATHGGTYRCFGSFRD SPYEWSNSSDPLLVSVTGNSRY LHALIGTSVVIIPFAILLFFLLHR WCANKKNAAVMDQEPAGNRT VNSEDSDEQDHQEVSYA*LDH CVFTQREITRPSERPKTPPTDTS MYIELPNAEPRSKVVFCPRAPQ
10155	40523	A	10216	3	1379	
10156	40524	A	10217	352	1825	
10157	40525	A	10218	1	1497	MGLEWRYGPGGADMDLEWRY GPGVEMWVWSGDMGLEVEIR AWSGDMGLEWRYEPGDGDMG LEWRYGPGGGQDKPLLSTWPS LVVPPEHVTLRCHSNLGFNNFS LYKDDGVPVPELYNRIFWKSLF MGPVTPSHTGTYRCRGSHTHSP SGGSAPSNPLVIVVTGFRRKPSL LAHPGPLVKSEETVILQCWSDV MFEHFLLHREGTFNHTLRLIGE HIDGVSKGNFSIGRMTQDLAGT YRCYGSVTHSPYQLSAPSDPLD IVITGLYEKPSLSAQPGPTVLAG ESVTLSCSSRSSYDMYHLSREG EAHERRLPAGPKVNRTFQADFP LDPATHGGTYRCFGSFRDSPYE WSKSSDPLLVSVTGNSSNSWPS PTEPSSETGNPRHLHVLIGTSVV KLPFTILLFFLLHRWCSNKKNA SVMDQGPAGNRTVNREDSDEQ DHQEVSYA*LDHCVFTQRKITP PSQRPKTPPTDSSMYIELPNAES RSKAVFCPRAPQSGLEGIF
10158	40526	B	10219	114	1944	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10159	40527	A	10220	20	1138	AGARPPVCTGSTMSLMVIIMAC VGFFLLQGAWPQEGVHRKPSF LALPGHLVKSEETVILQCWSDV MFEHFLLHREGKFNNTLHLIGE HHDGVSKANFSIGPMMPVLAG TYRCYGSVPHSPYQLSAPSDPL DMVIIGLYEKPSLSAQPGPTVQ AGENVTLSCSSRSSYDMYHLSR EGEAHERRLPAVRSINGTFQAD FPLGPATHGGTYRCFGSFRDAP YEWSNSSDPLLVSVTGNPSNSW PSPTEPSSKTGNPRHLHVLIGTS VVKIPFTILLFFLLHRWCSDKKN AAVMDQEPAGNRTVNSEDSDE QDHQEVSYA*LDHCVFTQRKIT RPSERPKTPPTDTSMYIELPNAE PRSKVVFCPRAPQSGLEGIF
10160	40528	A	10221	1	1334	MSLMVVSMACVGLFLVQRAGP HMGGQDKPFLSAWPSAVVPRG GHVTLRCHYRHRFNNFMLYKE DRIHIPIFHGRIFQESFNMSPVTT AHAGNYTCRGSHPHSPTGWSA PSNPVVIMVTGNHRKPSLLAHP GPLVKSGERVILQCWSDIMFEH FFLHKEGISKDPSRLVGQIHDG VSKANFSIGPMMQDLAGTYRC YGSVTHSPYQLSAPSDPLDIVIT GLYEKPSLSAQPGPTVLAGESV TLSCSSRSSYDMYHLSREGEAH ERRFSAGPKVNGTFQADFPLGP ATHGGTYRCFGSFRDSPYEWSN SSDPLLVSVTGNPSNSWPSPTEP SSETGNPRHLHVLIGTSVVIILFI LLLFFLLHRWCSN\KKNAAVM DQESAGNRTANSEDSDEQDPQ EVTYTQLNHCVFTQRKITRPSQ RPKTPPTDIIVYTELPNAESRSK
10161	40529	A	10222	50	492	RARHRVTRPSIRKHSGHIRRILC LTCSSGVFLQGLRAGSRGTGPG LRTGWRLSPRAPRRRLHTPSAS SP*CSQ*RGPSAGTAAGARRRW RCRGQLRHPAGTSPPGRRWTG TACGPPAAPPAPWHSSWSCPHS GAGPPWSPACRTASL

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10162	40530	A	10223	3	3159	QAEFAAASTTPALGSDGVRVT MDSALTARDRVGVQDFVLLEN FTSEAAFIENLRRRFRENLIYTYI GPVLVSVNPYRDLQIYSRQHME RYRGVSFYEVPPHLFAVADTV YRALRTERRDQAVMISGESGA GKTEATKKLLQFYAETCPAPQR GGAVRDRLLQSNPVLEAFGNA KTLRNDNSSRFGKYMDVQFDF KGAPVGGHILSYLLEKSRVVHQ NHGERNFHIFYQLLEGGEEETL RRLGLERNPQSYLYLVK
10163	40531	A	10224	1	2810	MLNGCAHAHPIFPTRILSECPRG MLRAGFHLNRREALPPSRSHIS AAVLAPGALLSWGPDHPLELY GLHSHQDPPTGYEGVKGAPVG GHILSYLLEKSRVVHQNHGERN FHIFYQLLEGGEEETLRRLGLER NPQSYLYLVKGQCAKVSSINDK SDWKVVRKALTVIDFTEDEVE DLLSIVASVLHLGNIHFAANEES NAQ\VTTENQ\VKYLTRLLSVE GSTLREALTHRKIIAKGEELLSP LNLEQAAYARDA
10164	40532	A	10225	1	416	FRGVARQLRTSAMTMPVNGAH KDADLWSSHDKMLAQPLKDSD VEVYNIIKKESNRQRVGLELIAS ENFASRAVLEALGSCLNNKYSE GYPGQ\GSPANFAVYTALVEPH GRIMGLDLPDGGHLTHGFMTD KKKISATSI
10165	40533	A	10226	135	840	GSPANF/AV/YTALVETHGCIMG LDLPDGGHLTHGFMTDKKKIS ATSIFFESMPYKGGPHNHTIAG VAVALKQAMTLEFEVYQHHV VANCRALSEALTELGYQTVTG CSDKHLILVDLHSIKGTDGRRA EKVLEACSIACNKNTCPDDRNT LRPSGLRLGNPALTSLGLLEKG FQKVAHFIHRGIELTLQIQSNAG IRATLKEFKERLAGHKYQGCV QALQEEVESFTLFPLPGLPDF

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10166	40534	A	10227	2	1355	QLRTSAMTMPVNGAHKDADL WSSHDKMLAQPLKDSDVEVYN IIKKESNRQRVGLELIASENFAS RAVLEALGSCLNNKYSEGYPG QRYYGGTEFIDELETLCQKRAL QAYKLDPQCWGVNVQPYSGSP ANFAVYTALVEPHGRIMGLDLP DGGHLTRGL\MTDKKKISATSIF F*SMPYKANPETGYINYGQLEE NARLFHPKLIIAGTSCYSRNLEY ARLRKIADENGAYLMADMAHI SGLVAAGVVPSPFEHCHVVTTT THKTLRGCRAGMIFYRKGVAV ALKQAMTLEFKVYQHQVVAN CRALSEALTELGYKIVTGGSDN HLILVDLRSKGT\DGGRAEKVL EACSIACNKNTCPGDRSALRPS GLRLGTPALTSRGLLEKDFQKV AHFIHRGIELTLQIQSDTGVRAT LKEFKERLAGDKYQAAVQALR EEVESFASLFPLPGLPDF
10167	40535	A	10228	2	243	GTACNPAWPPPGLAPHLTHYA DLLPGSPFHVALPPPESELWETP DVSLITG\PRLGQTPVTEAVSGR RGIAIAYEDEGSG
10168	40536	A	10229	1	1194	MESMFSSPAEAALQRETGVPGL LTPLPDLDGVYELERVAGFVRD LGCERVALQFPDQLLGDAVAV AARLEETTGSKMFILGDTAYGS CCVDVLGAEQAGAQALIHFGP ACLSPPARPLPVAFV/LSSTFCG LGALCQGL*GPEPRPQSACGAA \GEPACAHALDTGKTQDEGAR AGRLRARRRYLVERARDARVV. GLLAGTLGVAQHREALAHLRN LTQAAGKRSYVLALGRPTPAK LANFPEVDVFVLLACPLGALAP QLSGSFFQPILAPCELEAACNPA WPPPGLAPHLTHYADLLPGSPF HVALPPPESELWETPDVSLITGD LRPPPAWKSSNDHGSLALTPRP QLELAESSPAASFLSSRSWQGL EPRLGQTPVTEAVSGRRGIAIA
10169	40537	A	10230	35	429	KEKRYLVYLGCCDLPEK*ESV* TNPVQPIELSAMMAYPVAALSP HVA/RLNT*MTNVTEKLSF*S*L T*I*V*PHVFSGYCTGQCRSS*A SSSSSSSSSSSSSSSSSSSSSSSSS SSSASDK*WAEASPRVR

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10170	40538	A	10231	73	393	RTQAPKLSQGGPRCIPPPKLCL MESMFSSPAEAALQR\ETGVPG LLTPLPDLGRSVALQFPDQLLG DAVAVAARLEETTGSKMFILG\ DTAYGSCCVDVLGAEQAGAQ
10171	40539	B	10232	191	367	
10172	40540	A	10233	131	1681	RTQAPKLSQGGPRCIPPPKLCL MESMFSSPAEAALQRET\GVPG LLTPLPDLDGVYELERVAGFVR DLGCERVALQFPDQ\LLGDAVA VAARLEE\TTG\SKMFI/LGVDT AYGSCCVDVLGAEQAGAQALI HFGPACLSPPARPLPVAFVLSST FCGLGTLCQDLWGPKPRPQSAC GAA\GEPACAHALEALATLLRP RYLDLLVSSPAFPQPVGSLSPEP MPLERFGRRFPLAPGRRLEEYG AFYVGGSKASPDPDLDPDLSRL LLGWAPGQPFSSCCPDTGKTQD EGARAGGLRARRRYLVERARD ARVVGL\LAGTLGVAQHREAL AH\LRNL\VQAAG\KCSYVLALG RPTPAKLANFPEVDVFVLLACP LGALAPQLSGSFFQPILAPCELE AACNPAW\PPPG/LWVPHLTH/Y IADLLPGSPFHVALPPPESELWE TPDVSLITGDLRPPPAWKSSND HGSLALTPRPQLELAESSPAASF LSSRSWQGLEPRLGQTPVTEAV SGRRGIAIAYEDEGSG
10173	40541	A	10234	3	605	AAAREAAGRDMLAADLRCSLF ASALQSYKRDSVLRPFPASYAR GDCKDFEALLADASKLPNLKEL LQSSGDNPQTGPGDLVSLDFYP QKVLTNPQVQ/WECRSFEKDSK S*LGLLTRLFLHRTSCLKLST/SD PANAKFYETKGERDLIYAFHGS RLENFHSIIHNGLHCHLNKTSLF GEGTYLTSDLSLALIYSPHGHG WQH
10174	40542	A	10235	197	895	LGLLTRLFLHRTSCLKLST/SDP ANAKFYETKGERDLIYAFHGSR LENFHSIIHNGLHCHLNKTSLFG EGTYLTSDLSLALIYSPHGHGW QHSLLGPILSCVAVCEVIDHPD VKCQTKKKDSKEIDRRRARIKH SEGGDIPPKYFVVTNNQLLRVK YLLVYSQKPPKRASSQLSWFSS HWFTVMISLYLLLLLIVFCGLL ALQDRGLPQVCPQIPCGWRPPS EGSQVFETQPGL

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10175	40543	B	10236	1	1059	
10176	40544	B	10237	226	522	
10177	40545	A	10238	159	306	LGSGNLP*EINPLSSCSLFREEDP PTTSGPQTNQPKEHLTNFKSAA ED
10178	40546	B	10239	101	397	
10179	40547	A	10240	2	253	LQEFGTRKDPPTTSGPQTDQAR EHLTNFKSSA/CQIPWNSGPRLS E*LLPRSSRLSS*RLT/RAQSPW KPTGQSQMLWVTLTVEGT
10180	40548	B	10241	1	409	
10181	40549	C	10242	1	462	
10182	40550	A	10243	1	861	
10183	40551	C	10244	1	140	
10184	40552	B	10245	1	1773	
10185	40553	B	10246	1	320	
10186	40554	C	10247	1	420	
10187	40555	A	10248	273	485	LGSGDLPWGINPLSSCSLLREK DPLTISGPQTHQPKEHLTNFKSG P\TENRTVQL\TWQPLPEPLELW PKAL
10188	40556	A	10249	508	558	
10189	40557	B	10250	76	358	
10190	40558	C	10251	83	414	
10191	40559	B	10252	1	1111	
10192	40560	C	10253	1	411	
10193	40561	B	10254	1	1054	
10194	40562	B	10255	57	229	
10195	40563	B	10256	1	222	
10196	40564	A	10257	230	1272	LLCSSACKCLMLGLHFVIVGNI CATLKEKYSSMLHLDVTMKKN GEKRTRLQKRKKGMPPHPAYE DLNIAAITLPANVVLHQPSGFRT SGQLDPVWWSLDTDAHEIWCQ DPGLGSGDFPWEITPLSSYSLLH EKDPPTTSGPQTDQPKKHLTNF KSKTKETGFIHGPKTPAPVTDW EGSLPLVFNHCRDTSLIIHPCFK GVRPRRDACLGPSPLAASPAFL EKGQDLINLAFKVYNNRKKLQ FLASTVRQTAATSPAHKNFQMP EPQRPGVPPEPPPTGACYMCRK\ SGHW\TRNAGSPGFLLSRVPSV WDPTENRTVQLTWQPLPEPLEL WPKALCLTDSFPDLLGLAA

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10197	40565	A	10258	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKKHMKKCSP SLAIREMQIKTTMRYHLTPVRM AIIKKSGNNRCRRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DL\DPAIPLLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP
10198	40566	A	10259	1	1947	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGRQGWFNICKSIN VIQHINRAKDKNHMIISIDAEKA FDKIQQLFMLKTLNKLGIDGTY FKIIRAIYDKPTANIILNGKKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTQPSEITPHIYNYLIFD KPDKNKQWGKGSLFNKWCWE NWLAICRKLKLDPFLTPYTKIN SRWIKDLNVRPKTTKTLEENLG ITIQDIGMGMDFMSKTPKAMAT KDKIDKWDLIKLKSFCTAKETT IRVNRQPTKWEKIFTTYSSDKG LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAAKKH MKKCSPSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCW\WINWMKKTWH IYTMEYYASIKKNEFMSFAGA* MKLETII
10199	40567	A	10260	1	347	TNKIDRPLARLIKKKREKKQID AIKNDKGDITTDPTETQTTIKEY YKHLYANKLENLEEMDKFFDT YTLPRLNQEEVESLNRPIAGSEI EAIINSLPT/KKSPGPDGFTAKFY QRE

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10200	40568	A	10261	31	809	KPRLENYVKNAEASGADAINW KKGY/LVMEDEMNEMKREGKF REKRIKRNEQSLQEIWDYVKRP TLHLIDVPETLNAHKRKQERSK TDTLTSQLKELEKQEQTHSKAS RRQEITKIRAELKEIETEKTLQKI NESRSWFFERINKIDRPLARLIK KKREKNQIDAIKNDKGDITSDP TEIQTTIREYYKHLYANKLENL EEMDKFLDTYTLPRLNQEEVES LNRPITGSEIVAIINSLPTKKSPG PDGSTAEFYQRYKEEL
10201	40569	A	10262	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKIL
10202	40570	B	10263	1	2265	
10203	40571	A	10264	1	2832	
10204	40572	A	10265	1	2757	

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10205	40573	A	10266	1	2114	MKEKMLRAAREKGRVTHKGK PIRLTADLSAETPQARREWGPIF NILKEKNFQPRISYPDKLSFISEG EIKYFTDKQMLRDFVTTRPVLK ELLKEALNMERNNWYQPLQKH AKNMPNSIILIPKPGRDTTKKEN FRPISLMNIDAKILNKILANRIQ QHIKKLIHHDQVGFIPGMQGWF NIHKSINVIQHINRTIDKNHMIIS IDAEKAFDKIQQLFMLKTLNKL GIDGTYLKIRIKYLGIQLTREVK DLFKENYKPLLNEIKEDTNKW KNIPCSWVGRINIMKMAILPKVI YRFNAISNKLPMTFFTELEKTTL NFIWNQKRARIAKSILSQKNKA GGITLPDFKQYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYTYLIFDKPEKNKQWGKDSLF NKWCWENWLAVCRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEEILGITIQDTGMGKDFMSKT PKAMATKAKIDKWDQIKLKSF CTAKETTIRVNRQPTKWEKIFA TYSSDKGLIFRIYNELKQIYKKK TNNPIKKWAKDMNRPFSKEDIY AAKKYMKKCSPSLAIREMQIKT TMRYHLTPVRMAIIKKSGNNR QTESQIMSELPITIASKRIKYLGI QLTKDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWIGRINIVK/T WPYCPSPQMYMSPTWQPKTLQ LWRQPKYPWKGTHRRKK
10206	40574	A	10267	1	2952	MLLNQGRKLPRVFAEETLKFK GTSNKPQTLEQISTSIIAQKEAT VMVPGSNQEIPSGAYAIRALGF KHKTGRLFEQTLNYLQEFLFTP QWHLECQQERTVHSPGKAAEA REPSVIDRHLIQESSNWHLVGA ALGQSFQRKEQAAIFAVLQPLL VIPRQTGSGVDLQKTPTDLQQR GLIVRRKTNKQKGIVHNSTTRE QNWTENEFDKLTEGGFKRWVI TNSSELKEHVLTQCKEDKNLEK SAIKLELRIKNLIQN
10207	40575	A	10268	1	1797	

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10208	40576	A	10269	1	1751	MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRANYDKPTA NIILNGQKLEALPLKNGTRQGC PLSPLLFNTVLEVLARAIRQEKE IKGIQLGNVEVKLSLFADDMIV YLENPIVSAQNLLKLISKFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIMKMAILP KVIYRFNAIPIKLPMPFFTELEK TTLKFIWNQKRARIAKSILSQK NKAGGITPPDFKLYYKATVTKT AWCWYQNRDIDQWNRTEPSEI TPHIYNYLIFDKPEKDKQWGKD SLFNKRCWENWLAICRKLKLD PFLTPYTKINSRWIKDLKVRPKT IKTLQENLGFTIQDIGMGKDFM SKTPTAMGTKDKIDKWDLIKL KSFCTAKETTIRVNRQPTKWEK IFTTYSSDNGLISRIYNELKQIYK KKTNNPIKQWAKDMNRHFSIE DIYAAKKHMKKCSSSLAIREM QIKTTMRYHLTPVRMAIIKKSG NNRNHLDFKHIRILGICYL/D*KI YQP*LHLVSRNRKPEKLSPKQA
10209	40577	A	10270	1	4729	
10210	40578	A	10271	1	1428	

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10211	40579	A	10272	1	2718	MALFRVGMTTRRLGHANKFTR DLLVKRLLLYEFVVEIIPGLRTK TTLVGPLETGYTSSDSVNSPHF MLDIALSHNVKSTQLLLRPWR NIDCSRNHKNAKKEEQMGDDE INRQQECSSSPAMEQSWTENDF DELREEVFRRSNYSELQEEIRTN GKEVKSFEKKLDEWITRITNAE KSLKHLTELKTKARELQLEKQE LTHSKASRRQEITKIRAELKEIE TQKTLQKINESRSWFFEKINKID RPLARLIKKKREKNQTDTIKND KGDIITDPTEIQTTIREYYKHLY TNKLENLEEMDKFLDTYVLPRL NQEEVESLNRPITGSEIEAIINSL PTKKSPGPDGFTAEFYQRYKEE LVPFLLKLSQSIEKERILPNSSYE ASIILIPKPGRDTTKKENFRPISL MNIDAKILNKILANRTQQHIKK LIHHEQVGCIPGMQGWFNIRKS INVIQHINRTKDKNHMIISIDAE KLISKFSKVSGHKINVQKSQAF LYTDNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNKWKNIPCSWVG RINIVKMALLP\RFSAIPIKLPMT FFTELEKTTLKFIWN/QKRARIA KSFLSQKNKAGGITLPDFKLYY KATVPKTAWYCYQNRDIDQW NRTEPSEIMLLIYNYLIFDKPDK KKEWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKMNSRWI
10212	40580	A	10273	396	1227	SLGRNSTSQKRVGANIQHS*RK EFSTQNFISSQTTLHK*RRNKIL YRQANAERFCHHQACPKTAPE RSTK\LERNNRLPARLIKKKREK NQIDATKNDKGDITTDPTEIQTT IREYYKHLYANKLENLEEMDK FPDTYTLPRLNQEEVESLNRPIT GSEIEAIIKSLPTKKRPGPDRFTA EFYQRYKEELVPFLLKLFQSTE KEGILPNSFYEASIILIAKPGRDT TKKENFRPISLLNIDAKILNKILA NRIQQHIKKLIHHDQVGFIPGM QGWFNI
10213	40581	A	10274	1	2168	
10214	40582	A	10275	1	1845	

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10215	40583	A	10276	1	2877	MENDFDELREEGFRQSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKAQELR EEWRSLRSRCDQLEERVSAME DEMNEMKGEGKFREKRIKRNE QSLQEIWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQTTISEYYKHLYTN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRPITGAE
10216	40584	A	10277	1	1689	MIFSIDAEKAFDKIQQPFMLKTL NKLGIDGMYLKIIRAMYDKPA ANIILNGQKLEAFPLKTGTRQG CPLSPLLFNIVLEVLARAIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPITSAQNLLKLISNYSKV SGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLNKIKEDT NKWKNIPCSWVGRINIVKMAIL PKVIYTFSAIPIKLPMTFFTELEK TTSKFIWNQKRARIAKSILSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM PHIYNYLIFDKPDKNKQWGKDS LFNKWCWENWLDIWRKLKLD PFLTPYTKINSRSIKDLHVRPKTI KTLEENLGDTIQDIGMGKDFMS KTSKAMATKAKIDKWDLIQLK SFCTAKETTIRVNRQPTEWEKIF AIYSSDKGLIFRIYKELKQIYKK KTNSPIKKWVKDMNRHFSKEAI YAAKRHMKKCSSSLAIREMQIK TTLSLPAQVSVV/RHGLSFCWD SRG\CGKSGLFLAYSINPFPQSH WDQEQVM
10217	40585	A	10278	1	2142	

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10218	40586	A	10279	1	1722	MIISIDAEKAFDKIQQRFMLKTL NKLGIDGLYLKIIRAIYDKPTAN IILNGQKLEALPLKTGTRQGCPL SPLQFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLLADDMIVYL ENPIVSAQNLLKVISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWYQKRARITKSILSQRNK AGDITLPDFKLYYKATVNKTA WYWHQNRHIDQWNRTKPSEIT LHIYNYLFFDNPDKNKKWGKD SLFNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNIRPKTI KTLEENLGITIQDIGMGKYFMT KTPKAMATKAKIDKWDLIKLK SFCTGKETTIRVNRQPTKWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKKHMKKCSPSLAIREMQI KTTMRYHLTPT/RLIVIGIEECLR GKEKLETLYYWNSDTDHQV*W LGWP*WKSDHKKEQPSF

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10219	40587	A	10280	1	2076	MDKFLNTYTIPRLNQEEVESLN RSITGSEIEAIINNLPTKRSPGPD GFTPEFYQRYKEELVPFLLKLF QSIVKEGFLPNSFYEGSIILITKS GRDTTKKENLRPISLMNINAKIL NKILANQIQQHIKKLIHHEQVDF IPGMQGWFNIRKSINVIQHINRT NDKNHMIISIDAEKAFDKIQQLF MLKTLNKLGIDGTYLKIIRAIYD KHTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLARAIS QEKEIKGIQLGKEEVKLSLFAD DMIVYLENPIVSAQNLLKLIGNF SKVSGYKISVQKSQAFLYTNKR QTESQIMSELPFTIVSKRIKYLGI QLTRDVKDLFKENYKPLLNEIQ DETNKWKN\CSWVGRINIVKM VILP/KELEKTTLKFIWNQKRAR IAKTILSQKNKAGGITLPDFELH YKATVTKTACYLYQNRDIDQR NRTEPSEIMPHIYNYLIFDKSDK NKKWGKDSLFNKWCWENWLA ICRKLKLDPFLPPYTKINSRWIK DLNVRPKTIKTLEENLGNTIQDI GMGKDFMSKTPKAMSTKAKID KWDLIKLKSFCTAKETAIRVNR EPTEWEKIFAIYSSDKGLISRIYN EFKQIYKKKTNNPIKKWAKDM NRHFSKEDIYAANRHMKKCSSS LAIREMQIKTTQVGGSEEKSAS ELGNKLIELDQSEEWRGKED

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10220	40588	A	10281	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRIKNLTQNRSTTWKLN NLLLDDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLKELEKQEQTHSKASRRQ EITKIRAELKEIETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITTDPTEIQ TTIREYYKHLYANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKKSPGPDG FTAEFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELKKTTLNFIWNQK \RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSLFNKWC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKTLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLKSFCTAKE TTNRVNRQPTKWEKIFATYSSD
10221	40589	A	10282	1	1996	

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10222	40590	A	10283	1	1778	MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYLKIIRAIYDKPTAN IIPNGQKLEAFPLKTGTTQGCPF SPLLFNIVLEVLARVIRQEKEIK GTQLGKEEVTLSLFADDMIVYL QNPIVSAQNLLKLIGNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFKWNQKRACIAKSILSQKNK AGGIMLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNYLIFDKPDQNKQWGKDS LFNKWYWENCLAICRKLKLDP FLTPYTKINSRWIKDLNVRLKTI KALEENLGNTIQDIGMGKDFMS KTPKAMATKDKIDKWDLIKPK SFCTAKETTIRVNRQPTKWEKIF ATYSSDKGLISRNYNELKQIYK KKTIGPIKKWAEDMNRHFSKE DTYAAKKHMKKCSSSLAIREM QIKTTMRYHLTPVRMVIIKKSG NNRCWRGCGETGTLSHCWWD CKL/IQPLW/RFLRD*GPKTGGD S*MIQVKY*PQQKKKGCPNA
10223	40591	A	10284	3	2875	

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10224	40592	A	10285	1	1838	MIIPIDAEKAFDKIQQPFMLKTL NKLGIHGMYLKIIRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LPPLLFNIVLEILARAIRQEKEIK GIQLGKEEVKLSLFADDMIIYLE NPIVSAQNLLKLISNFSKVSGYK INVQKSQAFLYTNNRQTESQILS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLNEIKEDTNKW KNIPCLSIGKINIMKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRARIAKTILSQKNKDG GITLPDFKLYYKATVTKTAWY QYQNRDIDQWNRTEPSEIIPHV YNHLIFDKPDKNKKWGKDSLF NKWCWENWLAICGKLKLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKI PKAMATKAKIDKWNLIELKSFC TAKETTISVNRQPTEWEKIFAIC LSDKGLISRIYKELKQRHKKKT NNPIKKWAKDMNRHFSKEDIY AANRHMKKCSSSLAIREMPIKT TMRYHLTPVRMAIIKKSGNNRC WRGCGEIGTLSHCWWDCNLVQ PLWKAVWRFLKDLELEIPFDPA ISLLG/IYPKDYKSCCYKDTCTQ STFTCRQHLPL
10225	40593	A	10286	1	2046	

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10226	40594	A	10287	1	1700	MEDEMNEMKQEGKFREKRIKR NEQSLQEIWDYVKRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQTNIQIQEIQRMPQRYSS RRATPRHIIVRFTKVEMKEKMS RAAREKEIQTTIREYYKHLYAN KLENLEEMDKFLDTCTLPRLNQ EEVESLNRTVTGSEIVAIINSLPT KKSPGPDGFTAEFYQRQSESQI MSEFPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYTFNAIPIKLPMTFFTELEKTT FKFIWNQKRAHVAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYSYLIFDKPEKNKQWGKDS LFNKW\CWENW\LAICRKLKLD PFLTPYTKINSRWIKDLNIRPKTI ETLEENLGITIQDIGMGKDFMS KTSKAMSTKAKIDKWDLIKLKS FCTAKETTIKVNRQPTKWEKIF ATYSSDKGLISRIYNELKQIYKK K\TNNPIKKWVKDMNRHFSKE DIYAAKRHMKKCSSSLAIREMQ IKTTMRYHLTPV
10227	40595	A	10288	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10228	40596	A	10289	1	2019	MDTIKNDKGDITTDPTEIQTTIR EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPVRG SEIEAIINSLPT/KKSPGPDEFTAE FYQRK\AFDKIQQAFTLKTLNK LVIDGTYRKIIRAICDKPTANIIL NGQKLEAFPLKTGTRQGCPLSP LLFNIVLEVLDRAIRQEKEITCIQ LGKEEVKLSLFADDMIVYLENP IISAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKKIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWEN IPCSWVGRINIMKMAILPKVIYR FNAIPIKLPVAFFTELEKTTLKFI WDQKRAYIAKSILSQKNKAGVI MLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMLHIY NYLIFDKPDKDEQWGKDSLFN KWCWENWLDIWRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKTL EENLGNTILDIGMGKDFMSKTP KAMATKAKIDNWDLIKLKSFC TAKETTIRVNRQPTKWEKIFTT YSSDKGLISRIYKELKQIYKKKT NNPMNKWAKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIK TTMRYHLTPVRMVIIKKSGNNR PPLSKEQPPIFRLSIILATTRDGN PAAVENVLHIKATLSFQQTHKA FYFQPS
10229	40597	A	10290	1	3144	MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHVV GSKALLSKCKRTEIITNCLSDHS AIKPELRIKKLTQNRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDTFKAVS RGKFIALNAHKRKQKRCKIDTL ASQLKEVEKQEQTHSKASRRQ EITKIRAELKEIETQKTLQKINES RSWFLERINKIDRPLARLIKKKR EKNQIDVIKNDK
10230	40598	A	10291	1	2274	
10231	40599	A	10292	1	2250	
10232	40600	A	10293	1	822	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10233	40601	A	10294	1	2605	MKAEIKMFFETNENKDTTYQN LWDAFKAVCRGKFIALNAYKR KQERSKIDTLTSQLKELEKQEQ SHSKAGRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK GDITTNPTEIQTTIREYYKHLYA NKLENLEEMDTFLDTYTLPRLN QEEVGSLNTPITGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL PGRVPTKKENFRPISLMNIDAKI LNKILANRIQQHIKKLIHHDQV GFIPGMQGWFNIRKSINVIQHIN RAKDKNHMIISIDAEKAFDKIQ QPFMLKTLNKLGIDGTYFRIIRA IYDKPTANIILNGQKLEAFPLKT GTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYNFYVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGIQLTRDVKDLFKENYKPLL KEIKEDTNKWKNIPCSWVGRIN IVKMAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLYY KATVTKTAWYWYQNRDIDQW NRTEPSEIMPHIYNYLIFDKPEK NKQWGKDSLFNKWCWENWLA ICRKLKLDPFLTPYTKINSRWIK DLNVRPKTIKTLEENLGITIQDI GVGKDFMSKTPKAMATKAKID
10234	40602	B	10295	111	2440	

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10235	40603	A	10296	1	1795	MIISIDAEKAFDKIQQPFMLKTL NKLSIDGTYFKIIRAIYDKPTANI ILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLFAHDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSGVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKGACITKTILS\QKNK VGGITLPDFKLYYKATVTKTA WYWYQ\NRDIDQWNRIKPSEIM PI\IYNYLIFDKPEKNRQWGEDS LFNKWCWETWLAIWRKLKLDP FLTLYAKIN*RWIKDLNVRPKTI KTLEENLGIT\IQD\IGMGKDFM SKTPKAMATKAKIDKWDLIQL KSYCTAKENTIRVNRQPTKWE KIFATYSSDKGLITRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAAKKHMKKCSSSLAIRE MQIKTTMRYHLTPVRMAIIQKS GNNRTKRTIYRRNDDDDDNDD NDDDSLMSLSRTEIPFSSYSELN VVLHKPRPEPSASTILLLHTA
10236	40604	A	10297	1	2851	
10237	40605	B	10298	1	3220	

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10238	40606	A	10299	1	2047	MENDFEELREEGFRRSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTQKCLKELMELKTKARELR EECRSLRSRCDQLEERVSAMED EMNEMKREGKFREKRIQRNEQ SLQEIWDYVKRPNLRLIGVPET LHPRDEAHLKNLIDAIKNDKGD ITTDPTEIQTTIREYYKHLYANK LENLEETDKFLDTYTLPRLNQE EVESLNRPITGSEIVAIINSLPTK KSPGPDGFTAEFYQRYKEEL/PD KQLQQSLRIQNQCTKITSILIHQ QQTNREPNHE*TPIHNCFKENKI PRNPTYKGCEGPLQGELQTTAQ GNKRGYKQMEEHSMLMGRKN QYHENGHTAQGNLQIQCHPH* ATNAFLHRIGKNYFKVHMEPK KSPHRQVNPKPKEQSWRHHTT *LQTILQGYSNQNSMVLVPKQR YRSMEQNRALRNNAAYLQLSD L*QT*EKQEMGKGFPI**MVLG KLASHM*KAETGSLPYTLYKN QFKMD*RLKR*T*NHKNPRRKP RHYHSGHRHGQGLHV*NTKSN GNKSQN*QMGSN*TKELLHSK KKKNY*QTEQATCKMGENFHN LLI*QRANIQNLQ*TQTNLQEKN KQPHQKVGKGHEQTLLKRRHL CSQK\NHEKMVTITGHQRNAN QNHNEIPSHAS*NGNH*KVRKQ VLERMCRNRNTFTLLVGL*TSS

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10239	40607	A	10300	1	2704	MYSHVITVCRHVKNGDILLLNR QPTLHRPSIQAHRARILPEEKVL RLHYANCKAYNADFDGDEMN AHFPQSELGRAEAYVLACTDQ QYLVPKDGQPLAGLIQDHMVS GASMTTRGCFFTREHYMELVY RGLTDKVGRVKLLSPSILKPFPL WTGKQHINRTKDKNHMIISIDA EKAFDKIQQPFMLKTLNKLGID GTYLKIIRAIYDKPTASIILNGQK LEAFPLKTGTRQGCPLSPLLFNI VLEVLARAIRQEKEIKSIQLGKE EVKLSLFADDMIVYLENPTVSA QNLLKLMSNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSGLP FTITSKRITYLGIQLTRDVKDLF KENYKPLLKEIKEDTNKWKNIP CSWVGRINIVKMAILPKVIYRF NTIPIKLPMTFLTELEKTTLKFI WNQKRAHIAKSILSQKNKAGGI MLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMPHI/Y YNYLIFDKPEKNKQWGKDTLF NKWCWENWLAICRKLKLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKT PKATATKAKIDKWDLIQLKSFC TAKETTIRVNRQPTEWEEIFAIY SSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSEEDIYA AKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMVIIKKSGNNRC
10240	40608	B	10301	1	3345	

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10241	40609	A	10302	248	2623	RQWAGVVGRCSHLASWVSSNT SETGAIRSSTEVDAPDDSMLLST CDIDLTAARRAWLGCLPTKKSP GPDGFTAEFYQRCKEELVPFLL KLFQSI/EKEGILPNLFDEASIILI PKRGRDTTKKENFRPISLMNID AKILNKILANRNQQHIKKLIHH DQVGFIPGMQGWFNICKSINVI QHINRTKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLGIDGTYL KIIRAIYDKPTANIILNGQKLEAF PLKTGTRQGCPLSPLLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSAYKINVQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAG\GIT\LPDFK LYLQGLQ*PKTAWYWY\QNRD IDQWNRTEPSEITPHIYNYLIFD KPEKNKQWGKDSLFNKWCWE NWLATCRKLKLDPFLTPYTKIN SRWIKDLNVRPKTIKTLEENLGI TIQDIGVGKDFMSKTPKAMAT KAKIDKWDLIKLKSFCTAKETA IRVNRQPTTWEKIFATYSSDKG LISRIYNELKQIYKKK\TNNPIKK WAKDMNRHFSKEDIYAANKH MKKCSPSLAIREMQIKTTMRYH

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10242	40610	A	10303	1	2467	MGDFNIPLSTSDRSTRQKVNKD TQELNSALHQADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHIVG SKALLSKCRRTEIITNCLSDHSA IKLEIRIKKLTQNCSTTWKLNNL LLNDYWVNNEMKAEIKMFFEI NEDKDTTYQNRWDTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TEIRAELKEIETQKTLQKMNES RSWFFEKINNIDRLLARLIKKKR EKNQIDAIKNHKGDITTNPTEIQ TTIREYDKHLYANKLENLEETD KFLDTYILPRLNQEQVESLNRPI TGAEIEAIINSLRTKKSPG\PGGF TAEFYQRYKEKLIVLEVLARAI RQEKEIKGIQLGKEELKLSLFAD DMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSQAFLYSNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEV KEDTNKWKNIPCSWIGRINIVK MAILPKVIYRFSAIPIKLPMTFFT ELEKTTLKFIWNQKRS\RIAKSIL SQKNRAGGITLSDFKLYYKATV TKTAWYWYQNRDIDQWNKTE PSEIMPHIYNYLIFDKPDKNKK WGKDSLFNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NVRPKTIKTLEENLGITIQDTGM GKDFMSETPKAMATKDKIDKW DLIKLKSFCTAKETTIRVNRQPT
10243	40611	A	10304	2	2480	
10244	40612	A	10305	1	4793	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRAEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVNNEMKAEIKMFF ETKENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
10245	40613	A	10306	1	4320	

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10246	40614	A	10307	1	3229	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLQ PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNL\WDAFKAV CRGKFIALNAHKRKQERSKIDT\ LTSQLKELEKQEQTHSKASRRQ EIT\KIRAELKEIETKK\TLQKINE SRSWFFERIKKTDRPLARLIKKK REKNQIDTI
10247	40615	A	10308	1	3392	MGDFNTPLSTLDRSRRQKVNK NTQELNSALHQVQLIDIYRTLH PKSTEYTLFSAPHHTYSEIDHVV GSKALLSKCKRTEIITNCLSDHS AIKLELRIKKLTQNCSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYPNLWDTFKAVC RGKFIALNAHKRKQERSEIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQKTLQKINESR SWFFEKINKIDRPLARLIKKKRE KNQIDSIKNDK
10248	40616	A	10309	1	4137	MGKKQNRKTGNSKKQRASPPP KEHSSSPATEQSWMENDFDELR EEGFRRSNYSELREDIQTKGKE VENFEKNLEECITRITDIEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSAMEDEMNEMKQ EGKFREKRIKRNEQSLQEIWDY VKRPNLPPIDVPESDRENGTKL ENTLQDVIQENFPNLARQANIQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAAREKAFKQ ASRREDDIAKVTSG
10249	40617	A	10310	1	5195	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIHIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE IMKIRAELKEIETQKTL\QKINE\ SRSWFF\ERINKIDRPLARLIKKK REENQID\AI

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10250	40618	A	10311	1	2958	MKQEGKFREKRIKRNEQSLQEI WDYVKRPNLHLIGVPESDREN GTKLENTLQDIIQEDFPNLARK ANIQIQEIQRTPQRYSSRRATPR HTIVRFTKVEMKEKMLRAARE KGRVTHKGKPIRLTADLSAETL QARRELNQEEVESLNKPVTGSE VVAIINSLPTKKSPGPDGFTAEF YQKYKEEPVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFRPISLMNIDAKILNKILAN RI\QQHI\KK
10251	40619	A	10312	5211	7687	TDTSQKKTFYAAKRHMKKCSS SLAIREMQIKTTYHAGPDGFTA EFYQRYKEELVPFLLKLFQSIEK EGILPNSFYEASIILIPKPGRDTT KK\ENFRPISLMNIDAKILNKILA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSIN\VIQHINRAKDK NHMIISIDAEKAFDKIQQPFMLK TLNKLGIDGTYFKIIRAIYDNPT ANIILNGQKLEAFPLKTGTRQG CPLSPLLFNIVLEVLARAIRQEK EIKGIQLGKEEVKLSLFADNMI VYLENPIVSAQNLLKLISNFSKV SGYKINVQKSQAFLYTNNRQTE SQIMSQLPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSG\EGRINIVKMAIL PKNWKKTTLKFIWNQKRARIA KSILSQKNKAGGITVPDFQLYY KATVTKTAWYWYQNRDIDQW NRKEPSEIMPHIYDSLIFGKPDK NKQWGKDSLFNKWCWEDWLA ICRKLKLDPFLTPCTKINSRWV KDLNIRPKTIKTLEENLGNTIQD IGMAKDFMSKTPKAMATKAKI DKWDLIKLKSFCTRIAKEPTIRV NRQPTKWEKIFATYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKKHMK KCSSSLAIREMQIKTTMRYHLT PVRMAIIKKSGNNRCWRGCGE TGTLLHCWWDCKLAQPLWKS

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10252	40620	A	10313	1	4525	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH HKSTEHTFFAAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN LLLNNYWVHNEMKAEIKMFFE TNKNKDTTYQNLWDTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKQLEKQEQTHSKASRRQEI TKIRGELKEIETQKTLHKINESR SWFFERINKIDRLLARLIKKKRE KNQIDAIINDKG
10253	40621	A	10314	1	1185	MEDIKRTQNKLSEMKATLAEM KNTLDGINDHGRDSRRKIRKLQ DNGGDDPTGNTQRKKNLINGP SLSVHIGEKRGGRRSWAETLTP LQTKALRLGPTTPSARRKCGIV PNLQTRKTEAYRYPDTHPGETP VGTAVLSIQKPKLESVIDVRVN MSSFHPEPELQPTQTSVLPDQD ATVAGSTTKFPEEQEARQGRVR ERPATRERPVPGGVSVPGLHHI HFLRGPSLPLASLTRITVLEAVV CFFSVWSIVGLSGFHTYLISSNQ TTNEDIKGSWSNKRGKENYNP YSYGNIFTNCCVALCGPISPRT/ LSHTGQRPTPIECEPHLNLVTSA ETLLASKPD/PTEEGTSSPTRRS QQHPPMASPCTGPRSHRVTCTL EKREEEEGVGQRLSPLCKPRL
10254	40622	A	10315	44	302	GLLGPGPPTAC*CGPHCGIHPES SPQSWCLCHSHRSSRAPPLARL SGDRHPGWRTWGGRDARSVA RGQWWCLVEPVLPFSTRSAFW

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10255	40623	A	10316	3	2182	IRDPGKKPVMLFLHGGSYMEG TGNMFDGSVLAAYGNVIVATL NYRLGVLGFLSTGDQAAKGNY GLLDQIQALRWLSENIAHFGGD PERITIFGRYSQPGLSYHIAFGPV VDGDVVPDDPEILMQQGEFLN YDMLIGVNQGEG\LKFVEDSAE SED/GAFDFTVSNFVDNLYGYP EGKDVLRETIKFMYTDWADRD NGEMRRKTLLALFTDHQWVAP AVATAKLHADYQSPVYFYTFY HHCQAEGRPEWADAAHGDELP YVFGVPMVGATDLFPCNFSKN DVMLSAVVMTYWTNFAKTGD PNQPVPYDTKFIHTKPNRFEEV VWSKFNSKEKQYLHIGLKPRL WSRFRGVLYQVFHDTICEKEAP KSSLLRKQTQPPKKQSSPAVHL RCTMDPVMMTVSPPPAHRHRR RGSPTRCAHCPVAWAPDTDDE KPHQYPAICSYHWDVPEDWEG FQHTQGTWVPWSQDAPESPPQ TIRFQPTVEERPLKTGIWSELGL RAYVYPVNPPPPSPEAPSHKNG RIVYDARDMRRRLRELTREVE ALSGCYPLASGSSTAEETSKNW VYRSLTGSQKMSQLHRVPFFD QEDPDSYLEEEDNLPFPYPKYP RRGWGGFYQRAGLPSNVGLW GHQGGILASLPPPSLYLSPELRC MPKRVEARKCQDLGDSILLLLG SFILLNVWINVVTLLWKHLKSS
10256	40624	B	10317	37	241	
10257	40625	A	10318	2	815	
10258	40626	A	10319	1	943	RAGGQGVG*GWGPPSVPCSVH GGKGL/PPEEGPGQVTHLEF\GR GDGLLTPWWPLTGDGRGPSA/S LASQRTCSQ*GMWLPAAQPSPS HPGPAGTVGQSHLHL*GLLGPG PPHCLLMRPTLRDSSRVFTSKL VSVPQPQVQQGPTTRKTVWRS ASWMENLGRKGCQVCSTWPM VVPGGACTSIWEWEADRVTPG GHRGSSCSHSAAGGANAAPHG PRGRPGGHAAAGGRHSTDGRS SCSPRPPDPGAARPQSAVHTDY RSPSLGTFPLAQPFGESKSDQSA PGIRGQKAPLAVARRGQQTPRP RGQARGRGRGTRPR

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10259	40627	A	10320	39	621	SCPEEEESSLLSPGTSWPLHAW ACSAAQVTGRERVVADWPGY HPGGPTAPHWRAGPLSDKTRPS RDVGTWDTGRAGCPPPPGRNP GPPDQRKALGVVVTSFGSQLG NGTPNSCLSPRQCWIQRLGGSS RTGPPPPGSVPEAAVSCPGHHT LFGLRSGAGKIQG*LLGPGWEL GQAGTEPPLPLAPPPPHRSCG
10260	40628	A	10321	1	496	AAATYVQNQSEDCLYLNLYVP TEDGPLTKKRDEATLNPPDTDI RDPGKKPVMLFLHGGSYMEGT GNMFDGSVLAAYGNVIVATLN YRLGVLGFLSTGDQAAKGNYG L\LDQIQALRWLSENIAHFGGDP ERITIFGSGAGASCVNLLILSHH SEGLFQKAIAQSGT
10261	40629	A	10322	1	4304	MLPVWFTDNLGAAATYVQNQ SEDCLYLNLYVPTEDGPLTKKR DEATLNPPDTDIRDPGKKPVML FLHGGSYMEGTGNMFDGSVLA AYGNVIVATLNYRLGVLGRYS QPGLSYHIAFGPVVDGDVVPDD PEILMQQGEFLNYDMLIGVNQG EGLKFVEDSAESEDGVSASAFD FTVSNFVDNLYGYPEGKD/DW ADRDNGEMRRKT\LLALFTDH QWVAPAVATAKLHADYQSPV YFYTFYIIHCQAEGRPEWADAA
10262	40630	A	10323	1	2765	MDVGFSRTTVQTLSRSHCKNIK QKISQWEGRANGISNPEKWCPK DFGVRYNCHQEIRLKKNPIAER KSKNLDVTSRENVGLDINENTK SHDQSENENKKHEYDDTHFFK NESESNWVCSRVKEIESCKEDV LDPETSLPPGNFYTSQILWKKIE ALPPDKLLNLALEHCDSSEKEL NFRVLDSSYGITKSLENIYSEPE GQECGPSINPLPKPRRTFRYLSE SGVTPYKERNCDKKYCENNSC AQSSLASSQEPE
10263	40631	A	10324	2	597	RWLIPKVMRIYDTQKKMDREA SQAALQKMLTLLMLPPTFGDLL REEYIGDNGDPQTLQAQFQEM MADSMFVIPALQVAHFQCSRA PVYFYEFQHQPSWLKNIRPPHM KADHVKFTEEEEQLSRKMMKY WANFARNGNPNGEGLPHWPLF DQEEQYLQLNLQPAVGRALKA HRLQLW\KKALPQKIQELEEPE ERHTEL

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10264	40632	A	10325	2	1766	PGQPLGEQQRVRRQRTETSEPT MRLHRLRARLSAVACGLLLLL VRGQGQDSASPIRTTHTGQVLG SLVHVKGANAGVQTFLGIPFAK PPLGPLRFAPPEPPESWSGVRDG TTHPAMCLQDLTAVESEFLSQF NMTFPSDSMSEDCLYLSIYTPA HSHEGSNLPVMVWIHGGALVF GMASLYDGSMLAALENVVVVI IQYRLGVLGFFSTGDKHATGN WGYLDQVAALRWVQQNIAHF GGNPDRVTIFGESAGGTSVSSL VVSPISQGLFHGAIMESGVALLP GLIASSADVISTVVANLSACDQ VDSEALVGCLRGKSKEEILAIN KPFKMIPGVVDGVFLPRHPQEL LASADFQPVPSIVGVNNNEFGW LIPKVMRIYDTQKEMDREASQA ALQKMLTLLMLPPTFGDLLREE YIGDNGDPQ\TLPKRKF\QKMM ADS\MFVIPALQVAHFQ\CS\RAP VYLPTSSQH\QPSWLKNIRPPH MKADHGDELPFVFRSFF\GGNY IKFTEEEEQLSRKMMKYWANF AR\NGNPNGEGLP\HWP\LFDQE EQYLQLNLQLAVG\RALKAHRF \QFWKKALPQKIQ\ELEEPEERH
10265	40633	A	10326	2	435	ILAEFGSLHLEFLHLTELSGNQV FAEKVRNIRKVLRKIEKPFGLYP NFLSPVSGNWVQHHVSVGGLG DSFYEYLIKSWLMSGKTDMEA KNMYYEALET/HKLGPEAFWF NSGREAVATQLSESYYILRPEV VESYMYLWRQTHNTK
10266	40634	A	10327	3	583	

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10267	40635	A	10328	1	1299	MHLNQLPPILSRLGAVGFFGSM KAHLVSVSRQVRNIRKVLRKIE KPFGLYPNFLSPVSGNWVQLPI PGSVAAGEMPASYPYRHRAPE VRRVCEALPHHVSVGGLGDSF YEYLIKSWLMSGKTDMEAKN MYYEALEAIETYLLNVSPGGLT YIAEWRGGILDHKMGHLACFS GGMIALGAEDAKEEKRAHYRE LAVQITKTCYESYAR\SDTKLGP EAFWFNSGREAVATQLSEE/YT YILRPEVVESYMYLW\RQTHNP\ SYR\EWGWEVVLALEKYCRTE AGFSGDSKTCYSRHPQPRTTSR QSFFLAETLNRCLVSACNGPDT GLEARDTAESETVISPAVKGSR GEKAMVRETDKPAKCIGKKSK NGKSDLKAASKMDAQFRSLCF EEVTPLWFEKVLEMNGPASPSV SPGGLSLEVWSLVMWHKDARP
10268	40636	C	10329	186	401	
10269	40637	A	10330	194	482	
10270	40638	A	10331	224	495	
10271	40639	B	10332	138	1810	
10272	40640	A	10333	1	1351	MGGVGEPGPREGPAQPGAPLPT FCWEQIRAHDQPGDKWLVIER RVYDISRWAQRHPGGSRLIGHH GAEDATDAFRAFHQDLNFVRK FLQPLLIGELAPEEPSQDGPLNA QLVEDFRALHQAAEDMKLFDA SPTFFAFLLGHILAMEVLAWLLI YL\LGP\GWVPSALAAFILAISQ AQSWCLQHDLGHASIFKKSWW NHVAQKFVMGQLKGFSAHWW NFRHF\QHHAKPNIFHKDPDVT VAPVFLLGESSVEYGKKKRRYL PYNQQHLYFFLIGPPLLTLVNFE VENLAYMLVCMQWADLLWA ASFYARFLSLSYLPFYGVPGVL LFFVAVRVL\ES\HWFVWITQM NHIPKEIGHEKHRDWVSSQLAA TCNVEPS\LFTNWFSGHLNFQIE HHLFPRMPRHN\YSPVAPLV\KS LCAK\HGLSYE\VKPFL\TALVDI VRSLKK\SGDIVLDAYLHQ
10273	40641	A	10334	43	399	

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10274	40642	A	10335	1	2229	FLKVCPQNNAETFGCLGTG\EK GDRGNQTQKP\LHYKSWSLFHR SCPRDFYGSKVGDFQGKENGR G\GES\IYGGFFEDEGVSLVKDH\ KEFLLSMANRGKDTNGSQFFIT T\KPTPHLDGHHVVFGQVI\SGQ EVVREIENQKTDAASKPFAEVR ILSC\GELIPKSKVKKEEKKRHK SSSSSSSSSSDSDSSRYS\QSSSDS SDSESATEEKSKKRKKKHRKNS RKHKKEKKKRKKSKKSASSES EAEN/LLEAQPPVLLFRPEEIPLP IPENRFLMRK\SPPKADEKERKN RERERERECNPPNSQPASYQRR LLVTRSGRK\LKGRGPRRYRTPS RSRSRDLFRRS\ETP\PHWRQEM QRA\QRMRVSSGER\WIKGDKS ELNEIKENQRSPVRVKERKITD HRNVSESPNRKNEKEKKVKDH KSNSKERDIRRNSEKEDKYKNK VKKRAKSKSRSKSKEKSKSKER DSK\HN\RNEEKRMRFKELKGR DHENVKEKEKQSDSKGKDQER SRSKEKSKQLESKSNEHDHSKS KEKDRRAQSRSRECDITKGKHS YNSRTRE\RSRRRDSSSRVRSRP HDRDRSMSK\EYHRYRDQVYS RRVRSRSRERRTPPGRSRSRDR RRRRRDSRSSEREDSQSRNKDK YRNQESKSSHRKENSESEKRM YSKSRDHNSSNNSREKKADRD QSPFSKIKQSSQDDELKSSMLK
10275	40643	A	10336	3	3366	

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10276	40644	A	10337	3	2431	GCLQELSVLFARGEPRGPCHNL LHYMLALIGVPEVFWAFLFHCS LGLEEEKLAPLIKGEEKIVWLRS SFYFQHCLVDKSTLLPSSSVSLG IFHEEKNSGEFPIFAKAVRLALV PLRYVKLEDRDNWISVDSVTSE IKLAKLPDFESRYVQNGTYTVK IVAISEDYPRKTITGTVLINVEDI NDNCPTLIEPVQTICHDAEYVN VTAEDLDGHPNSGPFSFSVIDKP PGMAEKWKIARQESTSVLLQQ SEKKLGRSEIQFLISDNQGFSCP EKQVLTLTVCECLHGS\GCREA QHDSYVGLGPAAIALMILAFLL LLLVPLLLLMCHCGKGAKGFTP IPGTIEMLHPWNNEGAPPEDKV VPSFLP\VDQGGSLVGRNGVGG MAKEATMKRKVSSASIVKGQH EMSEMDGRWEEHRSLLSGRAT QFTGATGAI\MTTETTITARATG ASRDVAGAQAAAVALNEEFLK NYFTDKAASYTEEDENHTAKD CLLVYSQEETESLNASIGCCSFI EGELDDRFLDDLGLKFKTLAEV CLGQKIDINKEIEQRQKPATETS MNTASHSLCEQTMVNSENTYS SGSSFPVPKSLQEANAEKVTQEI VTERSVSSRQAQKVATPLPDPM ASRNVIATETSYVTGSTMPPTT VILGPSQPQSLIVTERVYAPAST LVDQPYANEGTVVVTERVIQPH GGGSNPLEGTQHLQDVPYVME
10277	40645	A	10338	5	354	RPRLTSQDIKKPDC/DGEDAIGR GFECDGLHLEKIVHFALHLEKN VNQSLLELHKLATDKNDPHLC DFIETHYLNEQVKAIKELGDHV TNMHEMGAPDSGVAEYLFDKH TLGDSDNES

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10278	40646	A	10339	1	2024	GEALMYHTHFSELLDEFSQNVL GQLLNDPFLSEKSVSMEVEPSP TSPAPLIQAEHSYSLCEEPRAQS PFTHITTSDSFNDDEVESEKWY LSTDFPSTSIKTEPITDEPPPGLV PSVTLTITAISTPLEKEEPPLEIEQ WGLIPRARPLFPKIKLEPHEVDQ FLNFSP\KEAKHLHIFPSWAACT CGSSGNSAIRIILAYSLALRVPT ETKKPRDLFGKTGREKGKEETS REKLYVAERERKAPVDHLHLPP TPPSSHGSDSEGSLSPNPRLHPF SLPQTHSPSRAAPRAPSALSSSP LLTAPHKLQGSGPLVLTEEEKR TLIAEGÝPIPTKLPLSKSEEKAL KKIRRKIKNKISAQESRRKKKE YMDSLEKKVESCSTENLELRKK VEVLENTNRASHGELVIGVLGK GRRWDPLLTSPHAGDQCLGSV QGWAGECTPRQLDGSRTTLISE EDPGSPEMGGGEALGAIVSYA WRGREALHASRVGAVIQAPIA AGSDICLSDIRESATSSQTNISVT RTLLQQLQKLQTLVMGKVSRT CKLAGTQTGTCLMVVVLCFAV AFGSFFQGYGPYPSATKMALPS QHSLQEPYTASVVRSRNLLIYE EHSPPEESSSPGSAGELGGWDR GSSLLRVSGLESRPDVDLPHFIIS NETSLEKSVLLELQQHLVSAKL
10279	40647	A	10340	1	489	.

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10280	40648	A	10341	1	2665	MESTLTLATEQPVKKNTLKKY KIACIVLLALLVIMSLGLGLGLG LRKLEKQGSCRKKCFDASFRGL ENCRCDVACKDRGDCCWDFED TCVESTRIWMCNKFRCGETRLE ASLCSCSDDCLQKKDCCADYK SVCQGETSWLEENCDTAQQSQ CPEGFDLPPVILFSMDGFRAEYL YTWDTLMPNINKLKTCGIHSKY MRAMYPTKTFPNHYTIVTGLYP ESHGIIDNNMYDVNLNKNFSLS SKEQNNPAWWHGQPMWLTA MYQGLKAATYFWPGSEVAING SFPSIYMPYNGSVPFEERISTLL KWLDLPKAERPRFYTMYFEEP DSSGHAGGPVSARVIKALQVV DHAFGMLMEGLKQRNLHNCV NIILLADHGMDQTYCNKMEYM TDYFPRINFFYMYEGPAPRIRA HNIPHDFFSFNSEEIVRNLSCRK PDQHFKPYLTPDLPKRLHYAKN VRIDKVHLFVDQQWLAVRSKS NTNCGGGNHGYNNEFRSMEAI FLAHGPSFKEKTEVEPFENIEVY NLMCDLLRIQPAPNNGTHGSLN HLLKVPFYEPSHAEEVSKFSVC GFANPLPTESLDCFCPHLQNST QLEQVNQMLNLTQEEITATVK VNLPFGRPRVLQKNVDHCLLY HREYVSGFGKAMRMPMWSSY TVPQLGDTSPLPPTVPDCLRAD VRVPPSESQKCSFYLADKNITH
10281	40649	A	10342	590	900	PLYSATVPSAFCSGQ/LVPHIKS FCRLNIFNR*LIELRHLVFFVLLL FRDLQHIMACNMRDAVRFFVC FLVIFFREGLSRSSCQKCSRKSQ NCGLFYNFFDVHVH
10282	40650	A	10343	1	804	
10283	40651	A	10344	207	299	
10284	40652	A	10345	738	1007	EDASCDEGSTARAVHSMEPAG ARNRQKPHPFQVRGAEPHPPW* RCSHPAVAVDPGIHALSGKPLC SWRLGSDLPTVWPLPTPDPPVS VS
10285	40653	A	10346	150	509	QLPAGSGEGPYHLEGQLSYCHR GGEKALAALLSSPTSKTRSPSEP DPEQDEQKLRFCKRHLYGQQP RSPVEIRLQHVAIAYQTHHAYD *FVQLYNQHVAQPVLEFPYPGA VVALLSRHL

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10286	40654	A	10347	120	620	SYVKYFPHQPAQKYFQQIHSAI GLHNADHVHKHLLGDNRYPIW IMQPSAHHPARQPEHDNHFR*V QQLYDGDSHRQFL*HQILFDRT PVSVDQSVEKKG*DHPVRPQ*A APGHVHYLTIPERSSQHYHPGA LQE*TSHPDHIQARGSILASVLS GSDRWRRTYRCL
10287	40655	A	10348	599	1185	MCQNLMTHSKSTEWKITKRFL TETEKHIRTFSSLSMKAIIHPA/H NHTLRDPHYVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFRKESQKLQQSAKKR DAELANGALGIIELNNDYTSEK SNEAADHFKHVPQAKGNNVVI TSYMTNRGFFEDKKATFAPSFL MNIKGNKTSVVKNSILEQGQLT
10288	40656	B	10349	1	975	
10289	40657	A	10350	1	1080	
10290	40658	B	10351	58	1128	
10291	40659	B	10352	1	1029	
10292	40660	A	10353	10	108	
10293	40661	B	10354	208	2237	
10294	40662	A	10355	1	1153	
10295	40663	A	10356	1026	1274	LHIEKSNEAADHFKHVACHR*R *ACTCHCNNPWFPRPLPQPDCP TSATVEPPLYPIRSRGRTRKPAE GSRAPGCCCCQRPGK
10296	40664	A	10357	434	1128	MCQNLMTHSKSTEWKITKRFL TETEKHIRTFSSLSMKAIIHPA/H NHTLRDPHYVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFRKESQKLQQSAKKR DAELANGALGIIELNNDYTLKK VMKPLITSNTVTDEIERANVFK MNGKWYLFTDSRGSKMTIDGI NSNDIYMLGYVSNSLTGPYKPL NKTGLVLQMGLDPNDVTFTYS HFAVPQAKSNNVVNYGA
10297	40665	A	10358	300	491	SYVKYFPHQPAQKYFQQIHSAI GLHNADHVHKHLLGDNRYPIW IMQPSAHHPARQPEHDNHFR*V QQLYDGDSHRQFL*HQPAQKY FQQIHSAIGLHNADHVHKHLLG DNRYPIWIMQPSAHHPARQPEH DNHFR
10298	40666	B	10359	1	1226	
10299	40667	A	10360	1369	1548	
10300	40668	A	10361	1	1365	

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10301	40669	A	10362	1560	2384	MCQILMTHSKSTEWIITKRFLTE TEKHIRTFSSLSMKAIIHPA/HNH TLRDPHYVEDKGHKYLVFEAN TGTENGYQGEESLFNKAYYGG GTNFFRKESQKLQQSAKKRDA ELANGALGIIELNNDYTLKKVM KPLITSNTVTDEIERANVFKMN GKWYLFTDSRGSKMTIDGINSN DIYMLGYVSNSLTGPYKPLNKT GLVLQMGLDPNDVTFTYSHFA VPQAKGNNVVITSYMTTRGFFE DKKATKAPSFLMNIKGNKASV VKNSILEQGQLAVN
10302	40670	B	10363	783	881	
10303	40671	A	10364	1	1359	
10304	40672	A	10365	1512	2010	ENFPHQPAQKYFQQIHSAIGLH NADHVHKHLLGDNRYPIWIMQ PSAHHPARQPEHDNHFR*VQQL YDGDSHRQFL*HQILFDRTPVS VDQSVEKKG*DHPVRPQ*AAP GHVHYLTIPERSSQHYHPGALQ E*TSHPDHIQAK*WHYR\GHYS YARN*RIHHRGSWCR
10305	40673	A	10366	62	368	TGARRVPWPRRGARLRGRARA RSDESGSAGDQPPSFPPWWGW RWVTTAASPANLWPSVARSTM VDRAINL/FFLKMKGDLALTED KREQAQNEQSAWKFTPGR
10306	40674	A	10367	2	305	CTINNPKSF/HGVGFKQHAPQA LTEIQKFAMKEMGTPDVRIDTR LIKAVWAKGIRNVPYRIRVRLS RKRNEDEDSPNKLYTLVTYVP VTTFKNLQTVNVDEN
10307	40675	A	10368	129	283	HLILLFLKHKYCFAREEEEK*R GVGGEEEEEEEEEEGEEEEEEI FKSIVY
10308	40676	A	10369	777	1755	DIWDQTEHQSSGPWSYGTSTDP E\PTSDLAVIVFEKRGGGEEEEE KEEEEGRR\EEEEKEEEE\GRRR EEEKEEEEEEEE\GRRAQEEEEE KKEEEEEEEEEWCLGEEESQPG HAEEVPSPHKMGALTLRVEGV KEQEAKLLRSSDLMKGDFSSTS QHPPQCSKRTNSESNADAKSKK KERPIMTFRQRKTFRIRILPLPQ GRIAGSNKLSAKLCTDGRGAG DVGVLTNVMLKRLHFTIDHFLF KIIQMSPSASWNLWSLLDQDSL KCQICLEGYAQGGKPDVQLLPP RLTADWKGHRWGQMMGLDE KLTPSSVMVTSVALFWFEVSAQ

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10309	40677	A	10370	1	444	
10310	40678	A	10371	1	3799	MNRQLSKEDIQMANKHEKML NITNDQGNANQNHNAIQPYSC KNGHNRKIDVSMNMVNREHFY TAVHKASDLSFKPTSEKDLDTK LQANFPNLVKAPDKARICFCGK PYQPYVQGSPNSPVEIVENEPSQ LLHFLCVGSSKEEIDLGNPKGS QHTGLGHSMGKCNYFYLPILLV HGWKSHLHPCVASMKVAGTQ RTQDQDEAQEKEKRDKRKAEA LVAALQTYKTQNPQGAPANCY KCGKLGHFKKDCHSSKRKPL
10311	40679	A	10372	1	990	MTQKKNQTEQKEQKNEQKKQ HNERKEHKKKQTEYKTHETNR PRKTERAEHDEQKRENEGKRR RHKKRT/RERKKTNEETETRKG REKPEQARQARKEKQKRQRGE RQ\KEEKKRKNNRQENEEEEAN EQDRREQKEETRKRGPRKRRE HKEEEGRRERKKRKRKTKEKG RRAQQKERREEEQQQRRRRRR GKRKKNESEDEEDKASNKHRQ QERERQKRKGA\ERARRPAETG RRRRKRKRQRKA\AKQRQERQ GDGVLPCAPWTAHPRQPSQCW SARAPGGSAHRPRRYLLTGQA NGSLAMWDLTTAIGRPRPGPCR WPDGARADGTAGTL
10312	40680	A	10373	99	1365	KEAEGRALARLLGPSEERFAAH EGMRPMRAVFTRQGHIFTTGFT RMSQRELGLWDPNNFEEPVAL QEMDTSNGVLLPFYDPDSSIVY LCGKVLTAGQGEQGTGWRCG GPCPGAPLNRLILQGDSSIRYFEI TDEPPFVHYLNTFSSKEPQRG\M GFMPKRGLDVSKCEIARFYKLH ERKCEPIIMTV\PRKVRAWDRD LGRRSDAVPRIRQGPEPALEAD EWLSGQGRRNPCSFSLR\DGYC CPPTHRD\LRVTKRNILDVRPPS GPRRKPSRPATPPCRSSTPLETL LEEIKPLRERVQAQEQRITALEN MLCELVDGPHYPRAPGRASGL PTDPFGGAVRRACPVPPPLVPL ARAVRTLPLRYASSIAALVERM KAHMWAKGRATRDATAKRCS PMAQTTTQHLHVPCDREDESR WNYICCSS

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10313	40681	A	10374	1	361	MINPNPERSDDLVFWGLFRAG GMWSAIIAPVMILLVGILLPLGL FPGDALSYERVLAFAQSFIGRV FLFLMIVLPLWCGLHRMHHAM HDLKIHVPAGKWV\FYGLAAIL TVVTLIGVVTI
10314	40682	B	10375	70	256	
10315	40683	A	10376	224	414	LRWRSLPAFQSGNLSVPAALM NRANARGEAVCVLGRSSRFLA H*LAALGRSAAASGISSLKGG
10316	40684	A	10377	439	595	RAISCCPSHLVKRKTTLAPNTQ TASPRALADSLMQLARQVSRLE SGQ*AQRN
10317	40685	A	10378	1	391	FSSGTVPGDRPDREFIGDTLME RRNRRTGRTEKARIWETANTL AITMLMST\AMPAAAADGVTFS VPVTPHTFRHSYAMHMLYA\GI PLKGLQSLMGHKCIRSTGRLPQ RFLGLEWGLPGHPGGRLAMAE
10318	40686	A	10379	278	694	GHRSPLAIAGCPTIQNGAGPQC AAITRVRAARWCGYPPGSGIPTI PEDSFMLYPRALTTHQTGFSPA WGKPSVDRLLATLSGPGGEGQ YSCCPSHLVKKKTTLAPNTQTA SPRALADSLMQLARQVSRLESG Q*AQRN
10319	40687	A	10380	2	371	SVQVFIRDKLMERRNRRTGRTE KARIW\EVTDRTVRTCDCGGGL PAAAADGVTFFCSAPPNIRFR\H SYA\MHMLYAR*YPLKGLLSPI G\HKCIRSTGRLPQRFLGLEWG LPGHPGGRLAMAEV
10320	40688	A	10381	276	508	
10321	40689	A	10382	464	763	
10322	40690	A	10383	1	715	MQHLSHGSRRHILISENFRGCQ DQAVSQTLLTRPPLVSKEASFF LLPFDLHVLGLPPAFNLSHDQT LQFKSLTLVTSVRVPLEVARPG LSMLGLLRFMSSLLAVGDMGQ GDQVEFQDTKGNSEGRASSQPP MTPLTPTRVRRCPGGPTWGAK AEGVGRAEAATADPGSEGDVV LSRTGLLLAGLLHYFRGRHHLE EIMYNENTRRSQLLMLFDKFRS VLV\VTTHEDPVIAVFQALLP
10323	40691	B	10384	72	195	
10324	40692	A	10385	1	2331	

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10325	40693	A	10386	1	706	MTTSRSDTRSQDDPSAHLASPK LPQRLPKDLSEAQVERLLQAPLI DQPLELRDKAMLEVLYATG\LR VSELVGLTMSDISLRQGVVRVI GKGNKERLVPLGEEA\VHWLET YLEHGRPWLLNGVPINVLFPSQ RAQQITRQALWRRINHYDEL\A GIDSEKLSPHVVRHAFATYFAG SGGCIADFCGGSCAGSSAAESC LWFAGTGLYLHHAWVSGVWS RECSGAAWRDRRDVGGGE
10326	40694	A	10387	39	209	EPGTYVYNETDKSHSPCRPCVL LS**GIYLGSV*R*NGITYGALL AHIPNKFQVDY
10327	40695	A	10388	2	930	AWTHAGILLKHKYSFLVGCASI SDVIAQVVFVAILLH\SHLECRE PLLIPI\LSLYMGALVRCTTLCL GYYKNIHDIIPDRSGPELWGDA TIRKMLSFWWPLALILATQRIR RPIVNLFVSRHLGGSSAATEAV AI\LTATYPVVHMPYGWLTEIR AVYPAFDKNNPSNKLVSTSNTV TAAHIKKFTFVCMALSLTLCFV MFWDTQRV*GKSLIDIIGSGLW PLQELCVV\PLWIFSFFPVPVTV RAHLTGWLMTL\KKTFVLAPSS \VLRIIVLIASLV\VLP\YLGVHG ATLG\VGFLL\AGFCGENSTMG
10328	40696	A	10389	1	1389	GDATIRKMLSFWWPLALILATQ RISRPIVNLFVSRDLGGSSAATE AVAILTATYPVGHMPYGWLTEI RAVYPAFDKNNPSNKLVSTSNT VTAAHIKKFTFVCMALSLTLKD SVQKPDISLTGRLVQTLPTRMR HQRGESKDVAPLASWLSEPSTS SEASQTSSKLTINSQGEGKAKQ KLECGTLSIVLRSCEKNQERIKA AEKRNRSWTTLCGLGAWRPLL FELPVIVQTPDQTNRFQFRYPA KTQSGLCSFFHSFDLLTLEAFV KVWFPGCLLILIEYASSKNRKS KMLQNLKLLSADMTLKLCFVM FWTPNVSEKILIDII\GVDFAFAE LCVVPLRIFSFFPVPVTVRAHLT G\FLMTLNY\TFVLAPSSVLRIIV PHRPASWVLPY\LGVHGATLGV G\SLLAGFVGESTMVA\LATCY VYRKQKKKMENESATEGE\DS AMTDMPPTEEVTDIV\EMREEN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10329	40697	A	10390	57	556	TGRCTCHDRHYWYSPVERIAY NVEAAR\VEQRTDLDKLVIEME TNGTIDPEEAIRRAATILAEQLE AFVDLRDVRQPEVKEEKPEFDP ILLRP\VDDLELTVRSANCLKAE AIHYIGDLVQRTEVELLKTPNL GKKSLTEIKDVLASRGLSLGMR LENWPPASIADE
10330	40698	A	10391	536	787	GRD*PDYAENAHVMPPVVIED ASDMLLAITQAGRMLMFPVSD LPQLSKGKGNKIINIPSAEAARG EDGLAQLYVLPPQSTLTIH
10331	40699	B	10392	868	900	
10332	40700	A	10393	1	278	MNPQEANYAYLRG/EVELVRLP DAEGRIAAE/GALPYPPGVLALE EGI/NLLPGFAPELQGVYIEE/HD GSGIIMLPTKLAEVGTI
10333	40701	A	10394	1	811	
10334	40702	A	10395	1	682	
10335	40703	A	10396	442	546	
10336	40704	C	10397	1	1776	
10337	40705	A	10398	2	1354	YFSPAAMKALDLLIKWTRSDQ NLGGCNTGLIRPISPIVLIYKLVI GEQMIDVLGPEKRRRRTTQEKI AIVQQSFEPGMTVSLVARQHG VAASQLFLWRKQYQEGSLTAV AAGEQVVPASELAAAMKQIKE LQRLLGKKTMENELLKEAVEY GRAKKWIAHAPLLPGDGDCTS FSDEPMTGWMAAAVVTLMIR MCFSVYTMLSESCQRMVIVGY GRR\PDRQNLMIQGSKP/SIFRQF C/PDFEHLQEPYE/LLWE/MYGN RGYLQLVSFMQKFIDQSIFANT QYDPSRFPSGKVPIQQLLKDLL TAYKFGVKTLYYQNTRDGAED AQDDLVPSIQDDGCESGACLIR RASVASGSGCRMQRERLILATA RICRPDKTRQRRIRHRMRRKMP YPALNSQQDTLMAYTTFSQTK NDQLKEPMFFGQPVNVARYDQ QKYDIFEKLIEKQLFFLLASGRS
10338	40706	C	10399	1	1269	

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10339	40707	A	10400	1	1909	MGFHHVAQAGFELLISSDLPAL ASQTARITAREARAPVEENKKA QLERDKQLSEQQKQAALAKEY KAQVKQLIEMNRITIANGDIGF NFTDGNLIKKIFVDKLTQAQLIN GRLAIARLLVDNNSEGEYAIIPA SVADKIAQRDASSIVLHSALSA EEQDEDDPYADFKVPDDLMWP TVYGRSVDRIRRSRRIRQSCAM PDATLCASYQAYGLRAKHPSFS SQGVPHCVPDVTLKIASEAPSPI VGGTLPVPMTSQLPSVTSMQLL LDLDTIPNEPLHYDWEALRESI KTHGLRNSTLSALMPSETSSQIS NATNGIEPPRGYVSIKASKDGIL RQVVPDYEHLHDAYELLWEMP GNDGYLQLVGIMQKFIDQSISA NTNYDPSRFPSGKVPMQQLLK DLLTAYKFGVKTLYYQNTRDG AEDAQDDLVPSIQ\DDG\CESGA CLIRRASVASGSGCRMQRERLI RPTARICRPDKTRQRRIRHRMR RVLPGRATRRDFPSLEAGYQW LPGRGLVIEPQAQVMYQGVQQ DDCTAASRARVSQSQGDDIQTR LGLHSEWRTAVHVIPTLDLNDY HDPHSTEIEEDGSTISDDAVKQR GEIKVGVTGNISQRVSLRGSVA WQKGSDDFAQTAGFLSMTVK
10340	40708	B	10401	1	1329	
10341	40709	A	10402	1419	1788	ALTSVLPRPSVHW*\SPKPRNVD WHIGRGVAIIMQKSGIPDIDQA NCMIKLESDGTFIVHSGGADIG TGLDTVVTKLAAEVLHCPPQD VHVISGDTDHALFDKGAYASS GTCFSGNAARLAAEN
10342	40710	A	10403	73	477	SMFPRIPFGY/WHI/GSRVAIICQ K/SGIPDIDQSNLHDQLESHGTFI VHSG/GFDYGTGLDTV/VLTKL AAEV/LHCPPQDVHVISGDTDH/ ALFDKGAYASSGTCFSG/NAAR LAAVNPRALAYSYGGGGGARV CIWGGWGRR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10343	40711	A	10404	1	756	MSIAYQEIPQNERLRLSDSSITS VVEYLLAVVARSVYTSPDMAIF REHHSYMSLSMAACRKIRPCPQ ELPRSIPHMISAMWSQSAPDHV VQHEREQQSGFGDGTESHSTSD SNTEVRQNCSPPIGGVRNHRAL RGHQPAELEPENILKLLLMVAE RKAHKGWYYSGDLCRMDEAG YIKITGRKKDIIVRGGENISSREV EDILLQHPKIPNA\CMGAMSDD RLGERSCAYV\VLKAPHHSLSL EEVLCWRGC
10344	40712	A	10405	252	1245	GSRILPGASITRS\LEFIAGQAVK FNPLLPVSLVKRNTTLAPTTHT ASPRALADSLMQLARQVSRLD SGQRSVVFVRWSRRSIIVDSHA GLITTQRALGQSDMYRGSLPISE LRIIGPRHLRGVLRVVRLCPFSE PMLVECNPLLPSSLIIREPSLEPT LRFASRIALPDSTVLQIFSGVLP LSSGQAYIQFTYSETPRSTPREA NSAHILSVHQWKCGHIVMAAR VKVGYPQWTPISLSAGLSAVLY KPVERGGRCSHSCSTALSPQGF LSSLLRFISEGVFKSFTDKQMLR DFVTTRPALIVLLWQPLNVEGT SSTSHCIIMPTCNDHRD
10345	40713	A	10406	269	432	
10346	40714	A	10407	332	933	RVSRGRKVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRGLYSV HINPYLIPFFIGLQNRFTQFRLSE TKEITNPYAMRLYESLCQYRKP DGSGIVSLKIDWIIERYQLPQSY QRMPDFRRRFLQDFRLLGQ\TS VDRLL\QLSQGQAVKGNQLLPV SLVKRKTTL\APNTQTA\SPRAL ADSLMQLARQVSRLESGQ*AQ
10347	40715	A	10408	1	531	MRWKIDLARISKEIIDFYITQGV NRIGFIAGEDEPGKADIREVAFA EYGRLKQVVREEDIWRGGFSSS SGYELAK\QILARKDYPKPLFV ASDSIAIGVLRAIHERGLNIPQDI SLISVNDIPTARFSFPPLSTVRIH SEMMGSQGVNLVYEKAPDGR ALPLLVFVPSKLKLRGTTR
10348	40716	A	10409	1	1059	
10349	40717	A	10410	2187	2429	

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10350	40718	A	10411	1	835	MRPFGDYPDGGIDDLKISFSVP AAGVGPHFDQYDVFIIQGTERR RWRVGEKLQMKQHCPHPDLL QVDPFEAIIDEELEPGDILYIPPG FPHEGYALENAMNYSVGFRAP NTRELI\SGLPDYVLQRELGGNY YSDPDVPPRAHPADVLPQEMD KLREMML\ELSTHPDPFKQWLG EFISQSRHDLDIAPPDPPYQPDE FSDALNQGKVLGALGGLRVLR MGDAVYPNGEKMDSPPRPALD ALASTIALTAKNFGDALEDPSF LAMLAALVNSGYWFFEG
10351	40719	A	10412	249	474	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQL\TRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI
10352	40720	A	10413	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDPAIPLL
10353	40721	A	10414	342	528	
10354	40722	B	10415	32	587	
10355	40723	A	10416	1	2141	
10356	40724	A	10417	1	748	
10357	40725	A	10418	321	411	RNRDRYKQWKQDFFHDSYNR QRCGCWRLYRRHHR*CRRYRR QQPHLCRLYES*KKSCFHCLYR SRF/RLRVKYPRDMYSCLGTFL RSPVAIRIPLSRNQVKR
10358	40726	A	10419	1	2235	

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10359	40727	A	10420	1	1884	MGKDFMTKTPKAMATKAKID KWDVIKLKSFCTAKETTIRVNR INKIDKPLARLIKKKREKNQIDT IKNDKGDITTDPTEIQTTIREYY KHLYTNKLENLQEMDKFLDTY TLPRLNQEEVETLNRPITGSEIV AIMNSLPTKKSPGPDGFTAEFY QRYKEEL\IILIPK/PGQDTTKKE NFRPISLMNIDAKILNKILAKRI QQHIKKLIHHDQVGFIPGMQG WFNIRKSINVIQHINRAKDKNH MTISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPTVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNKRQTESQ IMSELPFTIASKRIKYLGIQLPRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VTYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIAKSILSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIT PHIYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLNVRPKTI
10360	40728	A	10421	1	822	
10361	40729	A	10422	2738	2949	
10362	40730	A	10423	1	1134	
10363	40731	A	10424	1	2118	
10364	40732	A	10425	938	1147	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH*P*VIFL WSRRIHTASCLPSQRSITGHVH HQ
10365	40733	A	10426	2	1624	
10366	40734	B	10427	1	3690	
10367	40735	A	10428	1	1056	
10368	40736	B	10429	1	2265	
10369	40737	A	10430	1	2037	
10370	40738	A	10431	1	2406	
10371	40739	B	10432	670	2568	
10372	40740	A	10433	3	4072	
10373	40741	A	10434	1	3171	
10374	40742	A	10435	1	1542	
10375	40743	A	10436	1	1008	
10376	40744	A	10437	1	2241	
10377	40745	B	10438	1	2682	

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10378	40746	A	10439	644	949	MRKPTLGRTYPSRPPSPAAARG ASRAALGPGHGLETRKSAPCTI MFRICIAGCCWLPCGTPTSVLT KRWH*P*VIFLWSRRIHTASCLP SQRSITGHVHHQ
10379	40747	A	10440	1	1088	MARKDIQVLIIGTYEYYLVKGE KVLTILAIKLKVLKWSGYPGLC LPEYHLGEVEGEDDMEVTAMD GRCLEVKQGSERLQVADQECV GDGSGRLCPFDRCECEQRLQLV RPGLCNPRAIALTTKPQSPSPNI KRLVIGEQMIDVLGPEKRRRRT TQEKIAIVQQSFEPGMTVSLVA RQHGVAASQEGSLTAVDAGEQ VVPASELAAAMKQIKELQRLL GKKTMENELLKEAVFYGRAKK WIAHAPLLPGDGERTDDWMDG RRSRHTDDTDVL*SASWRQQV QRQEQPVLRRRQQ*DFLLGWL LHHVAGQRGRPSSPVQSSAEQL RSFPVWYAVCVSPALRHQSSVL
10380	40748	A	10441	1	2781	MGKKQNRKTGNSKKQSASPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSELREDIQTKGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRS RCDQLEERVSVMEDEMNEMN DGENGTKLENTLQDIIQENFPN LARQANVQIQEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKREKEGHYIM VKGSIQQEELTILKIYAPNTGAP RFTKQVLSDLQRDLD
10381	40749	A	10442	1	2445	
10382	40750	A	10443	1	1428	
10383	40751	A	10444	1	2478	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10384	40752	A	10445	1	1746	METQKTLQKINESRSWFFEKIN KIDRPLARLIKKKREKNQIDTIK NDKGDITTDPTEIQTTIREYYKH LYANKLENLEEMDKFLDTYTL PRLNQEEAESLNKPITGPEIEAII NSLPTKKIPGPDGFTAEFYQRY KEELQHIKKLIHHDQVGFIPGM QGWFNIHKLINVIQYINRTKDK NHMIISIDAEKASDKIQQPFMLK TLNKLGIDGTYLKIIRAIYDKPT ANIILNGQKLEAFPLKTGTRQG CLLSPLLFNIVLEVLARAIRQEK EKKCIRLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLISNFSKV SGYKINVQKSQAFLYTNNRQIE SQIMSELPFTIASKRIQYLGIQLT RDVKDLFKENYKPLLNEIKEDT NKWKNIPCSWIGRINIMKMAM LPKVIYRFDAIPIKLPMTFFTELE KTTLKFIWNQKRARIAKSILSQ KNKAGGITLPDFKLYYKAIVTK TAWYWYQKRDVDQWNRIEPS ETIPHICNHLIFDKPDKNKQWG KDSLFNKWCWEIWLAIGRKRK LDPFLTPYTKINSRWIKDFNIRP KTIKTLEESLG\IQDISMGKKFTS
10385	40753	A	10446	2	541	
10386	40754	B	10447	1	1533	
10387	40755	A	10448	753	1468	LVTSYSLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVVRRPK R\WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR
10388	40756	A	10449	753	1468	LVTSYSLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVVRRPK R\WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10389	40757	A	10450	753	1468	LVTSYSLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVVRRPK R\WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR
10390	40758	A	10451	753	1468	LVTSYSLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVVRRPK R\WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR
10391	40759	B	10452	1	2259	
10392	40760	B	10453	1	684	
10393	40761	A	10454	1	1419	
10394	40762	B	10455	1	462	
10395	40763	B	10456	1	915	
10396	40764	B	10457	1	1659	
10397	40765	A	10458	1	1659	
10398	40766	A	10459	1	1224	MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYPGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVERINIVKM AILPKTAKNGPVLPPLHSEEKIP FN\FH*LFR*TITATKA*QKRR* MCQNLMTH\QNQRSGRSQIYF* RRRKNISDRSAVYR*RQLYIRR QPYAERPS\HVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFCKESQKLQQSAKKR DAELANGALGIIELNNDYTLKK VMKPLITSNTVTDEIERANVFK MNGKWYLFTDSRGSKMTIDGI LPISDPTIKQDFRLLGQTSVDRL LQLSQGQAVKGNQLLPVSLVK RKTTLAPNTQTASPRALADSLM QLARQVSRLESGQ

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10399	40767	A	10460	1	2241	MEDEMNEMKQEEKFREKRIKR NEQTLQEIWDYVKRPNLHLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRMPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKDRSMRQKVNKDTQE LNSALHQADLIDIYRTLHPKSTE YTFFSAPHHTYTKIDHILGSKAL LRKCKRTEIITNYLSDHSAIKLE LRIKNLTQNRSTTWKLNNLLLN DYWVHNKMKAEIKMFFETNEN KDTTYQNLWDAFKA/EIQTTIK EYYKHLYANKLENLEEMDKFL DT\YTLPRLNQEEVESLNRPITG AEIVAIINSLPTKKSPGPDGFTA EFYQRYKEELVPFLLKLFQSIEK QGILPNSFYEASTILIPKPGRDTT EKENFRPISLMNIDAKILNKILA KRIQQHIKKLIHHDQVGFIPGM QGWFNIHKSINVIQHINRAKDK NHMIISIDAEKAFDKIQQRFML KTLNKLGIDGTYFKIIRAIYDKP TANIILNGQKLEAIPLKAGTRQG CPLSPLLFNIVLEVLARVIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPIVTAQNLLKLISNFSKV SGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGRINIMKMAIL PKVIYRFNAIPIKLPMTFFTELE KTK\FIWNQKSAHITKGILSQKN
10400	40768	B	10461	1	1254	
10401	40769	A	10462	551	868	SIQHWSRISSRLVYRSKAVAAA LLPMNCSLWSTQAGFLPRFG*R *TRHLSTIEPEDYNLLFRRVSLK LSVWLPTWQSKSNGWSQKCL WMHLKFDSLNALLPPTGF
10402	40770	A	10463	1	2985	MEDEMNEMKREGKFREKRIKR NEQSLQEIWDYVKRPNLHLIGV PESDVENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRYS SRRATPRHIIVRFTKVEMKEKM LRAAREKGHCNSGKSHRSLWE QNKGIFTTCICDDAEDLQSPSTA GPWFGVLYTKGGPYPQEDIFSE EVHTGPKLRKKIQEYQLTSKWS KSDVQVSVERRMAGGNPNQCH IGEVLLDGFTAEFYRRYKEELV PFLLKLFQSIEKEG
10403	40771	B	10464	1	2277	

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10404	40772	A	10465	1	1064	
10405	40773	B	10466	1	1827	
10406	40774	A	10467	1186	1208	ATKMVRLSVAALVQRMKEFCA AKFPAVITCWWSVWAQSA*WR *CWRKTKI
10407	40775	B	10468	1	1992	
10408	40776	A	10469	1488	1920	RVRVTAVITERDCVSRSRWTAV IVRHCTGRSLPAASTVKQYRTS CWERWN/CRFGNDLPSSPVEWL TDN/EFMLPG**NTPVRPDVGLE PT*TRAACQESRCN/RLTPGIVL EIIGVWMQRWSLECRLAIPCIFG WLPRVVGEESGA
10409	40777	A	10470	1	1659	
10410	40778	A	10471	1	987	
10411	40779	A	10472	1	1278	
10412	40780	B	10473	1	1556	
10413	40781	A	10474	1	1905	
10414	40782	A	10475	644	949	MRKPTLGRTYPSRPPSPAAARG ASRAALGPGHGLETRKSAPCTI MFRICIAGCCWLPCGTPTSVLT KRWH*P*VIFLWSRRIHTASCLP SQRSITGHVHHQ
10415	40783	A	10476	1	1217	
10416	40784	A	10477	83	1134	
10417	40785	A	10478	2450	2607	

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10418	40786	A	10479	1	2604	MPLRAFNPVSSFRWARGMTIV AALMTVFFIMQLVGQVPAALW VIFGEDRFRWSATMIGLSLAVF GILHALAQAFVTGPATKRFGEK QAIIAGMAADALGYVLLAFAT RGWMAFPIMILLASGGIGMPAL QAMLSRQVDDDHQGQLQGSL AALTSLTSIIGPLIVTAIYAASAS TWNGNRACSSSVTRIVSILSRFI GIITPMNRNPPYTEASVTKQEK TALNMARFIRSQTLTLLEKLNE LDADEQADICESLHDHADELYR SCLARFGDDGNSYDHDYAKLA CLQVEGRGGGTFAHELLAVEY AGWISPAFRLKVNQTFIDYRTG RLQPAIPQSLPEALRLAADLAE QKQRLEQKMLMDAPKVEFAER VATASGVLIGNYAKVLGLGQN YLFTWLRDNGILI/CNR*TQERP QTRIHISWVFH/LLKKP*SIQAM EAG/LSFTTRITGKGQQWLMKR LLDARNRDRYKQWKQDFFHDS YNRQSAGHILSQCANLAATTSE YFIHKPHRLIAAETGYSQSTVV RAFREAVNKGILSVEIVIGDHRE RRANLYRFTPSFLAFAQQAKNA LIESKLKISSAATKVKAVLAKTL ALFNFLSTPPCQNDTPSPCQDD VAIKNKKSQVKKTKRSVSGGA GTTSLKKLTSWIAKAKAKADN LRLSKKRTQKHEFKQKVEAAA RKYAYLKNKRSPDIGGISNFDN
10419	40787	A	10480	1	2559	

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10420	40788	A	10481	1	1676	MLNGEKLAVKQEALLAAISEK DANIALLELSSSKKKTQEEVAA LKREKDRLVQQLKQQVEGRGG GTFAHELLAVEYAGWISPAFRL KVNQTFIDYRTGRLQPAIPQSLP EALRLAADLAEQKQRLEQKML MDAPKVEFAERVATASGVLIG NYAKVLGLGQNYLFTWLRDN GILIATGERRNVPKQEYISRGYF TLKETVIDTSNGSRISFTTRITGK GQQWLMKRLLDADVVRTTSIV MLAKVTFLSCITMSDFTFSGYE LACFVTHSGLSRSAGHILSQCA NLAATTSEYFIHKPHRLIAAETG YSQSTVVRAFREAVNKGILSVE IVIGDHRERRANLYRFTPSFLAF AQQAKNALIESKLKISSAATKV KAVLAKTLALFNFLSTPPCQND TPSPCQDDVAIKNKKSQVKKTK RSVSGGAGTTSLKKLTSWIAKA KAKADNLRLSKKRTQKHEFKQ KVEAAARKYAYLKNKRSPDIG GISNFDNLPHCMTVNEALNAVL AKNKDNEQWGAVAGAYIADIT DGEDRARHFGLMSACFGVGM VAGPVAGGLLGAISLHAPFLAA AVLNGLNLLLGCFLMQESHKG ERRGELLKIVVLPGDHVGQEIT AEAIKVLKAISDVRSNVKFDFE NHLIGGAAIDLQGGGGKPRCVS KSLMLH/CWHSCRLEPRWR*QR VQRIRL*VHP*AFFAPAVAFALP
10421	40789	A	10482	1	3213	
10422	40790	A	10483	1089	1373	
10423	40791	A	10484	2720	2968	TTTLVRLPCRSPKRRIKALRSQL RRKSILKPLLS*SR*STTK*RNTP CSQVSSLSRLSTRYRRRMKHSV NLVWTWVPYSSAP
10424	40792	A	10485	2	2264	
10425	40793	A	10486	1693	1980	
10426	40794	A	10487	1776	2026	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH*P*VIFL WSRRIHTASCLPSQRSSNRACSS SVTRIVSILSRFIGI
10427	40795	A	10488	1323	2064	
10428	40796	A	10489	53	243	WTVPLGAVPPVRMHEGLGCW CKLNGEVCMSGMCLLCWWDC D*RHDLKANLDRLMNVCQDGR KR
10429	40797	A	10490	1	3117	
10430	40798	A	10491	1	1227	

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10431	40799	B	10492	1	2119	
10432	40800	A	10493	938	1147	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH*P*VIFL WSRRIHTASCLPSQRSITGHVH HQ
10433	40801	A	10494	1	2822	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ
10434	40802	A	10495	2	163	
10435	40803	A	10496	4051	4355	MRKPTLGRTYPSRPPSPAAARG ASRAALGPGHGLETRKSAPCTI MFRICIAGCCWLPCGTPTSVLT KRWH*P*VIFLWSRRIHTASCLP SQRSITGHVHHQ
10436	40804	B	10497	1692	1781	
10437	40805	B	10498	1	3477	
10438	40806	A	10499	179	439	KKELVNLTTD*SLENR/WIDVL GPEKRRRRTTQEKIAIVQQSF/G TGDDGLPRCPATWCSSQPVISL A*AIPGRKSYCCRRRRTGCSCL
10439	40807	A	10500	1	7456	MYQANGKQKKAGVAILVSDKT DFKPTKIKRDKEGHYIMVKGSI QQEELTILNIYAPNTGAPTFIQQ VLSDLQRDLDSHTLIIGDFNTPL STSDRSTRQKVNKDTQELNSAL HQADLIDIYRTLHPKSTEYTFFS APHHTYSKIDHILGSKALLSKC KRTEIITNYLSDHSAIKLELMIK NLTQNHSTIWKLNNLLLNDYW VHKEMKAEIKMFFETNENKDT TYQNLWDTFKAVCRGKFIALN AHKRKQERSKIDT
10440	40808	A	10501	2476	2718	WPLRGRGGHRAAPGRHLHLQQ RLLLRLHLTACLLQDALDG/GP PRCWRGSCRWRCSAGPPRSWA RRPSATRSPSWPALECS

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10441	40809	A	10502	2	4517	HRLANWIKSQDPSVCYIPETHL TCRDTHRLKIKGWRKIYQANG KQKQAGVAIHISDKTDFKPTKI KRDKEGHYIMVKGSIQQEKLTI LNVYAPNTGAPRFIMQVLSDLQ RDLDSHTLIMGDFNTPLSTLDR LTRQKVNKDTQELNSALHQVD LIDIYRTLQPKSTEYTLFSAPHH TYSKIDHILGSKALLSKCKRTEII TNYLSDHSAIKLELRIKKLTQIR STAWKLNNLLLNDYWVHNEM KAEIKMFFKNNEN
10442	40810	B	10503	88	501	
10443	40811	A	10504	1	971	MWALFMIRNVKKQRPVNLDLQ TIRFPITAIASILHRVSGVITFVA VGILLWLLEYRLSYLKGSSKLR DYGQLLTLEIPAALLPIHTGIVN QNINCTETLTASSDNLLRRAFC GDTHLHEVHLNTLFFNHFLCFA VIFDETRNKDICATSGQHAHFV DKKRKRELLSHMIGKGNWQQV LVFTRTKHGANHLAEQLNKDG IRSAAIHGNKSQGARTRALADF KSGDIRVLVATDIAA/RGLDIEE LPHVVNYELPNVPEDYVHRIGR TGRAAATGEALSLVRSFFDWC DDCAAAGGMGNRNAQLADGI YHLRCIELYLGDGMADFL

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10444	40812	A	10505	1	2201	MSFDSLGLSPDILRAVAEQGYR EPTPIQQQAIPAVLEGRDLMAS AQTGTGKTAGFTLPLLQHLITR QPHAKGRRPVRALILTPTRELA AQIGENVRDYSKYLNIRSLVVF GGVSINPQMMKL\RGGVDVLV ATPGRLLDLEHQNAVKLDQVEI LVLDEADRMLDMGFIHDIRRVL TKLPAKRQNLLFSATFSDDIKA LAEKLLHNPLEIEVARRNTASD QVTQHVHFVDKKRKRELLSHM IGKG\NWQQVLVFTRTKHGAN HLAEQLNKDGIRRAAKHGNKC KCAYSKFQKPSPHIFTMLIGVC GVNQSAITNVSNVSNMAKISGS GSHRLTKRVIKRDMRPIINHPV AYSDRRRLQTELLFWHARWLN HTRRQFRIKEGDNGGQCFLFLW TGRFNFNLPSFGRIQHQQRNNA VGFSLGAFVITFIAGRACMPSLF VISTVCLTVMVYVFPAYDGVT GRFYRASGSSLPVALQYTPNGA SRRYNQWRPSRMLSSLKKQKW RKGMSESLHLTRNGSILEITLDR PKANAIDAKTSFEMGEVFLNFR DDPQLRVAIITGAGEKFFSAGW DLKAAAEGEAPDADFGPGGFA GLTEIFNLDKPVIAAVNGYAFG GGFELALAADFIVCADNASFAL PEAKLGIVPDSGGVLRLPKILPP AIVNEMVMTGRRMGAEEALR WGIVNRVVSQAELMDNARELA
10445	40813	A	10506	1	168	MCEKNLAYAHKVKAALEKGA SPGDFPREDYETNWEG\RFTLA DLNIHGKRALGMDV
10446	40814	C	10507	1	3861	
10447	40815	A	10508	1	7407	
10448	40816	A	10509	290	661	QPLPEGRW/THLWHNDELDGS RWHK/QQHGFLSLPVYVRDNT LRALGNNDQRPDYVWHE/GTA FHLFN\LKAARTGNTITAIDASE ANNWTLCLRNGVKVNGLQDG SQAESEQGLVVKPQGNALTITL
10449	40817	A	10510	3	510	KFHFMSPFPAHSMVQALE*LYA LGGLDKDCRLTEPLGMRIAEFP LNPMFAKMLLESGNFGCSQEIL SIAAMMQIQNIFVVPPNHKSHAI RVHRKFAVEEGDHLTMLNIYE AFIKHNKDSKWCQEHFLNYKG LVRAATVREQLKKLLVKFQVP RKSSEGDPDLVLRCIVS

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10450	40818	A	10511	1	1920	MIWGRAWWLTPVIPALWAAK VAGRVAEERGAVLGHEVGYCI RFDDCTDQLATRIKRLTESFSLI LSVIMLDEAHERTLYTDIAIGLL KKIQKKRGDLRLIVASATLDAD EEVETVVSMLIEQARALARTG MKRHLRVLPMYAGLPSFEQMK VFERVSRSVRKVIVATNVAETSI TISGIVYVIDCGFVKLRAYNPRT AIECLVVVPVSQASANQRAGR GGRSRSGKCYRLYTEEAFDKLP QSTVPEMQRSNLAPVILQLKAL GIDNVLRFHFMSPPPAQSMVQA LELLYALG\SLDKDCRLTEPLG MRIAEFPLNPMFAKMLLESGNF GCSQEILSIAAMMQIQNIFVVPP NQKSHAIRVHRKFAVEEGDHL TMLNIYEAFIKVSTTTARSAAST HHPLEHNKDSKWCQEHFLNYK GLVRAATVREQLKKLLVKFQV PRKSSEGDPDLVLRCIVSGF\FA NAARFHSTGAYRTIRDDHELHI HPASVLYAEKPPRWVIYNE\LL QTSKYYMRDVTAIESAWAVGS WLHTFYSTRERTCSLESQKGPR SRDPLRREPTVYSCRDCWRPLL HAAAPGPRWGELAPAPVECLV ALKWAAACSLVLSSRCPQHLH PCWDPGGLCAWAGILLCCSGQ SGSWLTQHAH
10451	40819	A	10512	3	414	
10452	40820	B	10513	62	1408	

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10453	40821	A	10514	1	1388	MGTSSIFLCVLFLCGALGLTMS PARGRLRCYICGFTKPCHPVPTE CRDDEACGISIGTSGCRGIFQVP DGQRDSRSHFPADVTKITWAC GQSPPGFKPLFPSCSSPKTGQM DVLIDLDFGFELRNRGIWGEGA IRDTEEKSADNLEPCSSPPPLEE VICCEGNAGFYEVGCVSTPLEA GYSVLGWNHPGFAGSTGVPFP QNEANAMDVVVQFAIHRLFFH PQDIIIYA\LAIGGFTATWAAMS YPDVSAMILDASFDDLVPLALK VMPDSWRGLVTRTVRQHLNLN NAEQLCRYQGPVLLIRKTQDG NLTPTVP\KDICSNRANCLLVKA LQ\HRYPG\VMAEEGLLVARQW\ LEASSQLEEASIYSRW\EVEED WCL\SVLR\SY\QAEHGADFPW\ SVGEDMSA\DGR\RQL\ALFLAR KHLHNFEATHCTPLPAQNFPRC PWHPLGTQLGLIMEEWGERRH
10454	40822	A	10515	1	1519	MGFLPKLLLLASFFPAGQASWG VSSPQDVQGVKGSCLLIPCIFSF PADVEVPDGITAIWYYDYSGQR RVFMGNPEHRVCNLLLKDLQP EDSGSYNFRFEISEVNRWSDVK GTLVTVTARSLSPPGRHLETLH MAMSWQDHGRILRCQLSVAN HRAQSEIHLQVKYAPRGVKILL SPSGRNILPGELVTLTCQVNSSY PAVSSIKWLKDGVRLQTKTGV LHLPQAAWSDAGVYTCQAENG VGSLVSPPISLHIFMAEVQVSPA GPILENQTVTLVCNTPNEAPSD LRYSWYKNHVLLEDAHSHTLR LHLATRADTGFYFCEVQNVHG SERSGPVSVVVNHPPKTPTMM VFVEPEGGLRGILDCRVDSEPL ASLTLHLGSRLVASSQPQGAPA EPHIHVLASPNALRVDIEALRPS DQGEYICSASNVLGSASTSTYF GVRALHRL/LSVPAAALGPGTA/ VWASCSCCWAWGPATPGGTG YYLTGTYKSGGQTQMLSASLF
10455	40823	A	10516	3	615	
10456	40824	A	10517	373	631	SGGPDTDVVSIPYSCSRMHLCS *LCELLSFSWETLCRAVKENEL PKKE*RAPANQGPTGESSLSGL SDSPLQPGGDGVEERRALLF

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10457	40825	A	10518	1	5521	MANRFRSGEDSGGAIWQDCVE EGASELGFLESLLYTQGNDRKQ CSLTNQGRQVFALLMLRKGHL HVFVILFGPAGPAPPQPLPSVEQ VPLSLVPGPKGVAVSRTPPFFH QVHDCPFQDPKWEEQGSWDKI AALAIAELTLTSPVARDTSDPQ CAQQAAFLHGQASWGVSSPQD VQGVKGSCLLIPCIFSFPADVEV PDGITAIWYYDYSGQRQVVSHS ADPKLVEARFRGRTEFMGNPE HRVCNLLLKDLQPEDS
10458	40826	A	10519	1	1149	
10459	40827	A	10520	111	370	SHRRSLGEAARHPSFRPAGTAF E*VSQKVVHPRDLEDRSACVPV GCSLTRESFFRLNNQPHGTRFLP IPSNPESSRRAVPSAHLTV
10460	40828	A	10521	1	220	
10461	40829	A	10522	654	967	
10462	40830	A	10523	2	1415	
10463	40831	A	10524	2	293	CGKAFTQHSRLIQH/QRMHTGE KPYEYWEFGEKPRIYLQRKTFM KLDTTTGEGQSYQRNQMPECP YGEKPCKCKECGKSFRR/SSELT RHQRAHTGEKP
10464	40832	A	10525	51	378	GDFSPQKPPMAPHGCLTYLAFQ KVKEGKKEEKKEKKKRKKERK KERKKERKKERKKERKRKEKK E\EGKEGRKEGRKEGRKEGRKE KKEISKKEIVAPTSLNPLKCSVL
10465	40833	A	10526	1	235	
10466	40834	A	10527	545	793	NKEMHWPCTGLCSHQPWGFK DCSLLE*RLPGQQEQNSIERKK RKKEKKEKKEKRKKRKKGKKE ERKKERKYHFILLLGMPTS
10467	40835	A	10528	127	376	
10468	40836	A	10529	3	710	EPG/NPERLK/GFSYPEFEDLDA LFSTLGLNEESVDSFDDYLPRR GVDSFGDKYQD/RCNSDQYHD GCQDRFRDGSHQDMGQCGGR D*DDD*GSRDYDRGYDSATGS CRRAFGSGYLRDDDY\WESSET EQQPPTGSEGKVPPVQPSEERP AKKDENKVDGMN/APKVQSGN SGRGPGDGGNKDCWRESDRKD GKKDQVCRSAPESKKPEENPAS KFSSASKCAAVSVDGEDEKEG

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10469	40837	A	10530	1	548	MQRSENDILGMDLRPLICIKDE KEEVGEKEEGEKEEEECEEQEE EGGKEWEEPGNYHLGQSLSHD WQSSETEQQPPTGSEGKVPPVQ PSEERPAKKDENKVDGMN/APK VQSGNSGRGPGDGGNKDCWRE SDRKDGKKDQVCRSAPESKKP EENPASKFSSASKCAAVSVDGE DEKEGADYTK
10470	40838	C	10531	37	289	
10471	40839	A	10532	1	1062	
10472	40840	A	10533	1	1977	
10473	40841	A	10534	1	2050	LPLLHAGFNRRFMENSSIIACYN ELIQIEHGEVRSQFKLRACNSVF TALDHCHEAIEITSDDHVIQYV NPAFERMMGYHKGELLGKELA DLPKSDKNRADLLDTINTCIKK GKEWQGVYYARRKSGDSIQQH VKITPVIGQGGKIRHFVSLKKLC CTTDNNKQIHKIHRDSGDNSQT EPHSFRYKNRRKESIDVKSISSR GSDAPSLQNRRYPSMARIHSMT IEAPITKVINIINAAQENSPVTVA EALDRVLEILRTTELYSPQLGTK DEDPHTSDLVGGLMTDGLRRL SGNEYVFTKNVHQSHSHL\AMP INHSMDV\PPCISQLLDNEESWD FNIFELEAITHKRPLVYLGLKVF SRFGVCEFLNCSETTLRAWFQV IEANYHSSNAYHNSTHAADVL HATAFFLGKERVKGSLDQLDE VAALIAATVHDVDHPGRT\NSF L\CNAGSELAVLYNDT\AV\LES HHTALAFQ\LTVKDTK\CNIFKN ID/RGNHYRTLRQAIIDMVLATE MTKHFEHVNKFVNSINKPMAA EIEGSDCECNPAGKNFPENQILI KRMMIKCADVANPCRPLDLCIE WAGRISEEYFAQTDEEKRQGLP VVMPVFDRNTCSIPKSQISFIDY FITDMFDAWDAFAHLPALMQH LADNYKHWKTLDDLKCKSLRL PSDRLKPSHRGGLLTDKGHCES
10474	40842	A	10535	2	445	ERTFNCCYPGCHFKTVHGMKD LDRHLRIHTGDKPHKCEFCDKC FSRKDNLTMHMRCHTSVKPHK CHLCDYAAVDSSSLKKHLRIHS DERPYKCQLCPYASRNSSQLTV HLRSHTGPGP\ADLLEHSRLHQ ADHPEKCPECSYSCSSAA
10475	40843	A	10536	1	957	

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10476	40844	A	10537	1	1438	MSRRKQAKPQHLNSEEPRPARR ECAEVAPQVAGEPASELDDDV PKANCLSTESTDTPKAPVITLPS EAREQMATLGERTFNCCYPGC HFKTVHGMKDLDRHLRIHTVP FCFSKVYWNGFQLGMISPPKGT MSGDIFDCYNWRRKGSTGICIW TGGGGTPICPGYHLGQIFVAILT KKPLTLTPYVFEGDKPHKCEFC DKCFSRKDNLTMHMRC\HTSV KPHKCHLCDYAAVDSSSLKKH LRIHSDERPYKCQ\VCPYASRNS SQLTVHLRSHTA\GDTPFQCWL CSAKFKISSDLKRHMIVHSGEK PFKCEFCDVRCTMKANLKSHIR IKHTFKCLHCAFQGRDRADLLE HSRA/LHQADHT\EKCPECSYSC SSAAALRVHSRVHCKDRPFKC DFCSFDTKRPSSLAKHVDKVHR DEAKTENRAPLGKEGLREGSSQ HVAKIVTQRAFRCETCGASFVR DDSLRCHKKQHSDQSEKQNLT
10477	40845	A	10538	1	1427	MIAFDSMSHIQVMLMQEESTAP ATLEHILGHSQLCGSDGLAHAA VWVLAHLHYWFTGLSPGPMD VLPLHPAISSSFHLWRVAFISKA GKPRAAGHLLKRFLRCQFQRA ASSLLFTTVEAMLGTESGTEKV MRGAGTWYHIIIENWPSAECV WTEEYQQGRGQEDSAEDRKLF VGMLNKQQSEDDVRRLFEAFG NIEECTILRGPDGNSKGCAFVK YSSHAEAQAAINALHGSQTMP GASSSLVVKFADTDKERTMRR MQQMAGQMGMFNPMAIPFGA YGAYAQALMQQQAALMASVA QGGYLNPMAAFAAAQMQQMA ALNMNGLAAAPMTPTSGGSTP PGITAPAVPSIPSPIGVNGFTGLP PQANGQPAAEEI\FANGIHPYPA QSPTAADPLQQAYAGVQQYAG PAAYPAAYGQISQAFPQPPPMIP QQQREGFVSFDNPASAQTAIQA MNGFQIGMKRLKVQLKRPKDA NRPY

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10478	40846	A	10539	1	547	AAAPMTPTSGGSTPPGITAPAV PSIPSPIGVNGFTGLPPQANGQP AAEAVFANGIHPYPAQSPTAAD PL\QQAYAGVQQYAGPAAYPA AYGQISQ\AFPQPPPMIPQQQRE GPEG\CNLFIYHLPQEFGDS\EL MQ\MFLPFGFRE/RFDNPASAQT AIQAMNGF\QIGMKRLKVQLKR PKDANRPY
10479	40847	A	10540	96	1080	WFKCYGCNSS/RDWQRSTYLLS WEVR/G/RPVPDSGCKAVVALC SQPAHPSNICKGVGGCLTK\HLL LMGAMGIRVACLEVWRDGEER GGEEATFFTSLAERQVGTAHRH LHQPALYIQIRKVPAALHMCVV QKPSLFQADSRAPLEQGLRQQA SLATARPIVSGANAGPAGLKVP QAAQLQLSPYLHRGVGDEACR YGRSQPTRKAFALCICAAPALP CPALDGSWMVCGLGQETRTSL ANVQSFTQRPQQQPLTVWMLN RGRKPAQGTLTVICPIGPGHLLT STITESVCVPRRNKYHSRTLPA AQHCQWLVTAVPTALGLVIRA GSKKLC
10480	40848	A	10541	1	392	
10481	40849	A	10542	1	110	FFWSHS*VYYTCFLLQN*KHLK PGPSGSLSPSISGN
10482	40850	A	10543	1	978	MAAATRGCRPWGSLLGLLGLV SAAAAAWDLASLRCTLGAFCE CDFRPDLPGLECDLAQHLAGQ HLAKALVVKALKAFVRDPAPT KPLVLSLHGWTGTGKSYVSSLL AHYLFQGGLRSPRVHHFSPVLH FPHPSHIERYKN\DLKSWVQGN LTACGRSLFLF\DEMDK\MPPGL \MEVLRPFLGSSWVVYGTNYR KAIFIFISNTGGEQINQVALEAW RSRRDREEILLQELEPVISRAVL DKPAPLPSPNSGHHWKERLLD AVVPFLPLQRHHVRHCVLNEL AQLGPGAKGMRVVQAVLDSTT FFPEDEQLFSSNGCKTVASRIAF

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10483	40851	A	10544	1	560	ATSPHQSQQSTVDVGQLHDPQP YPQHAIQVQHIQVSEPTASAPSS AQGSSSTQGQG\LQQQQQQQQ NSSVQHTYLPSAWNSFRGYSSE IQMMTLPPGQFVITDSGVATPV TTGQVKAVTSGHYVLSESQSEL EEKQTSALSGGVQVEPPAHSDS LDPQTNKQQQTTQYIITTTTNG NGSSEVHITKP
10484	40852	A	10545	3	205	
10485	40853	A	10546	2	348	ADQARGKPTEWAVSATQFQLD FPIT*CYGLL*QRVSRRHIGALQ GKPVPLLHVLLYPITPREGGLG DRARLCLKQQQQQQQQQQQQ QLLLLLLLLLLLLLLLLQQCEGT EGRPFPD
10486	40854	A	10547	1	1146	MVTYKLVLIRCGESTWNLENH FSS\WQKRA/IRILWTVLDAIDQ MRLPVVRTWCLKEWHYGSLA GLNKAETSAKHGEAQSNISKGC RYADLTEDQLSSGESLKEIVPQI KEGKWVLTAAHGNSLRGIVKH LEGLSEEAIMELNLPTGIPIVYE LDKNLKPIKPMQFLGDEVTLCK AMEAVAAQSKAKKRRPAGML LSPGTPSLAIPSSAPAPCTCHTD HIWNSPVYSDLAILRANPFCVHI SKANYLVNELHTAVNVAGLYI GWRCPHYLWDCFRIGDESRCF CGHLLREHRIISDISVPCKVSQC RCFMFCFIPSRPEEVGCCCGCFE SNFLCAACDRRWEEHETFFDTQ KTRQRGGRPRGADYVPFAEMA VLREAILSNSDF
10487	40855	A	10548	2	516	GRLNERHYGGLTGLNIAETAA KHGEAQVKIWRRSYDVPPPPKE PDHPFYRNIRMDRRYADLTED QLPSCESLKDTIARALPFWNEEI GPQIKEGKRVLIATHGNSLRGIV KPWEGLSEEAIMELNLPTGIPIV YELDKNLKPIKPMQFLG\DEET VRKAMEAVAAQGKAKK
10488	40856	B	10549	123	237	

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10489	40857	A	10550	1	952	PAAPQVAGRLGLGCPLHLVF AVVSAMLPLLRCVPRVLGSSV AGLRAAAPASPFRQLLQPAPRL CTRPFGLLSVRAGSERRPGLLRP RGPCACGCGCGSLHTDGDKAF VDFLSDEIKEERKIQKHKTLPK MSGGWELELNGTEAKLVRKVA GEKIPVPF\NINNSIPP\TFYGEKD PSQSQKV\EDREPELTSLPKF\VV EVIKNDDGRKA\LVLDCHYPED EVGQEDEAESDIFSI\REVSFQS\ TGESEWKDTNYTLNTDSLDWA LYDHLMDFLADRGVDNTFADE LVELSTALEHQEYITFLEDLQEV LSRAHRADRC
10490	40858	A	10551	1	879	AAGCRKENSLDLRSQFPRGRDS EDFNVKEEANAAAEEIRYTHIL NRVLPPDIRILAWAPVEPSFSAR FSCLERTYRYFFPRADLDIVTM DYAAQKYVGTHDFRNLCKMD VANGVINFQRTILSAQVQLVGQ SPGEGRWQEPFQLCQFEVTGQ AFLYHQVRCMMAILFLIGQGM EKPEIIDE\LLNIEKNPQKPQYSM AC\EFPLVL\YACKFENVKWIYD QE\LRSSNITHLQQLWANHAVK THMLYSMLQGLDTVPVPCGMG PKMDGMTEWGNVKPSVIKQTQ CLCRRSEDAHI
10491	40859	A	10552	231	358	
10492	40860	A	10553	2	319	
10493	40861	A	10554	573	1660	MAAPTPARPVLTHLLVALFGM GSWAAVNGIWVELPVVVKELP EGWSLPSYVSVLVALGNLGLL VVTLWRRLAPGKDEQVPIRVV QVLGMVGTALLASLWHHVAP VAGQLHSVAFLALAFVLALAC CASNVTFLPFLSHLPPRFLRSFF LG\QGLSALL\PCVLALVQGVG RLECPPAPINGTPGPPLDFLERF PASTFFWALTALLVASAAAFQG LLLLLPPPPSVPTGELGSGLQVG APGAEEEVEESSPLQEPPSQAA GTTPGPDPKAYQLLSARSACLL GLLAATNALTNGVLPAVQSFSC LPYGRLALPPGLWCWAVLPIP WACFLGHGCCCAGPWQGWGG LLSAGRVLWGLPDGRWQS

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10494	40862	A	10555	154	850	QFFRVITCLPFKGPDYRLYKSEP ELTTVAEVDESNGEEKSEPVSEI ETSVVKGSHFPVGVVPPRAKSP TPESSTIASYVTLRKTKKMMDL RTERPRSAVEQLCLAESTRPRM TVEEQMERIRRH\QQACLREKK KGLKCFSVLSDQSPLQSPSNLR DNPFRTTQTRRRDDKELDTAIR ENDVKPDHETPATEIVQLKETE PQNVDFS/IRGLLDCPSVSILPGR SIKRAKNQNS
10495	40863	C	10556	39	436	
10496	40864	A	10557	2	959	
10497	40865	A	10558	34	1044	QGCAVAGPLHPARLPCCVHGC PVRMHALSLCHVRCHFAVTFR LMYLDWLPTVIEPCGVGSNKV PVVQHPHHVHPLTPLITYSNEH FTPGNPPPHLPADVDPKT/GMC SCGTGRCAVARTCRIRSCVPCE ALSPCDARGAHSAGIPRPPHPPD ISPYYPLSPGT\QGQPVYPITTGG FRHPYPTALTVNASMSRKHQD SKKEEKKKPHIKKPLNAFMLY MKEMRAKVVAECTLKESAAIN QILGRRLGYNARAFGLKRGWR LDKYRGFVWMEMAVWSLPPA FSFQGKKKKRKRDKQPGETND KPESSLGASSLMVVGNWTYRN QEKHIPTLELDHTVSV
10498	40866	A	10559	2	398	
10499	40867	A	10560	174	362	
10500	40868	A	10561	14	266	
10501	40869	B	10562	67	474	

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10502	40870	A	10563	1938	3291	ERRKRFGMLDATDGPGTEDAA LRMEVDRSPGLPMSDLKTHNV HVEIEQRWHQVETTPLREEKQV PIAPVHLSSEDGGDRLSTHELTS LLEKELEQSQKEASDLLEQNRL LQDQLRVALGREQSAREGYVL QATCERGFAAMEETHQKKIED LQRQHQRELEKLREEKDRLLAE ETAATISAIEAMKNAHREEMER ELEKSQRSQISSVNSDVEALRG QYLEELQSVHRELE\VLSEQYS AKCLENAHLAQALEAERQALR QCQRENQELNAHNQELNNRLA AEITRLRTLLTGDGGGEATGSP LAQGKDAH*LKGLM\RVKESEI QYLKQEISSLKDELQTALR\DK KYASDKYKDIYTELSIAKAKA\ DC\DISRLKEQLKAATEALGEKS PDSATVSGY\DI\MKSKSNP\DFL KKDRSCVTRQLRNIRSKSLKEG LTVQERLKLFESRDLKKD
10503	40871	B	10564	58	4405	
10504	40872	A	10565	3	156	NSSHHCHHHHHHNHHHQHH QHNHC\HQHHHYNHHYDYHH DDNYYHHHHHHH
10505	40873	A	10566	10	445	HRSTITRQCPSGLETRIALLPPA VFPSGSRTLPPSTPGSSSPQPR/P PLTRGPGPPRTHALASGTRGPA RGEEKVADTPHHGEGGCPNSE KEPFLHPTAPPPRLPTPSPESGP VPHTLQQAPPLRRHLGGTPAGA PASPQSSEWGG
10506	40874	A	10567	1	288	
10507	40875	A	10568	50	542	TLSPERLSPELRLLPYMITLGDA VHNFADG\LAVGAAFAI\SWKT GLATSLAVFCHELPHELGGLRP LAAPGAVPCAKELLLNLASALT AFAGLYVALAVGVSEESEAWI\ LAVAT\ALFLYVAICDMLPAML KVRDPRPWLLFLLHNVGLLGG WTVPADAVPVRG
10508	40876	A	10569	1	690	
10509	40877	B	10570	34	465	
10510	40878	A	10571	1	624	
10511	40879	A	10572	3	933	

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10512	40880	A	10573	1	1481	RRFPPAGAVAVIERGVRGGSQR CRTMADQLYLENIDEFV\TDQN KIVTYKWLSYTLGVHVNQAKQ MLYDYVERKRKENSGAQLHVT YLVSGSLIQNGHSCHKVAVLRE DKLEAVKSKLAVTASIHVYSIQ\ KAMLKDSGPLFNTDYDILKSNL QNCSKFSAIQCA\AAVPRAPAES SSSSKKFEQSHLHMSSETQANN ELTTNGHGPPASKQVSQQPKGI MGMFASKAAAKTQETNKETKT EAKEVTNASAAGNKAPGKGN MMSNFFGKAAMNKFKVNLDS EQAVKEEKIVEQPTVSVTEPKL ATPAGLKKSSKKAEPVKVLQK EKK\RGKRVALSDDETKETENM RKKRRT\IKLPESDNSEYEVFPD SSGAYEAESPSPPPPPSPPLEPVP KTEPEPPSVKSSSGENKRKRKR VLKSKTYLDGEGCIVTEKVYES ESCTDSEEELNMKTSSVHRPPA MTVKKEPREERKGPKKGTAAL GKANRQVSITGFFQRK
10513	40881	A	10574	1	100	

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10514	40882	A	10575	2	2271	PELLTEGVKEPIMDSQERDSGD PLVDESLKRQGFQENYDARLSR IDIANTLREQVQDLFNKKYGEA LGIKYPVQVPYKRIKSNPGSVII EGLPPGIPFRKPCTFGSQNLERIL AVADKIKFTAT\RPFQGLIPKPD EDDANRLGEK\VILREQ\IKELF\ NEKLR*GPWGLNRPVLVPYKL\ IRDSPDAVEVPGLPDDIPIRNPN TYDIHRLEKILKAREHVRMAIIS QLQLLQQQQHHISEGRPFAEIC NDAKVPGESEARKPPFCPVGTR LFLLKKREPEVSMNKDRYPQE APRNLQSLRTLLDILDDPRGGC VHLRQSQSRWRGADTRELPRG MLEGLRQLLSAIGCPRDPTCAP AQPGDQPLQRLAFTLANEPQTV LEKPPPRFRRRGAARSPEQLYTP RRGGVLPAEPERTQSASADAGS LACRALEVDSGCPTGPPCPKGS RRLTITSGVDCGLLKQMKELEQ EKVVLLQGLEMMAGSRLQRLQ PVQDRQCRLGQSRASADFGPA GSPHPLGRLLPKVQEVARCVGE LLAAAGASRALPTSSSGPLCPA LTFTSFPGWQQQTILMLKEQNR RLTQEVTEKSGRVMQLEQKSA LIMKQLFEAQALSQQDGEASGL HLHLARLGWAEPQGSSVTQPFE GGRPVSPNVSGWRPPAAQAVP EWAPSCPTCHPGFPGPPPAGPR TEPLTRFWLLVLTWAGALLSLH
10515	40883	A	10576	346	3136	ALRTKRLWPGGHCRAEAPQWP P/ASPLAPATALAAHSRHLSLCR SDKGSMSEDCGPGTSGELGGLR PIKIEPEVLDIIQVTVPDALPTSE EMTDSMPGHLPSEDSGYGMET LTDKKWTWDGAKAIGISEPIKV LYSKFLMHPEELFVVGLPEGISL RRPNCFGIAKLWKILEASNSIQF VIKSGEEIRWDRELFCRACSMP GGSLLQIAKSYTTGLESKSCDP AVESKASAGQDEMQPHARPKL LTEGVKEPIVD
10516	40884	A	10577	60	352	
10517	40885	B	10578	1	720	
10518	40886	B	10579	1	1478	
10519	40887	B	10580	1	1895	
10520	40888	A	10581	2	413	

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10521	40889	A	10582	2	969	WGSWAPQSRGCPYQPGAAQGR ALAPQHRGSCSPPWTGGGKE/Y LMRAHFGLPSVEAEDKEGKPPI SVKFEIPYFTTSGIQVRLAPGSL YGRKRSSLGKSHPSLLQVDGQ YSQQQGAGHPRGTKRGSQTPG ARQRVEPGKCWPVVCVPHVPC PPTSTALRKHLRPQRAIYTSRLA PGALGGHCSVCLLPGLAGLAC GAFPGPAWVTRCCHSARSVLT HQGAPPGPDITVPARLPEPEVE VSCRGRRPALLNAQQSPPSLPPP PPSAAAEASCSHHVRQRRLRAG PEGQGFYLFHDRNKHSILKLAK PREPFCVVTDSRIQFGPPH
10522	40890	A	10583	50	1083	NPRAIFKSVRTCPVPPTQPCRNV KARSCGVGAGTTSFTLSVWPH RYITQEGHKLETGAPRAPGTVT NAVCWRSEGIKYRKNEVFLDVI ESVNLLVSA\NGNVLRSEIVGSI KMRVFLSGMPELRLGLN\DKVL FDNTGRGK\SKSVE\LEDVKFHQ CVRLSRFENDR\TISFIPPDG\EFE \LMSYRLNTHVK\PLIWIESVIEK HSHSRIEYMIKAKSQFKR\RSTA NNVGDPHFPLPNDCRLNPSFK\T TVGERLSWVPENSEIVWSIKSFP GGKEYLMRAHFGLPSV\EAEDK EGKPPDSVFKF\EIPYF\LTSGIQ VRYLKIIEKSGYQALPWVRYIT QNGDYQLRTQ
10523	40891	C	10584	175	454	
10524	40892	A	10585	1	193	LLPRPGSGLDFLLSPVLPS/HSAS WACPLPRPSPMPSSCC*R*RKE MASGFSKGPTLGCCPTCPP
10525	40893	A	10586	2780	2965	SPSQGESIPT*WRPTGPSPPTSSP GPA*SSLSPRPSPSSASASPSMC VRPSMWAASLLKSL
10526	40894	A	10587	1	1502	
10527	40895	A	10588	1256	1990	RCAPMTTCAWASCCSPWPTPF GTGPPSTSVSTSWPWQPWGWG WL*VGAAPAGGRQHPSPPALPR RSSGRSKLSRPSLCQLVPGIL*T RLLSPPQKESLPWRGSWREFPL PQLNTLPATEADPGVSSLPSAQ RHLHSYKIKVLSRQESLAPAPA SGYPESTALPQNGRGPWAVGF GQIPFLCIHNVGRSLGAGPGSG KPLPCVFRSTFSSSHQYCRLGR KHNFHFTKGKLRCGCGPGDGR

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10528	40896	A	10589	375	678	RCCCCTTRPARKCRTTMGIRHS TWPAPTATRTTHSGSRSPGSTA ASPRGLCPRPALTDCPCGHLSG LPVASV*AGSCPHVPGDQTTRK SGTVFPTQCTRP
10529	40897	B	10590	1	2452	
10530	40898	B	10591	1	1140	
10531	40899	A	10592	1	1617	
10532	40900	A	10593	1	1448	RERSCLHLVCIRCSCDVVEMGS VLGLCSMASWIPCLCGSAPCLL CRCCPSGNNSTVTRLIYALFLL VGVCVACVMLIPGMEEQLNKIP GFCENEKGVVPCNILVGYKAV YRLCFGLAMFYLLLSLLMIKVK SSSDPRAAVHNGFWFFKFAAAI AIIIGAFFIPEGTFTTVWFYVGM AGAFCFILIQLVLLIDFAHSWNE SWVEKMEEGNSRCWYAALLS ATALNYLLSLVAIVLFFVYYTH PASCSENKAFISVNMLLCVGAS VMSILPKIQESQPRSGLLQSSVIT VYTMYLTRS\CMTNEPETNCNP SLLSIIGYNTTSTVPKEGQS\VQ WWHAQG\IIGLILFLLCVFYSSIR TSNNGQVNKLTLT\SGESTLIGR WVGAR\SDGITGRDGGTDVSPE AVRINGK/RDGCSLYSYSFFHF MLC\LASLYIM\M\TLTSWYRYE P\SAWMESQWTAVL/WVKISSS WIGIVLYVWTLVAPLVLTNRDF
10533	40901	A	10594	3	343	GVLLCRL*QGQNYW/NFLQTK VTGNMRDKRTTPMPEFLHASW PNTELRYWKENCPESQKGP*PM MALS*GCPLPWPAPNVTSSSKG WSPGQLWMYRFGRPLRISSETG WSLWLT

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10534	40902	A	10595	1	2500	MEDAWGIRKETGRVKEEAEKV TGWGNNWRNVEKSSMSRKVK AARPGFKKLPMTSDIPPKCTIKD LLPKEKSSTEAVFHTVVLERHE SPDIEDFSFKEPQKNVHDFECQ WRDDTGNYKGVLMAQKEGKR DQRDRRDIENKLMNNQLGVSF HSHLPELQLFQGEGKMYECNQ VEKSTNNGSSVSPLQQIPSSVQT HRSKKYHELNHFSLLTQRRKA NSCGKPYKCNECGKAFTQNSN LTSHRRIHSGEKPYKCSECGKT FTVRSNLTIHQVIHTGEKPYKC HECGKVFRHNSYLATHRRIHTG EKPYKCNECGKAFRGHSNLTT HQLIHTGEKPFKCNECGKLFTQ NSHLISHWRIHTGEKPYKCNEC GKAFSVRSSLAIHQTIHTGEKPY KCNECGKVFRYNSYLGRHRRV HTGEKPYKCNECGKAFSMHSN LATHQVIHTGTKPFKCNECS\Q VFTQNSQLANHRRIHTGEKPYK CNECGKAFSVRSSLTTHQAIHS GEKPYKCIECGKSFTQKSHLRS HRGIHSGEKPYKCNECGKVFA QTSQLARHWRVHTGEKPYKCN DCGRAFSDRSSLTFHQAIHTGE KPYKCHECGKVFRHNSYLATH RRIHTGEKPYKCNECGKAFSM HSNLTTHKVIHTGEKPYKCNQC GKVF\IQNSHLANHQRTHTGEK PYRCNECGKAFSVRSSLTTHQA
10535	40903	A	10596	330	432	
10536	40904	A	10597	1	147	
10537	40905	A	10598	1	380	RTRGRGQRGKMELVQVLKRGL QQITGHGGLRGYLRVFFRTNDA KVGTLVGEDKYGNKYYEDNK Q/FFWHRWLHSMTDDPPTTKPL TARKFIWTNHKFNVTGTPEQY VPYSTTRKKIQEWIPPSTPYK
10538	40906	A	10599	9	536	VLKRGLQQITGHGG/LFRGYLR VFFRTNDAKVGTLVGEDKYGN KYYEDNKQFFGDERLQASGLA LTLCEQTEEGSCLWSQRSKLGK SQSMNFKNSKTRSFQRTVSAGK TKYYHPVVAGRQQQARATCD HVDPRTQEHGPGAAWPYWPRL GLKHALLTFTVALQYRAQPLFR LPNLPL
10539	40907	A	10600	239	263	
10540	40908	A	10601	1	600	

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10541	40909	A	10602	1	1178	
10542	40910	A	10603	1	1038	MHLEVNSSPEPLDENLDNTVTS ALSGHEQRIQTSLPVLLTTKTEI LARFSQLQFPEEQSSFAYPANC VKSKGMNTKLPLRPLKVCREL TIDSDRDILYRTLFMGDSGMGK VQFEFGEEVHIVIKSTGFGPFSS YATLEPFVAVQLWGGGQHYQ GQQPPMGMMGQVNQGNHMM GQRQIPPYRPPQQGPPQQYSGQ EDYYGDQYSHGGQGPPEGMN QQYYPDGHNDYGYQQPSDPEQ GYDRPYEDSSQHYYEGGNSQY GQQHDAYQGPPPQQGYPPQQQ QYPGQQGYP\KQQQGYGPSQG GPGPQYPNYPQGQGQQYGGYI PTQPGPPQPPQQRPYGYDQGQY
10543	40911	A	10604	130	213	LKVST*AMPLPR*TPSRRCQP*R TGTSP
10544	40912	A	10605	124	208	LKVST*AMPLPR*TPSRRCQP*R TGTSP
10545	40913	B	10606	140	589	
10546	40914	A	10607	1	302	
10547	40915	A	10608	2	98	
10548	40916	A	10609	2	190	
10549	40917	B	10610	1	856	
10550	40918	A	10611	123	1287	AFSLGK\MSEKKLFGPNGERMP FSKVKALCAGLQATVAAPKNA EENKAIQDVAKDTAFLGITDEA TEGQFMYLTGGRLTYSNWKKD EPNDHGSGEDCVILLNNGLWN GISCTSSFIAIFQWAHYQYRQAE NYPKGELHTLRVKLCGPSWPT NAIHFRSRLLMPLGPTVLLMTM AVFQLSQAVAMCSWCCGLVLP PAGCLQDKASKPRETQAPGL CVRGNFRIPSRQDFAAALARAL SGLDLWASLWVPFADFLGSSLS VPWFSYLENDEEDLTRLSLRLN GERTFLESPGKKRIGAGTPPMS QEAVMLAVMERDPGQCRGEE GPTECRAMWPGWGGRHSLPGH PAMLCSFLGSDLEIRGSNGGWE PPFIPGLQPELARGIQGSGRGAE
10551	40919	A	10612	292	445	LSICLQSAVCTPGMD/PAAPCSL GILDWGTLPSTAEPGREGPADA WVDPGVR
10552	40920	A	10613	363	575	HLLPTQGALCPAEGWPAPWQG YTPTCDCAEDTTQLERAGQLPP VF*SCHRGGVSSQ*GSPGVPQL LHQPE

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10553	40921	A	10614	3	638	SSKLSGLTTNVVDIILAHHFGQE ELQANLDLIQTYRMHIAQDINQ DNLQLFLNSYNGRRDLEIERPIL GQNDNKSKTLKG\STLLVVGDN SPAVEAVVECNSRLNPINTTL\L KMADCGGLPPG*FSPGKLTEAF KYFLQGMGYIPLVLCYST\SGS MTSVARSR\THSTSSSLGSGESP FSRSVTSNQSDGT\QES\CESPDV LDRQQTMEVSC
10554	40922	A	10615	3	1152	KSCFNAFFNFEDMQEITQH\FAV CHVDAPGQQEGAP/SPFPTGYQ YPTMDELAEMLPPVLTHLSLKS IIGIGVGAGAYIL\SRFALNHPEL VERPLCSLMVDPC/ALKGWIDW AASKLSG\LTTNVV\EIILAHHFG QEELQANLD\LIQTYRMHIAQDI NQDNLQLFLNSYNGRRDLEIER PILGQNDNKSKTLKCSTLLVVG DNSPAVEAVMADCGGLPQVVQ PGKLTEAFKYFLQGMGYIPVCA AQSPEHRVST\SASMTRLARSRT HSTSSSLGSGESPFSRSVTSNQS DGTQESCESPDVLDRHQTMEIS LDDVLLSALLRNNGKSAQQKKI SAKPKLEFLCPRPGTCDHGSRE KQGHSRGPGQFPGRWPGRAVA ETRGAIDHRL
10555	40923	A	10616	169	270	GICPFLQLSFYHLLD*DTRYLQI LRLQLKPHSFH

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10556	40924	A	10617	1	1551	MRKDSCASSMHQQVSRSKKRA GQKTPPEDQEGGQRALRSSHIR LGQFLLIEDCKTPSPSSLGADAI AKQRKTSVSAAASVSATIPIRR VQGPTVVGSWARGVSAAASGP RGTGPKGKARSEKGCSLSHGPQ TNKPLVVQKGQKMEQANHPV GLVISVVYKDILKKIVQRETSHP LIHVRYAEAITGRRTAPEDKGS LGRDMLAKAGAIIYMNMGNKL PIWCHLLEEGIYLEVWALEGQF GRAKNACPVQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSPCNTPILGVQKP NGQWSLVQDLRLISEAVIPLYP VVPNPYTLLSQIPEEAEWFPVL DLKDAFFCIPLHYDSHDSQFLF AFEDPTDHTSQLIWTVLPQGFR DSPHLFGQALAQDLGHFSSPGT LVLQYVDDLLLATSSEASCQQA TLDLLNFLANQGYKASRSKAQ LCLQQVKYLGLILARGTRTLGK ERIQPILAYPHPKTLKQLWGFL QIT/GFCQLWIPR*SKI
10557	40925	A	10618	1	1022	MKPSVWALIQLNLSPYEKGILG LTKRHQGRLCTDGRQGIQPLPP SQAHTGIPLLHPYSIQVDCAIDR GKLCFCCCIGECNYSDQQGPGT VAGSWARGISAAVSVSATILISR VQGPLHVLGQEVFLLLRRQTNL AGSERTENGAGQSPGGACYQC GLQGHFTKDCPMRNKLPPRPCP LYQGNHWKDGEPIEHDCQQIIV QTSAAREDLLEVPLANPDLNLY TDGSSFVENGEVAKAVIAQFPT TVGVSCLDGRLRVLEVLARAIR /LGEGNKGYSIRKRGSQIVPVCR *HDCISRKPHHLSPKSP*ADKQL QQSLRIQNQCAKITSILIHQ*QT
10558	40926	A	10619	1	2091	
10559	40927	B	10620	1	2269	
10560	40928	A	10621	1	1776	

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10561	40929	A	10622	112	1465	LLKGARCLIQRPSFA/LQQETHR AHTLLLEWEPQAETAFTTLKQA LLQAAALTLPTRQNFSLYVTDR AEIALGVLIQTCGTTPQPVAYLT IEKGKERGEQQHKQLAEAAER KERKRQEVREREKEKETERQSK KEREEETKMESERKRETEKEVS TLAALEEPFSPPQPSLGLAEAGA GSLFSWGGVEGEVRGGGRAAH SAHRLVQVPGGQVRVQVFENP LLKAIKSDLPRSSLWSGRKTSV SAAALKEIRKEISKGTQIPLGYR LCPLQAVGGGEFGPTKIHVPFS LSDLKQIKADLGKFSDDPDRYI DVLQGLGKTFDLTWRDVMLLL DQTLAFNEKNAALAAASEFGGI WYLSQVNDRMTAEERDQFPTG QQAIPSMDPHWDLDSDHGDWS HKHLLTCVLEGLRGIRKKPMN YSMMSTIIQGKEENPSAFLQQL WKSLRKYTPPSSKSL
10562	40930	C	10623	52	690	
10563	40931	C	10624	199	285	
10564	40932	A	10625	59	411	SWPSDKQTLVVQRGQKMEQA NHPDPTDHMSQLMWT/VLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLLATSSEASCQ QATLALLNFLANQGYK/LSRSK AQLCLQQVKYLCL
10565	40933	A	10626	280	571	DIYVPIRII*KLPQAYAD/PAVPP CTSGRIWL*IHAGAWSSFWLVS Y*LLPQFQILLLVYSEIQILPGLV LGECMCQGICPFLLDFLVYLRR GVCSIL
10566	40934	A	10627	60	148	WGRGEPLCLAQGL*THQSAPC QNRPLGSL
10567	40935	B	10628	1	397	
10568	40936	A	10629	55	219	LGNKHLLGSIDPRGSWVTGEYI FLRPPIAA*GRQ*DFLPFPELWW TSLNNSWAFS
10569	40937	A	10630	3	494	
10570	40938	A	10631	2	689	
10571	40939	A	10632	157	277	DV*SNNSMTSLQVRCRTSMYLS GSSENFPRSTWICDAVAETPLA QEPATVPGP
10572	40940	A	10633	230	543	PSDRQTLVVQRGQKIEQANHL VGLVTSVVWKDTLKKIVHGMA FSMLISC/PRQLSSRSITIQGILGR AVTRYFSHLLSCNWETLLQIDQ GHQATDGLTNGTPNELN
10573	40941	B	10634	1	669	

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10574	40942	A	10635	119	409	GDICHHLGLTPVGSHSLLSCSR* QVA*VGAVTAATIGTGILLQQL AFLVCNWLLLSGSSENFPRSALI CFKSEREKGTCIQVGPNSPPPTA CKGHN
10575	40943	A	10636	3	482	LSSYSGGDLEKLYV*LRDCKYT NQHSVSSSRFVNIPISTLCLTQG L*MHPMDTLYLATLGGDLENL CVHTLYLANLVGMWRTFVSSS GIVNAPISTLSKQTT*LSVKWTN QQDVGGARQENKSRLPEPAVT TPLGSPPTPWKLCSFALCNKSC YCPKKKK
10576	40944	A	10637	1	2331	
10577	40945	A	10638	879	1353	SNNRTEGARGKRQLMSSP/STE PRVRLTIEGQETDFLLDTGAAFS VLISCLGRLSSRSVTIR*ILGQPV TRYFS/QPLSCNWETLLFSHAFL IMPESSTPLLGRDILAKAGAIIYI NMGNKLPICCP\LLVEGINPEV WALEGQFGRAKNARPLQIRLK
10578	40946	A	10639	345	1996	
10579	40947	B	10640	97	1110	
10580	40948	A	10641	728	5171	
10581	40949	C	10642	1	2049	

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10582	40950	A	10643	1	2019	MNAHPEFRMAMKDGELVIWD SVHPCYTVFHEQTETFSSLWSE YHDDFRQFLHIYSQDVACYGE NLAYFPKGFIENMFFVSANPWV SFTSFDLNVANMDNFFAPVFTM GKYYTQGDKVLMPLAIQVHHA VCDGFHVGRMLNELQQYCDE WQGGAQYPLRPEAHKGIQDIV KYLKAQGLGRKCSSPCNTPILG VQKLNGQWRLVQDLRLIN/EGF F*SSKLQAMQAMFAENSMSSV YSPTQEAEYWLPHGILQPADCF FEAASTSRSMWPRE/DWLSTT/S LTTWNMDFADFGTTIKQDFRLL GQTSVDRLLQLSQGQAVKGNQ LLPVSLVKRKTTLAPNTQTASP RALADSLMQLARQVSRLESGH LDHGSHSYRRSDNSLDPRSHSC CRSDIGLGPRSHLYCRSDYQRE TTIPSMPVKGNQAPCMKSNNA LIVILGTVTLDAVGIGLVMPVLP GLLRDIVHSDSIASHYGVLLAL YALMQFLCAPVLGALSDRFGR RPVLLASLLGATIDYEIMATTPS WEDEEPIEHDSQQIIVQTYATR DDLLEVPLANPDLNLYADGSSF VENGIRRAGYAIVSDVTVLENS LAAVTLQNRQGLDLLTAEKGG LCTFSGKECCFYTNQSGISSPLE DTTTAGPFLHPIQQEVARAIIGQ FPTAFGVSCLEGRLRGEASWTS
10583	40951	A	10644	803	1171	
10584	40952	A	10645	1	2148	
10585	40953	A	10646	1094	3886	SNDRTEDDCGKHPFMSSPP\TEP WVCLIIEGQEIDFLLDTGTTFSV LIPCLGRLSSRSVTIQGILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPTPLLGRDILAKAGAIISM KTGNKLPICCPLLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPEEAEW FTVLDLKD
10586	40954	A	10647	762	1298	

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10587	40955	A	10648	893	2165	GPRGTGPKGKARSEKGRSLSHG PQTNKPLVVQKGQKMEQANHP VGLVISVVYKDILKKIVQRETS HPLIHVRYAEAITGRRTAPEDK GSLGRDMLAKAGAIIYMNMGN KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDPTTFP YQRQYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPILGVQ KPNGQWSLVQDLRLISEAVIPL YPVVPNPYTLLSQIPEEAEWFP VLDLKDAFFCIPLHYDSHDSQF LFAFEDPTDHTSQLIWTVLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLLATSSEASCQ QATLDLLNFLANQGYKASRSK AQLCLQQVKYLGLILARGTRTL GKERIQPILAYPHPKTLKQLWG FLEITGFC*LWIPGYSKIARPLYT
10588	40956	A	10649	2	403	
10589	40957	B	10650	51	1038	
10590	40958	A	10651	581	1128	SPCRAQRHSCMWGLWQQSPCS PGSWQDSSPAQSGPPPR*PFSVP SSPWCLPSTWPLSPSPLPASWR RKTSAPSLLSLATAGPP*AGVC E/AKTPKKKYSDDDEEEESEEN SRDSESDFSDDFSDDFVETRRR RSRRNQKRQINYKEDSESDGSQ KSLRRGKEIRRVHKRRLSSSESE GYFFIKS
10591	40959	B	10652	1	4296	
10592	40960	A	10653	2	447	KEKKRNKKKKTIGSPKRIQSPL NNKLLNSPAKTLPG/AC/GSPQK LIDGFLKHEGPPAEKPLEELSAS TSGVPGLSSLQSDPAGCVRPP\V VKYCTDLIEEKDLEKLDLVIKY MKRLMQQSVESVWNMAFDFIL DNVQVVLQQTYGSTLKVT
10593	40961	C	10654	286	336	
10594	40962	A	10655	421	638	

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10595	40963	A	10657	1	888	MMNEKNLEKGLGVDSVDKDA MNAAIQQAIKAQPSMSPKKAPP APAKEARNVVAVGTGGRGTHD RDPSEKPPRLQWFEQQAKKLA KQQEEDSEEEEEDLDGDVLEIG KSKIKVLAESVSDWEDIDSDEE LECEDTEAMDDVVEQDAEEEE AEEGPPLGAIPITDCLFCSHHSSS LMKNVAHMTKDHSFFIPDIEYL SDIKGLIKYLGTHSSSSNVCKGL WDLEKRPSIDLK/CRT*YSTKRH /CTRTLSASSHFILCQWFSVLS/P VHASTDQEIQEMHDDQSNPQN AVVREHCVGWGWGV
10596	40964	A	10658	1	1545	MATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAP VTAEGFQERVRA\HGPSRRRRA RARP/LYCTVCSKKFASFNAYE NHLKSRRHVELEKKAVQAVNR KVEMMNEKNLEKGLGVDSVD KDAMNAAIQQAIKAQPSMSPK KAPPAPAKEARNVVAVGTGGR GTHDRDPSEKPPRLQWFEQQA KKLAKQQEEDSEEEEEDLDGD VLEIGKSKIKVLAESVSDWEDI DSDEELECEDTEAMDDVVEQD AEEEEAEEGPPLGAIPITDCLFC SHHSSSLMKNVAHMTKDHSFFI PDIEYLSDIKGLIKYLGEKVGVG KICLWCNEKGKSFYSTEAVQA HMNDKSHCKLFTDGDAALEFA DFYDFSWRLAVGGHDWVERLT ASHYFYGYYPGARVGHRSLMR YYKQRFGLSRAVAVAKNRKAV GRVLQQYRALGWTGSTGAAL MRERDMQYVQRMKSKWMLK TGMKNNATKQMHFRVQGSQK EIQIFHSSEIDGIATAVEDDFASP TPTKDAKN
10597	40965	A	10659	3	943	

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10598	40966	A	10660	1	2427	MATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAP VTAEGFQERVRA\HGPSRRRRA RARP/LYCTVCSKKFASFNAYE NHLKSRRHVELEKKAVQAVNR KVEMMNEKNLEKGLGVDSVD KDAMNAAIQQAIKAQPSMSPK KAPPAPAKEARNVVAVGTGGR GTHDRDPSEKPPRLQWFEQQA KKLAKQQEEDSEEEEEDLDGD DWEDIDSDEELECEDTEAMDD VVEQDAEEEEAEEGPPLGAIPIT DCLFCSHHSSSLMKNVAHMTK DHSFFIPDIEYLSDIKGLIKYLGE KVGVGKICLWCNEKGKSFYST EAVQAHMNDKSHCKLFTDGD AALEFADFYDFSWRLAVGGHD WVEVEGRIRGCGSREDNECLL VCNFSVIGVAIQITRKGRTPIRA EELPSEKNLEYDDETMELILPSG ARVGHRSLMRYYKQRFGLSRA VAVAKNRKAVGRVLQQYRAL GWTGSTGAALMRERDMQYVQ RMKSKWMLKTGMKNNATKQ MHFRVQMDCRGIAVLVFKAPS FYLIMAPKHKSGDAGDSNMPK GSRKVLPLSEKVKVLKEKKLY AEVAKIHGVKLQTFGVSVTAH KGSVDPKSEQQQDLLQRVKEQ SFHSVEADPAAEGAGSGLSQLR KGLPQCSSRLNGSSSATKVGAQ AEEAPRASEGCEGCQHAVTSQ
10599	40967	A	10661	3	658	GTKGWAFPITDCLFCSHHSSSL MKNVAHMTKDHSFFIPDIEYLS DIKGLIKYLGEKVGVGKICLWC NEKGKSFYSTEAVQAHMNDKS HCKLL\QDGDAALEFADFYDFR SSYPDHKEGEDPNKAEELPSEK NLEYDDETMELILPSGARVGH\ RSLMRYYKQAIWLVKNLWQLP KIRKAVGRVLQQYRSPGIGLGS TGAALMRERDMQYVQRMKSK MGC
10600	40968	A	10662	1	221	MNPLANSTLTDVHPHFIFKQMA ELDRDMDEAGNHHSQQTNTRT ENQTPHVLTHKWELNNENTRT QGREHHTSEEFIAIQPEYYQKE KSNSDINLEGTSYWTENHCSGI YKVINCLESEIHSEEN*CQN*IFL SDNIQVELR*IPLMCDVPCPVSV CSHCSTPTYE

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10601	40969	A	10663	1	1815	MHEAGNHHCQQSNTRKENQTP DVLTHKWEGFDQLRLEGLLCD VTLMPGDTDDAFPVHRVMMA SASDYFKAMFTGGMKEQDLM CIKLHGVSKVGLRKIIDFIYTAK LSLNMDNLQDTLEAASFLQILP VLDFCKVFLISGVTLDNCVEVG RIANTYNLTEVDKYVNSFVLKN FPALLSTGEFLKLPFERLAFVLS SNSLKHCTELELFKATCRWLRL EEPRMDFAAKLMKNIRFPLMTP QELINYVQTVDFMRTDNTCVN LLLEASNYQMMPYMQPVMQS DRTAIRSDTTHLVTLGGVLRQQ LVVSKELRMYDEKAHEWKSLA PMDAPRYQHGIAVIGNFLYVV GGQSNYDTKGKTAVDTVFRFD PRYNKWMQVASLNEKRTFFHL SALKGYLYAVGGRNAAGELPT VECYNPRTNEWTYVAKMSEPH YGHAGTVYGGVMYISGGITHD TFQKELMCFDPDTDKWIQKAP MTTVRGLHCMCTVGERLYVIG GNHFRGTSDYDDVLSCEYYSPI\ LDQWTPIAAMLRRQSDVGVAV FENKIYVVGGYSWNNRCMVEI VQKYDPDKDEWHKVFDLPESL GGIRACTLTVFPPEETTPSPSRES
10602	40970	A	10664	1	1226	MNEIEFRLERTPVDESDDEIQH DEIPTGKCIAPIFDKRLKHFRVT EGSPVTFTCKIVGIPVPKVYWF KDGKQISKRNEHCKMRREGDG TCSLHIESTTSDDDGNYTIMAA NPQGRISCSGHLMVQSLPIRSRL TSAGQSHRGRSRVQERDKEPLQ ERFFRPHFLQAPGDMVAHEGR LCRLDCKVSGLPPP\DMTWLLN GQPVLPDASHKMLVRETGVHS LLIDPLTQRDAGTYKCIATNKT GQNSFSLELSVVAKEVKKAPVI LEKLQNCGVPEGHPVRLECRVI GMPPPVFYWKKDNETIPCTRER ISMHQDTTGYACLLIQPAKKSD AGWYTLSAKNEAGIVSCTARL DIYAQWHHQIPPPMSVRPSGSR YGSLTSKGLDIFSAFSSMESTM VYSCSSRSVVESDEL
10603	40971	C	10665	166	229	
10604	40972	B	10666	251	371	

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10605	40973	A	10667	79	1391	PWEGSAPATSPLGEDSAWGSA DGSESWSCRELLQPGDVLGESC GLTPPALPAHCIQEGCLPPLTQE LRCCQPPRMGRWALDVAFLW KAELTLGLELLYY\CFFIGINFY NKWLTKSF/HIFPLFMTMLHLA VIFLFSALSRALVQCSSHRARV VLSWADYLRRVAPTAALREVA SLFRKPSAEEMLCPPARQRGEA RELSQNPIIRAGEGRLQGHRQV ATVICAPAPFSVMGLSPELQQCI VGNFASRYTMTKSSAVLFILIFS LIFKLEELRAALVLVVLLIAGGL FMFTYKSTQFNVEGFA\WCWG PRSSVAFAGPSPRCSCRRLNSAS RIPSTPCSTCSHSCS/WGLFPLFA VFEG\TGLLLRVLGSLFLGGILA FGLGFSEFLL/VSSRTSSLTLSIA GIFKEVCTLLLAAHLLGDQISLL NWLGFA\SASREYPSTLPS
10606	40974	A	10668	1	1129	MGRWALDVAFLWKAVLTLGL VLLYYCFSIGITFYNKWLTKSF HFPLFMTMLHLAVIFLFSALSR ALVQCSSHRARVVLSWADYLR RVAPTALATALDVGLSNWSFL YVTVSLYTMTKSSAVLFILIFSLI FKLEELRAALVLVVLLIAGGLF MFTYKSTQFNVEGFA\WCWGP RSSVAFAGPSPRCSCRRLNSASR IPSTPCSTCSHSCSWGLFPLFAV FEGLHLSTSEKIFRFQ\DTGLLR RVLG\SLFLGGILAFGLGFSEFLL VSRTSSLTLSIAGIFKEVCTLLL AAHLLGDQISLLNW\LGFA\SAS REYPSTLPSKPCIPEVTQSPFQK PLVSVLLPVTLSDSDAGSVPGG SAAVTPLGRCGGHLQSGWVGP
10607	40975	A	10669	566	1026	PVMPKLIYVIRTGKQLKISLGH VDFQTVPSFLQQLNV/WQTIKA SEHPDRNDCVAVLRQKRSLGS VENTSGKRKCWGGQSGFTTSE LEETEEDSDLSDYGDDVDGRK DALAEPCFMLIGEIFELRGKPQY QLEIWQVPTGTPDHLEEEANEK

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10608	40976	A	10670	1717	2340	GIDVQGKKNSFSLSSFLERLPRD FFSHQEEETEEDSDLSDYGDDV DGRKDALAEPCFMLIGEIFELR GMFKWVRRTLIALVQVTFGRTI NKQIRDTVSWIFSEQMLVYYINI FRDAFWPNGKLAPPTTIRSKEQ SQETKQRAQQKLLENIPDMLQS LVGQQNARHGII/NKYSNALQE TRANKHLLYALMELLLIELCPE LRVHLDQL
10609	40977	A	10671	181	399	NRYIVPISQIMKRKRRKVSIVLN VTGY*/RGM/RKPGLLNLASGFL LSTSPTSENSNRCRGLWQIDPW EEGETYV
10610	40978	A	10672	66	535	CWWQDPLQRTRQKSVTATSTK ID\ISNVKIPKHPADAYFKKQQL WKPRNRKLAGKLSTPAARDAP RARPPHEAPPPPPPPELRYRVPP RPAPSSWRHPSGKGRRGPPGIG GRIVGERQLRTEYGNDRPGREG DPAPGCCGGARTLSLYGEIKLR VKF
10611	40979	A	10673	67	585	SAAKSEMAGEKVEKPDTKEKK PEAKKVDAGGKVKKGNLKAK KPKKGKPHCSRNPVLVRGIGRY SRSAMYSRKAMYK\RKYSAAK SKVEKKKKEKVLATVTKPVGG DKVGGTRG\VKLRK\MPRI\YPT EDVPRKLLSHGKKPFSQHVRKL RASITPGTILIILTGRHRGKRVVF
10612	40980	A	10674	2	282	CIALYCHLLNICSKVKAEMQNL GREFIVPGMDSATSLIWATK/DL MNAVIEAPEKKPLLKREKQDES QSEIKWASQKKHLNPVQALSEF KAMDSI
10613	40981	A	10675	2	2798	
10614	40982	A	10676	14	2858	PDWRETKQRPSASGLWNLALA QLAAEMTAVHAGNINFKWDPK SLEIRTLAVERLLEPLVTQVTTL VNTNSKGPSNKKRGRSKKAHV LAASVEQATENFLEKGDKIAKE SQF\L*E*LLAAVEYVRKQGDL MKTAAGEFADDPCSSVEQGNM VQAA*TLLSAVTCLLILA\DMG NVYTLLIQLKVVEDDILKLRNA GNEQDLGI*YKALKPEVNKVNI MAVKRQQELKDVGHRDQMAA ARGILQKNVLIFYTASRA
10615	40983	A	10677	1	4545	

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10616	40984	A	10678	1	1921	MAGLGMGEEGIPGGERWEHKR RAHIVSNHRITRTGTHPYTHSPY PHKDNVHTARREHKTQDLGTI RSVGHSSEHTQHTTPDTVPPLV VIVCRVCYRPPHGETRAEYTRH RGQNRRTKFWVGIKEEKNLAQ QERTEEQLANIARGGYVLKDC AGQPELIFIATGSEVELAVAAYE KLTAEGVKARVVSMPSTDAFD KQDAAYRESVLPKAVTARVAV EAGIADYWYKYVGLNGAIVGM TTFGESAPAELLFEEFGFTVDNP LASRAVRLRLPFNNDQVEAAV GWKLAVERHNGPTALILSRQN LAQVERTPDQVKEIARGGYVL KDSGGKPDIILIATGSEMEITLQ AAEKLAGEGRNVRVVSLPSTDI FDAQDEEYRESVLPSNVAARV AVEAGIADYWYKYVGLKGAIV GMTGYGESAPADKLFPFFGFTA ENIVAKAHKVLGVKAGSHIPRK KYDVPGKKSFSPVKYSTIGSPSP ERPVSITTIPNSFVIITANRVLHC NADTPEEMHHWITLLQRSKGD TRVEGQEFIVVEKLIRGLAMED SRNMFAL/S*IQRPRRQSH*KSN RRS*CLSQV*KRASW*AFTNI* WPDRHGLRKYSF/WSPGNIHHL RHCRML*VVRLLLRLLNAVYE
10617	40985	A	10679	1	2940	
10618	40986	A	10680	2	404	
10619	40987	A	10681	2	546	WCPHRWRPHTLTPTAAPAVTK SPEATHLYGQVSWNSQNLHLE GQLQSASLQGSFMLK**GDPLD F/VMSPPRPLFERLKARISQSTK TFTPCERLEKRRTSFLEGTLRRS FRTGSVVRQKVEEEQMLDMWI KEEVSSARASIIDKWRKFQGMN QEQAMAKYMALIKEWPGYGST LFDVEGTDT
10620	40988	A	10682	1	555	
10621	40989	A	10683	1	627	

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10622	40990	A	10684	1	7232	MPEPPTHSMGSCAAGASLTSTA PCSTAPSPIDHLRAKECERTAQ DWQAAPPAALVRDPLAALVRT WRTFMSSSRIVNTPIGTLCLAQ GFQWFSVLSQVHASTDQEIQE MHDEQANPQNAVGTLDVGLID SVCASDSPDRPNSFVIITANRVL HCNADTPEEMHHWITLLQRSK GDTRVEGQEFIVRGWLHKEVK NSPKMSSLKLKKRWFVLTHIPG LLQEFREDALNWGPDEKIFKET ELVNDMDKINGRIERAE
10623	40991	A	10685	1	2146	IDSVCASDSPDRPNSFVIITANR VLHCNADTPEEMHHWITLLQR SKGDTRVEGQEFIVRGWLHKE VKNSPKMSSLKLKKRWFVLTH NSLDYYKSSEKNALKLGTLVL NSLCSVVPPDEKIFKETGYWNV TVYGRKHCYRLYTKLLNEATR WSSAIQNVTDTKAPIDTPTQQLI QDIKENCLNSDVVEQIYKRNPIL RYTHHPLHSPLLPLPYGD\INLN LLKDKGYTTLQDEAIKIFNSLQ QLESMSDPIPIIQGILQTGHDLRP LRDELYCQLIKQTNKVPHPGSV GNLYSWQILTCLSCTFLPSRGIL KYLKFHLKRIREQFPGTEMEKY ALFTYESLKKTKCREFVLSRDEI EALIHRQDMTSTVYCHGGGSC KITINSHTT\AGEVVEKLIRGLA MEDSRNMFALFEYNGHVDKAI ESRTVVADVLAKFEKLAATSEV GDLPWKFYFKLYCFLDTDNVP KDSVEFAFMFEQAHEAVIHGH HPAPEENLQVLAAHATSSIMQG DYT\LHA\AIPP\LEEVYSLQRLK ARISQSTKTFTPCERLEKRRTSF LEGTLRRSF\RTGSVVRQKVEEE QMLDMWIKEEVSSARASIIDK WRKFQGMNQEQAMAKYMALI KEWPGYGSTLFDVEVRTGCHV LGWAGCWHLRTWITAKFMWR EDKMEHFALSTSFFRAPKIVPLT PPFSSQFLFSCVVNASVILGMN

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10624	40992	A	10686	28	561	MDIVQDATFVYATLQTAHYHR DAGLPVYLYEFEHHARGIIVKP RTDGADHGDEMYFLFGGPFAT GAKVPPDTPTGCPVSHLWMQT HPSIGWPQGAHQFLICYALPNE SLLLRKQQKQQE*GGRNPNDG NLPCWPRYNKDEKYLQLDFTT RVGMKLKEKKMAFWMSLYQS QRPEKQRQF
10625	40993	A	10687	148	444	
10626	40994	A	10688	1	1531	PLPGARRCLHEFWGQLASMYV STRERYKWLRFNEDCLYLNVY APARAPGDPQLPVMVWFPGGA FIVGAASSYEGSDLAAREKEGL VFLQHRLGIFSFLSTDDSHARG NWGLLDQM\AALRWVQENIAA FRGRPREILTLFGQSAGAMSISG LMMSPLASGLFHRAISQSGTAL FRLFITRNPLKVAKKVAHLAGC NHNSTQILVNCLRALIR\AKVM RVSNKMRFLQLNFQRDPEEIIW SMSPVVDGVVIPDDPLVLLTQG KVSSVPYLLGVNNLEFNWLLP YIMKFPLNRQAMRKETITKML WSTRTLLAKNSWGAEHGSKSL VGPPLAQLAPRPQNITKEQVPL VVEEYLDNVNEHDWKMLRNR MMDIVQDATFVYATLQTAHYH RDAGLPVYLYEFEHHARGIIVK PRTDGADHGDEMYFLFGGPFA TGLSMGKEKALSLQMMKYWA NFARTGNPNDGNLPCWPRYNK DEKYLQLDFTTRVGMKLKEKK MAFWMSLYQSQRPEKQRQF

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10627	40995	A	10689	138	1898	ICKYIMNDQWARQNCLHSPTY GPSENVLSSAESKPEIQLSPSCPL IFSSQQALSQHVWLSHLSQLFSS LWAG\NPLHLGKHYPEDQKQQ QDPFCFSGKAEWIQEGEDSRLL FGRVSKNGTSKALSSPPEEQQP AQSKEDNTVVDIGSSPERRADL EETDKVLHGLEVSGFGEIKYEE FGPGFIKESNLLSLQKTQTGETP YMYTEWGDSFGSMSVLIKNPR THSGGKPYVCRECGRGFTWKS NLITHQRTHSGEKPYVCKDCGR GFTWKSNLFTHQRTHSGLKPY VCKECGQSFSLKSNLITHQRAH TGEKPYVCRECGRGFRQHSHL VRHKRTHSGEKPYICRECEQGF SQKSHLIRHLRTHTGEKPYVCT ECGRHFSWKSNLKTHQRTHSG VKPYVCLECGQCFSLKSNLNK HQ\RSHTGEKPFVCTECGRGFT RKSTLITHQRTHSGEKPFVCAE CGRGFNDKSTLISHQRTHSGEK PFMCRECGRRFRQKPNLFRHKR AHSGAFVCRECGQGFCAKLTLI KHQRAHAGGKPHVCRECGQGF SRQSHLIRHQRTHSGEKPYICRK CGRGFSRKSNLIRHQRTHSG
10628	40996	C	10690	160	294	
10629	40997	A	10691	3	82	SWACAIHPTGYLIEQAGG*WVT ARRD

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10630	40998	A	10692	1	1399	MLRRYRPDITSCHGSTAESKGG VVLDVSGRARPLRRTRNSPSPT SLTSSKMSGLDGGNKLPLAQTG GLAAPDHASGDPDRDQCQGLR EETEATQVMANTGGGSLETVA EGGASQDPVDCGPALRVPVAG SRGGAATKAGQEDAPPSTKGL EAASAAEAADSSQKNGCQLGE PRGPAGQKALEACGAGGLGSQ MIPGKKAKEVTTKKRAISAAVE KEGEAGAAMEEKKVVQKEKK VAGGVKEETRPRAPKINNCMD SLEAIDQELSNVNAQADRAFLQ LER\KFGRMRRLHMQRISFIIQNI PGFWVTAFRNHPQLSPMISGQD EDMLRYMINLEVEELKHPRAG CKFKFIFQGNPYFRNEGLVKEY ERRSSGRVVPFSTPI\RWH\RGQ\ DPQAHIHRNREGNTIPSFFNWFS DHSLLEFDRIAEIIKGELWPNPL QYYLMGEGPRRGIRGPPRQPVE SARSFRFQSG
10631	40999	A	10693	3	441	
10632	41000	A	10694	190	2716	
10633	41001	A	10695	1	793	MARQKKMGQSVLRAVFFLVLG LLGHSHGGFPNTISIGKRKRASR RSRLSLTRDHCPGKAFPAVFRA ERSTGGEQEAGMLQGGEESRLF GSLLWTLPWRACSSWKLSQGD ADCLAAPGRITRARGAQSVVSG CRETGW\GLFMRNTVQEHSAFR FAVQLYNTNQNTTEKPFHLNY HETSPIPLKSPPVSFCCALVVHS TLHRPSLCSVSSLAHRSHIPSPH CHCKNCCCTPLQPTNVLVDYA LFARSREKANVTLKLPLTEVIPF
10634	41002	A	10696	2	2744	
10635	41003	A	10697	2	2740	
10636	41004	B	10698	47	7237	

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10637	41005	A	10699	426	2118	GFGHTVHAAEGGDFGGSWQG DSVLLCSTVDPGSWAASRGKG SPCRGPLCGCCPGRSS\QPSKVE VAVSCSCGALLGMCMPPVVLA LEGCPRGVAAKGKGSPQAQTV RRSPSADQSLEDSPSKVPKSWS FGDRSRARQAFRIKGAASRQNS EEASLPGEDIVDDKSCPCEFVTE DLTPGLKVSIRAVCVMRFLVSK RKFKESLRPYDVMDVIEQYSAG HLDMLSRIKSLQSRQEPRLPVQ QGTRTGIDMIVGPPPPSTPRHKK YPTKGPTAPPRESPQYSPRVDQI VGRGPAITDKDRTKGPAEAELP EDPSMMGRLGKVEKQVLSMEK KLDFLVNIYMQRMGIPPTETEA YFGAKEPEPAPPYHSPEDSREH VDRHGCIVKIVRSSSSTGQKNFS APPAAPPVQCPPSTSWQPQSHP RQGHGTSPVGDHGSLVRIPPPP AHERSLSAYGGGNRASMEFLR QEDTPGCRPPEGTLRDSDTSISIP SVDHEELERSFSGFSISQSKENL DALNSCYAAVAPCAKVRPYIA EGESDTDSDLCTPCGPPPRSAT GEGPFGDVGWAGPRK
10638	41006	A	10700	1	774	
10639	41007	A	10701	124	815	HPGTAMDALNSMQNFLRGRPK TFKSLENAIEWSVKSGQIRNLES ARVSMVGQVKQCEGITSPEGSK SIVEGIIEEEEEDEEGSESISKRK KEDDMETKKDHPYTWRIELAK TEKYWDGWFRGLSNLFLSCPIP KLLLLAGVDRLDKDLTIGQMQ GKFQMQVLPQCGHAVHE\DAP DKVAEAVATFLIRHRFAEPI\GG FQCVFPGLLVTCCPPLLQHRAL LVNTFAPEAHC
10640	41008	A	10702	69	370	
10641	41009	A	10703	1	224	MCNTPAYCDLGKAAKDVFNK GYGFGMVKIDLKTKSCSGVEFS TSGHAYTDTGKASGNLETKYK VCNYGLTFTQK*NTPAYCDLG KAAKDVFNKGYGFGMVKIDLK TKSCSGVEFSTSGHAYTDTGKA SGNLETKYKVCNYGLTFTQK
10642	41010	A	10704	2	171	

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10643	41011	A	10705	1	740	MCNTPTYCDLGKAAEDVFNKG YGFGMGKIDLKTKSCSAVEFST SGHAYTDTGKASGNLEPECKV CNYGLTFTQKRNTDNTLGTEIS LENKLAKGLKLSLDTILVPNTG KKSGELKASYKWDCFSVGSNV DLDFSGPTIYGWAVLVFEGWL AGYQMSFDTAKSKLSQNNFAL GYEAADFQLHTHVTDGTEFGG SIYQKVNGIEMSINLAWTA/GSN NTHFGIATKYKLDCRTSLSAKA VVLGTRVGSC
10644	41012	B	10706	1	318	
10645	41013	A	10707	2	100	
10646	41014	A	10708	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVYTKVF ALDVAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIIERYQLPQSYQLY YFELAIPVGYFYPGSFSTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMVLKNVVRETDEVG KARLTWGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEPDVRILLTKYSN SNGSQSPWMEEQIRDAWGSMV LKNVVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
10647	41015	A	10709	284	969	RVSRGRKWFFIALKRMPAMKK AMNLFLGLSNVRTVHPEGFTV YISTHISFPSLSGYRTGLRSFGLV KQKKSPIRMPCVYTNPCVSIHP LWLRLRSPSARWLRCGSPSLG WTRTEPAPSPPRGGRTEKARIW EVTDRTVRTWIGEAV/AAHAA DGVTFSVPVTPHTFRHSYAMH MLYAGIPLKVLQSLMGHKSISS TEVYTKVFALDVAARHRVQFA MPESDAVAMLKQLS

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10648	41016	A	10710	2817	3297	AGCVRHRLSENRLDHRALPAA SKLPAYA*LPPPLPAGRL*RIPH RQFL*HQI/RL/PTERRCLLTRRT EKARIWEVTDRTVRTWIGEAV ARLAADGVTFSVPVTPHTFRHS YAMHMLYAGIPLKVLQSLMGH KSISSTEVYTKVFALDVAARHR VQ\FAMPES
10649	41017	B	10711	1	963	
10650	41018	A	10712	1	1296	
10651	41019	A	10713	1	1167	
10652	41020	A	10714	349	3195	
10653	41021	A	10715	163	864	
10654	41022	A	10716	576	754	
10655	41023	A	10717	1	1449	
10656	41024	A	10718	1422	1600	
10657	41025	A	10719	489	726	ISCCSFFSPRPPH\TFRHSYAMH MLYAGIPLKVLQSLMGHKSISS TEVYTKVFALDVAARHRVQFA MPESDAVAMLKQLS
10658	41026	A	10720	1	1596	
10659	41027	A	10721	1	1572	
10660	41028	A	10722	2	100	
10661	41029	A	10723	561	804	TLRQTKPDNSADPPHT\FRHSY AMHMLYAGIPLKVLQSLMGHK SISSTEVYTKVFALDVAARHRV QFAMPESDAVAMLKQLS
10662	41030	A	10724	1	867	
10663	41031	B	10725	1	825	
10664	41032	A	10726	1	942	
10665	41033	A	10727	2	100	
10666	41034	A	10728	39	359	RILGKGAGQTRAESLVWGRGV PARCC*PGGPFLVPGPPP*VR/H LSYARPM\L*PGIPLKVLQSLMG HKSISSPEVYRKVFALNVAARH RVQFAMPEFDAVAMLKQLS
10667	41035	B	10729	41	724	
10668	41036	A	10730	1	1023	
10669	41037	A	10731	1	1314	
10670	41038	A	10732	1	1128	
10671	41039	A	10733	892	1611	
10672	41040	B	10734	78	1099	
10673	41041	A	10735	1	936	
10674	41042	A	10736	766	1056	
10675	41043	A	10737	1	1422	
10676	41044	A	10738	1214	1721	

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10677	41045	A	10739	2592	3233	RWGRWRTGGSSRSEPTMELRA PAWPRGRPGQGGARPAGSELR GNATAPSPACLCRNILCRMEES PNTDGKRPETGSNKRGKAGDK WWKIKTGI\IRDKLMERRNRRT GRTEKARIWEVTDRTVRTWIGE AVAAAAADGVTFSVPVTPHTF RHSYAMHMLYAGIPLKVLQSL MGHKVISSTDFYTKVFALDVA ARHRVQFAMPESDAVAMLKQL
10678	41046	A	10740	6323	7130	
10679	41047	A	10741	319	522	RNTRYWVINSISVIPPSSALISKR SPRLMAKKTAHFLGISRTSVAE FTFTRSGISRDHCVKGAGAADR RPNAPPRAEFQSGWFLIMECFA R*VGDPQL/TA/HFDAV/RRE/IM PL/PREG/KTL/QTEVREMPRKC AVFLAINLGDRFDIKADEGGIT DIEFITQYLVLRYAHEKPKLTR WSDNVRILELLAQNDIMEEQEA MALTRAYTTLRDELHHLALQE LPGHVSEDCFTAERELVRASW QKWLVEE
10680	41048	A	10742	2	640	
10681	41049	C	10743	1	2358	
10682	41050	A	10744	1264	1894	RGDKPQHIVTVHRADVVKAQL FKQRARHYHAFNMFFGAFEQL FNWRHARENFFPAGKQLCQMV VERADIFGNRHFIVVENHQHIR TDIARVIHRFKRHACGNRAIAN DTDGAAIFAFTAILYGIQFSCAS FYLFVVYEHGSLKTVGCPLQEV /WRTALESCKPAHIQLSGVLAI/S SIVMQSVNAMPSWSGYSSSQA ASAARWLLARSGLIC

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10683	41051	A	10745	872	3111	VLKPNHLTERKGC/GFACGRYG KLGAWELDYSPDLDIIFLNDCP MNAMTAGERKIDGRQFYLRLA QRIMHLFSTRTSSGILYEVDARL RPSGAAGMLVTSAEAFADYQK NEAWTWEHQALVRARVVYGD PQLTAHFDAVRREIMTLPREGK TLQTEVREMREKMRAHLGNKH RDRFDIKADEGGITNIEFITQYL VLRYAHEKPKLTGWSDNVRIL ELLAQNDIMEEQEAMALTRAY TTLREPRFSRFSLFWGCSPLGLF DYLADLFKIDNSHGGRFKTVLL TFLPPALLYLIFPNGFIYGIGGA GLCATIWAVIIPAVLAIKARKKF PNQMFTVWGGNLIPAIVILFVLP WFYFIPPGLICTSLVYRASPPIS MPAKAVAYCVLRISGGDGSCD VICRGKVADRSKFWNPNWSKT HTEPTQQSQTATSNRTSATTAE QRSDEKEGNNRTRHEEQRSQN ATQHKRRERATTTQKTCSETVT PTTMNMCNEPELRRHARVLPP VLYIVQRRYDESHLRISISACNV CRTERHAVHTDETIHSTVVADC KERVAVMRLRLPLCAACRHIG DVIVYSAYVCEHRCMRLLATR RHYVVTLTTHLRRRLFLTEVNA RYVCIYDDEHSRSSTVTHAHPI DHQSAHYDTYVYDIGTVSYMR LNTSVRLIRRRAHTCTSRALMD SHSKDGRPMDYASAVVVTHPL
10684	41052	A	10746	1577	1668	TINPPELAFVKTVH*SPRICLGFI HIFLLN
10685	41053	A	10747	486	674	HWWKNWRRCWIPVIWH*RRSR TIWRCCKKWITASTLLSRSSPSK LPPCMSGFQPVVAGRKRR
10686	41054	A	10748	254	396	ADDQIPHSKTHLKLSLEVEENQ Q*EI*RPLLQ*GGMSVPRCVHG RSG
10687	41055	A	10749	3	674	ISAELNRPFAIRGDLG/VVWERQ KQETGWRSWVP/WPHVHAEDII LGNPPDI/PEVTMVHLPRVEATL /APLALLTKTVWLPWIKLESPRI RFQFSHHVRRAVLCEDAYYKL TLAQVEKLKNGGKVIASDELM TKFRIPNTLEFCAPVMADAPAI ALLRLSLACLDLAQAMMPAFH KPISSSFVNDYAGTSFACAASD MDERRMLNAPLSLRLTLVEKL RRCWIPVIRH

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10688	41056	A	10750	1	1755	
10689	41057	A	10751	1	1662	MSKPKYPFEKRLEVVNHYFTT DDGYRIISARFGVPRTQVRTWV ALYEKHGEKGLIPKPKGVSADP ELRIKVVKAVIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNIAISVDPE KAASALELSKDRRIEDLERQAL SKPDKYADVKKRISEIYHENRG RYGYRRVTLSLHREGKQINHK AVQRLMGTLSLKAAIKVKRYR SYRGEISSTTKLFLTAFRMIVVA IILIATFDWNRLKPTINQKVSAE LNRPFAIRGDLGVVWERQKQE TGWRSWVPWPHVHAEDIILGN PPDIPEVTMVHLPRVEATLAPL ALLTKTVWLPWIKLEKPDARLI RLSEKNNNWTFNLANDD/NKD ANA\NRRHGRFGWIIFFSIKGGS PLMTNDIHGSLVYTTGKPRPKL EGDVESRQLRLADLGPLIGVDS GKGAEKSKRSEQKKGEKSVQP AGKVLPYDRFETDKWDVMDA DVRFKGRRIEHGSSLPISDLSTHI ILKNADLRLQPLKFGMAGGSIA ANIHLEGDKKPMQGRADIQAR RLKLKELMPDVN
10690	41058	A	10752	1	477	SELGHAGLNGDILVWNPVLED AFELSSMGIRV\D\ADTLKHQLA \GDEDRLELEWHQALLRGEMP QTIGGGIGQSRLTMLLLQLAHI GQVQCGVWAAAVRESVPSLPL QLFHFTRHVVRQPLSDKIRNHQ RIGIKPFPALQAFHNGAKTTGKI GADTKLLA
10691	41059	A	10753	414	794	RPSPLPTGLGDTGLGFLPRFIEM EKLPF\DVAEAEQELQEGPLPEY SGPGLALAKWG\LG\LKQVVM ASLFVALFLPFGR\AQELSLACL LTSLVVTLLKNINSMTAGILVC LVTVVSPGLIKVLIYDQ
10692	41060	A	10754	88	227	
10693	41061	A	10755	26	261	
10694	41062	A	10756	164	361	
10695	41063	A	10757	1347	1656	RVGRPGHRASAQSGGNPQNHR RLGEPVSARHPAYLSTGSGDAA AARYRRSA*SLRR*SRASSHPPE RAGTPVAPGTIDIFRWRTAARQ HRPRLYRRLPHSAA

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10696	41064	A	10758	2096	2248	RLIGLHGQNSRSVPQLPMESAS VA*RCTAALDGGVSSTSTRWLF ASCTRL
10697	41065	A	10759	1	2240	
10698	41066	A	10760	1	1082	MEHERYVGISNLMLKPELYLA VGISGQIQHMVGANASQTIFAI NKDKNAPIFQYADYGIVGDAG ALMSEDIFDAIIVGAGLAGSVA ALVLAREGAQVLVIERGNSAG AKNVTGGRLYAHSLEHIIPGFA DSAPVERLITHEKLAFMTEKSA MTMDYCNGDETSPSQRSYSVL RSKFDAWLMEQAEEAGAQLIT GIRVDNLVQRDGKVVGVEADG NRVMKKILTTPIKAEDLQDIRV GDVIYL*RHRSLSVG*RAESGG* RSGRIVKRTG
10699	41067	A	10761	987	1191	
10700	41068	B	10762	1	1506	
10701	41069	A	10763	204	527	GPDRCQIGPLAE*NTGNSHKAA LRQQRAEGRWWQKPHGEWRA ATADGRTYAAISAQATAPQSPA GQSTMPRPPRWLSTPALPVMPA VTVDRQITPASVSTTKQAISA
10702	41070	A	10764	1041	3024	
10703	41071	B	10765	1	763	
10704	41072	A	10766	729	989	HLTRQGIPTDLQLRVLSVRRKT NKQKGHPHRKRICTSPSSKTKS R*NHKDGEKTEQKNWKL*NAE HLSSSKGTQFLTSNGPKLDGE

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10705	41073	A	10767	89	1755	LSEGKLTNRKDIHTKTPSVRHH HQRPKCWKFWPGHSGRRRK*R /CIQVGKEEVKLSLFADDMIVY LENPIVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNNRQTESQ IMTELPFTTASKRIKYLGIQLTR DVKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILP KVIYRFNAIPIKLPMTFFIELEKT TLKFIWNQKRARIAKSILSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYNYLIFDKPEKNKQWGKDS LFNIWCWENWLAICRKLKLDPF LTPYTKINSRWIKDLNVRSKTIK TLEENLGNTIQDIGMGKDFMSK TPKAMATKAKIDKWDLIKLKSF CTAKETTISVNRQPTEWEKIFAI YSSDKGLISRIYNELKQIYKKKT NNPIKKWVKDTNRHFSKEDIYA AKRHMTKCSSSLAVREMQIKT TMRYHLTPVEEVRAGEMAKTR RCQNVKGASEEGIRALALFLIN LTVHMEGNHIDGDIEIQTNRSPL QAPGEICESFTALMAMQLLSKL FWS
10706	41074	A	10768	533	760	
10707	41075	A	10769	1067	1225	
10708	41076	A	10770	1080	1250	SSGLHSWDARLVQYTQINKYN PAYKQSQRQKPHDYLNRCRKS L*QNSTTLHAKNSQ
10709	41077	C	10771	55	1842	
10710	41078	A	10772	1575	1745	SSGLHPWDARLVQYTQINKCN PAYKQSQRQKPHDYLNRCRKS L*QNSTTLHAKNSQ
10711	41079	A	10773	2798	2871	
10712	41080	A	10774	601	876	
10713	41081	A	10775	1194	1421	

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10714	41082	A	10776	587	1683	GWKFWPGQSGRRRK*R/CIQLG KEKVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNI PCSWVGRISIVKMAILPKVIYRF NAIPIKLPMTFFTELEKTTLKFI WNQKRARIAKSILSQKNKAGGI TLPDFKLYYKATVTKTAWCWY QNRDIDQWNGTEPSEIMPHIYN YLIFDKPEKNKQWGKDSLFNK WCWENWLAICRKLKLDPFLTP YTKINSRWIKDLNVRPKTIKTLE ENLGITIQDIGVGKDFMSKTPK AMATKAKIDKWDLIKLKSFCT AKETTVRVNRQPTTW
10715	41083	A	10777	1260	2176	SSGLHPWDARLVQYMQINQCN PAYKQNQRQKPHDYLNRCRKG L*QNSTTLHAKNS/AIN*CWKF WPGQLGRRRK*R/CIQLGKEEV KLSLFADDMIVYLENPIISAQNL LKLISNFSKVSGYKINVQKSQA FLYTNNRQTESQIMSELPFTIAS KRIKYLGIQLTRDVKDLFKENY KPLLNEIKEDTNKWKNIPCSWI GRINIVKMAILPKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNQKR ARITKSILSQKNKAGGITLPDLK LYYKAIVTQNSMVLLPKQRYR PMEQNRALRNNAAYLQLSDL
10716	41084	A	10778	3813	3983	SSGLHPWDARLVQYTQINKCN PAYKQSQRQKPHDYLNRCRKS L*QNSTTLHAKNSQ
10717	41085	A	10779	1312	3348	
10718	41086	A	10780	1636	1815	
10719	41087	A	10781	67	403	KFLCRPPIIRPPKTFNTLIVLARR CIQCFRFFDIACFNRVGKGFGV GHQLRGFRHDIRGFAQWTHLP DGCAFRDRCYAAGAQCENVPA LTACGDNNQR\GACWYPQQEV
10720	41088	A	10782	506	915	WASVKSPVPCWNCWISHRRRV TCRHVRFAPGFNLAKAV/QGAA LVITGKGRIDSQTAGGKAPLGV ASVANQFNVPVIGIAGVLGDGV EVVPQYGIDAVFSILPRLAPLAE VLASGETNLFNSARNIACAIKIG QGIKN
10721	41089	A	10783	1	906	

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10722	41090	A	10784	2	597	SILKVACDVDNPLVGARGAAA VFGPQKGATPEMVEELEQGLQ NYARVLHQQPEINVCQMAG\A GAAGGMGIAAP\VFFNGDIKPGI EIVLNAVNLAQAVQGAALVITG EGRIDSQTAGGKAPLGVASVA KQFNVPCDLGLLAYVGDGVEV VHQYGIDAGFNILP\FLAPLAEV LASGETNLFNSARNIACAIKIGQ
10723	41091	A	10785	1	1140	
10724	41092	A	10786	13	628	LLIPARPPGINPYYWKVSEANLI RYFQQVGDSVTLPVMLYNFPA LTGQDLTPALVKTLADSRSNIIG IKDTIDSVAHLRSMIHTVKGAH PHFTVLCGYHDHLFNTLLLGGD GAISASGNFAPQVSVNLLKAW RDGDVAKAAGYHQTLLQIPQM YQLDTP\FVNVIKEAIVLCGRPV STHVLPPASPLDEPRKAQLKTL LQQLKLW
10725	41093	A	10787	3	1185	EQSGRGARDGGARDGVREGG\ SWTQQHGLPLTKVELATVAEY PVCLWQRLTL\SPQYGSIP/RGD QSDGWKVDYNGPFSLWKGQH FVINGIDTCSGCKFAIPVCSASA KLLPMSSQNVYHRDILHRIDSE QGTHFRVKEVQQWALGRGFY WSYYISHHPEAAGLVEQCNGIL KTPSQFQMGRNTLQGWGKVLP SLEGCAFSSSKSNLCSVVLKVF VPKEGMVPPGDTTMIILNCKLR LPP\MPLNLLASKEVTVLD/YQG EIGQLLHNRGKEECVWNTGDC LTYLLILPSSVIKVKEKPQPHPG RTINGPDPSGMKTWVTPPAGA VFLIGSWLRYDYGQYTWRAAS SQMLDRKGMNLASNLFHIGILG IFVGHFFGMLTPHWMYEAMTY GSCDTDNANV
10726	41094	A	10788	396	504	WKRLERRAIQGDSPVHKNARA GELDE*AATRAIPG
10727	41095	A	10789	24	611	EILPVPGPVVIAW/AIFRRIAGES WSAIVISGLSIARHAQQKRIITFT ASLAARLEIALKIVRNADGTES ASEQLYQVVGAGCKMPWQSE AMKDVLICDKRRLMRRTGGTE TSKYPEEKKSTEIPPVAASERGG AQSLNQCATEAVVLTRVDSHL KVGDSLSHTTSFLKKFAARFGG QLEKALGLGSMQAFSDIRGL
10728	41096	A	10790	212	578	

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10729	41097	A	10791	1	1707	
10730	41098	A	10792	3	313	NAE/TVKMFTTSSKEDATFGL/G WRVNGNATMTPTFGT/LASPQT YGHTGSPPLPPICPVRPPGYLRR LSPRFPRLFGISLPQRPPGILERS LQRRRNPSGWRRRNQ
10731	41099	A	10793	1	1992	MDVQSAADDTGLPMLVVRGPF NVVWQRLPAALEKVGMKVTD STRSQGNMAVTYKPLSDSDWQ ELGASDPGLASGDYKLQVGDL DNRSSLQFIDPKGHTLTQSQND ALENAILAVIRHEICLSDVVRIR ASRRFDKTSGTPDRQKILKLGY LLPAGWLADVDPRLVGVMNV WTLLVPAALFFFGAGMLFPLAT SGAMEPFPFLAGTAGALVGGL QNIGSGVLASLSAMLPQTGQPG VVDDLNGIVDRAVLAAAGDAD VASGAARLSARHRSIVISSMGE RCCFIRSRITRICGFLAAGVGLD QLAPDFATPVIRELLALLLCLFS GGLAMYGYLRWLRNEKAMRL KEDLPYTNSLLIISLILMVVAVI VMGLWIPPTCIVDDRMAKYIPG LADSPNDTIKGKNTLRISDLLH HSGGFPADPQYPNKAVAGALY SQDKGQTLEMIKRTPLEYQPGS KHIYSDVDYMLLGFIVESVTGQ PLDRYVEESIYRPLGLTHTVFNP LLKGFKPQQIAATELNGNTRDG VIHFPNIRTSTLWGQVHDEKAF YSMGGVSGHAGLFSNTGDIALF NAETVKMFTTSSKEDATFGLG WRVNGNATMTPTFGTLASPQT\ YGHTGWTGTVTVIDPVNHMTI VMLSNKPHSPVADPQKNPTMF
10732	41100	A	10794	2	137	NCLSPVSAN*WPAKTGRPILPS ATVTASTRNVLSKHWRIWVST VC
10733	41101	A	10795	271	553	ATQRQDLHFVRSPGDAVYTQIT PEAADAVVARNPDTAQHLHC/ VYP/HTSNAALAQKYLHIAASP EVMVPLSAFHAASYSMFFMEF NLIAMWANFS

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10734	41102	A	10796	1	747	MLLGLHSLAAFLQRESFSGKQS WGCQLAALLQRRITKMTEAMK ITLSTQPADARWGEKATYSINN DGITLHLNGADDLGLIQRAARK IDGLGIKHVQLSGEGWDADRC WAFWQGYKAPKGTRKVVWPD LDDAQRQELDNRLMIIDWVRD TINAPAEELGPSQLAQRAVDLIS NVAGDRVTYRITKGEDLREQG YMGLHTVGRGSERSPVLLALD YNPTGDKEAPVYACLLGDIITY RNGKKVEVMNTDAEGRLVL
10735	41103	A	10797	444	548	
10736	41104	A	10798	951	1648	TTGRFPPSVQDSFVNESSRMGL PDEFTLQREFERARQQGALAQ W/IAAFEGGFTGIVATLDTGRPG PVMAFRVDMDALDLSEEQDVS HRPYRDGFASCNAGMMHACG HDGHTAIGLGLAHTLKQFESGL HGVIKLIFQPAEEGTRGARAMV DAGVVDDVDYFTAVHIGTGVP AGTVVCGSDNFMATTKFDAHF TGTAAHAGAKPEDGHNALLAA /AQATLALHAIAPHSEGASRV
10737	41105	A	10799	1495	2282	FDRHVGEFFLNQLETTNSLAKL HALIGVARRIFKGAHRRTVVGE GYQETFMVELFFDAVKAVTFPT EHVFLVQFHVVKGDFTAAIHTQ TELFKFGHFDARFAHINKPFGV DRFVRRSPVARHHHDVRGVGA AGNKTLTTIKINLTISTGISRFQA THVGARARFGDR*VRTDSTTTV GHRDCIITGGHR/HKSFQPGHEA PQAVPLPGRFHHH*PSHDHCR* LVSLAGAAYRSPQDPVPYMPIS PGLDWVRQIVCCVMASDAD
10738	41106	B	10800	1	3618	
10739	41107	A	10801	3	490	TGIVATLDT/GRPGPVMAFRVD MDALD/LSEEQDVSHRPYRDGF /ASCNAGMMHACGHDGHT/AIG LGLAHTLKQFESGL/HGVIKLIF QLHRYAAHAGAKPEDGHNALL /AAAQATLALHAIAPHSE/GASR VNVGVMQAGSGR/NVVPASAL L\RQPTRSALNTTQQLNAR

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10740	41108	A	10802	1	513	MGIESLQAFLRSAGALGVWVY TFLERILIPTGLHHFIYGQFISGP AAVEGGIQMYWAQHLQEFSLS AEPLKSLFPEGGFALHGNSKIFG AVGIYLAMYFAAAPENRVKVA RLLIPTPLAAMLVVIPEPL\EFTF LFISPILYAVHAVLTASMSPVM YLPGVVGNMGEGKID
10741	41109	A	10803	1	4941	
10742	41110	A	10804	1	1083	
10743	41111	A	10805	1	1363	MPVRKNMIMNEGNITTPTNGC RIRASCGVPMICINQLKDGNKK PSPLTAARMKQKAIILFLIRTVR TDTHVVEDTGRKGSRKANSRE RFPDAFPEFHGFADFRVLRQAM IQIWLVSMVQHVHNVCTTDAC RIVQTRIVVTAGFQLSNASLVA MRRWVYRVRRIQYRRTTQTAV FHSTHGNYREGQPVGTLIDDRY KANENVELVHYAQPLLNEADS LAKVMPSDIPLKQRRWLGLQM LEGDIYSRAYAGEASQHLDAAL ARLRNEMDDPALHIADARYQCI AAICDVVSNTLTAEPSRFTTAV DKIVLNRFLGLPIFLFVMYLMF LLAINIGGALQPLFDVGSVALF VHGIQWIGYTLHFPDWLTIFLA QGLGGGINTVLPLVPQIGMMY\ CFSSFLKTPALACREIFVPLMRL RVNLRWYPPVL*RISWWTNSRI PTTFSTRGSACWRATPAK
10744	41112	A	10806	199	1083	RLFEHPRLGVAAVENGALGKR SAVVLPGFDAVNHKTRFIEFVK SAIEGNRLTVRAIGPQFFTQTPV IVFNQGVSGAQNIAGRAVVLLQ TNSFGTGEIIKETLNILHLRPAPA VD*LVVITDDHHFAGVARQQA DPRVLNVVGILEFVHQDIGKTF AVVLQDMRLVKPQLVSAQQQL GEVHQARAVTRFLIRLIHLLPGL LHRITVALNMMRTQAFIFLAVD VPHCLPRRPLLLVEVHGFDQTQ KVAAWRGHRFALFVIKAVEQV RNVHWHRRVKIGWAEKRNAL RQKAGNFQMRQ
10745	41113	A	10807	49	273	DFLGRGAFNVINIGAWASRPVQ GSTVDLSHGLHLVLHLKNNL*F YGFDSHFLKSFFYKGTSISIQVE VGISQGNL
10746	41114	B	10808	91	2183	

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10747	41115	A	10809	8	219	FSLWPL/KKFSNRFLKKKPMEF GSWTTREILIASFAGVRGAITLA GVLSIPLLLPDGNVFPARYELVF LAAV
10748	41116	A	10810	84	509	
10749	41117	A	10811	3	163	ENTTWLYAD*NAGRDADFGHA KRKWTLWLAILAAVATAMAN RQPGAGLFALFT
10750	41118	A	10812	1	707	MGWRMGIWLRVFTVAKHLQR AESDQIGFRLKEHCWKRYAVR HPVKDVSGFSPVLTVNMRAPQ SN/PARRTVGWLRMFRRLRKR/ RKPRPLPLSPLHMDV/HAGNLV HSASGLKLIDW/EYAGDGDIAL E\LAAVW/VENTEQHRQLVNDY ATR/AKIQPAQLWRQVRRWLP/ WLLMLKAGWFEYRWRQ/TGD RQFIRLADDSWRQLHRSNKESS RELVARLRVFAQSSGGAVDQE GGRVQCFREGL
10751	41119	A	10813	1	227	SFINVERYRAEPQTADAAPLKR GAFGSWLPEPDHYAED/DHQQ YLHKNPYGYCGIGGIGVCQAY KIVQIQYIARTA
10752	41120	A	10814	1	283	
10753	41121	A	10815	315	569	
10754	41122	A	10816	65	580	SDRS*IPVRPTHRDSGNRHDGSS GYCRCYG*HG*HRGIRYRCWPE KSQTRSGLLP\LTVNYQERTYA AGRIPGSFFRREGRPSEGETLIA RLIDRPIRPLFPEGFVNEVQVIA TVVSVNPQVNPDIVAMIGASAA LSLSGIPFNGPIGAARVGYINDQ YVLNPTQDELKESK
10755	41123	A	10817	235	1236	TDHDGRNDTQRIGSGERNRPFS NANTAHHQCRFAGFALFCGEIF TTNQRRQPHPQRRDTNTHGSD GHHGINTLSNANQHEGIGHFVN RTAHIERQHQTHDHRQHNNAA NSGTEVSQ*AR*HAAV*RYVAE REIHSGDRCGKRNSAHKIMPG WWCALPDTAPSLSKVVFFKGC PHLCPWCANPESISGKIQTVRRE AKCLHCAKCLRDADECPSGAF ERIGRDISLDALEREVMKDDIFF RTSGGGVTLYRGEDPAEDARY AHTNQPRQNKAVVDDEATDV GGAGTVKLNRCQIARISRQDVI TVASRCEHGFCHPCDTVHRHD GDHTGTEDFVF
10756	41124	A	10818	1	400	

1451

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10757	41125	A	10819	783	1116	SVLHLYYEQNTE\HDTRGYRPI KTLDIVPAFEASHLLWQSYENS WEQIFSASVGASWQKHYGTDV LTQLGYGQRIIWNDIIDAGATL RWEKRPYDGDREHNLYVEFD MTFRF
10758	41126	A	10820	3	474	TCGE/AASIVDRIRGFFEPSSILV STLVLTLRPTGLLPLVTDSLPM RLLPTEIMAGSPIRS/RDISLGDD PGINGQRAQGTWERWTVRADE PQAFHIEGVMFQIRNVNGAMPF PEDRGWKDTVWVDGQVELLV YFGQPSWAHFQFYFNSQTHKV GPRAVA
10759	41127	B	10821	93	786	
10760	41128	A	10822	191	748	GPATPRQPFKVLASLGRLVQHG GRWDAQHLHNAVHLVDLIGAT EEGLSGVHLHKDAAQGPHVNG QVVGCAQEHLR*AVEAALDIL VDPLAKLAGAAEVHNLDGAAL GVAQQDVFGLEVAVNDAEAQ AWPERAVPCRAAAPASGSGSA RRRGSGCCAGGRTGCRTAAQIP STSGFRNMKCRFRCTI
10761	41129	B	10823	1	2724	
10762	41130	B	10824	116	2458	
10763	41131	A	10825	1	1317	

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10764	41132	A	10826	99	2052	NPADGRTGFTLCATGEALSSAT IAAAERRQALQEGCDDILS/HG DADMVSMAR/PFLADAELLSK AQSGRA/DEINTCIGCNQACLD Q/IFVGKVTSCLVNPRACH/ETK MPILPAVQKKNLA/VVGAGPAG LAFA\FNIAKQIPGKEEFYD/TL/ RYYRRMIEVTGVTLKL/NHTVT ADQLQAFDETILAVG/IVPRTPPI DGIDHP/KVLSYPDVLRDKAPV/ SN/KVAIIGCGGIGFDTAM/YLS QPGESTSQNIAGFC/NEWGIDSS LQQADCDAPAKASKPGQGLGK TTGWI/HRTTL/LSRGVKMIPGV S/YQKIDDDGLHVVINGANQGS DMLRLQGELDSASRIGRRSAAP KLGSLNDGRCFINCHILDRLPY KGLVPACSWNGGSLDPLEGRP DEPHVEVLGIPPAAMLDQAPRL ASTLNGCLGVAGPYEDERTQE GLPGPRDTAAEEVLGVQTGGA GSRGRVRGPQPADLPSASGPGA ACWSMSPPPDQPPCVLAHGFFR RTPTSTQQRPAEQCFHSPAPLEL PLSSTSSILSFAEYGNAMAWLY RGKILPSGTPDDLKAQSANDGN PDPTMEKAFIQLIHDGIRSIAMS NPILSCRRYGRYQEWCLTIPAV FISAPYVRRYVRFHEHQEGGGV RQEATVREIPLAIAVIPNSRTPC
10765	41133	A	10827	1	525	DAMVSSWNRAAPNTIPTAAKA GGNYLSSLLVGSEARRHGYQE GIALDVNGYISEGAGENLFEVK DGVLFTP/PGFTSSALPGITRDAI IKL\AKE\LGIEVREQVLSR/EKS LYLADEVF\MSGT\AGEITPR\RS GNGYSGLAKGRCGPVTKRIQH ALQGVYSWVTPGYFESVRCTA
10766	41134	A	10828	8	573	REPAGENGPPVCDGAMLDLKA/ WGSECHQQLTGRDNQQIKRSIY LLPERAKLAELRLLVIPGQVDY LQHIEELAAFIKGLGDVPVRLN AFHAHGVYGEAQSWASATPED VEPLADALKVRGTCRPDKTRQ ASHQALCANCRMRRERLIRPTV RHKPVGMIRRDKRRIRHYAPTA GCGVNALSGLRFGTDL

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10767	41135	A	10829	1	479	SNATNGIEPPRGYVSIKASKDGI LRQVVPDYEHLHDAYELLGEM PGNDGYLQLVGIMQKFIDQSIS ANTNYDPSRFPSGKVPMQQLL KDLLTAYKFGVKTLYYQNTR/G RR*RRTRRSGAVNPGTMGCESG ACKNPGYLRMPGCRRKTPLIPA LPGFGFW
10768	41136	A	10830	1	443	MDSLMDMLAST\QGRRMDDQR VTVSSLPGFQPVGSKAYKPSRR PDKAFTPHPASQYQILHAPLVA AIVSGLTAARVVFVRLQQPSLG VLSNTSGCDATNVVGRLQDNA SVSPGIVHTDSVIWRSCQVRRS AVHTLWRQKTRLFDAVDA
10769	41137	A	10831	1	323	MDLVTGSRKVIIAMEHCAKDG SAKIL\RRCTMPLTAQHAGHML VTELAVVRSFDGKMWLTEIAD GPTSQAQPAATYRIPLSNSRVR RRYRHRYYRYNLSIRKKRHRPL
10770	41138	A	10832	526	975	TPYPAYVQHVTPGRIRRGKRRI RQCLPVLESRFHNTQKSRGETE GASGFSLQHHLGDSSRAAPGPY RVSTAAADSGGRAGSSAPSALV PRGC*GPSLAPAGRSQR*HRGG GQLSPAAPRTANKAAGLGPPA RLNFFIRAQCDSRINDITR
10771	41139	A	10833	1906	2049	PLSIIEADFRIWANAG*RMVAGI KPSIARVPLVLQVSALEVPEQC YRH
10772	41140	A	10834	1	808	MPKPNTRWSAWGLRRLKRKW SVARGSNLNRSVQYEFTGRGD RIGWVKGIDDNWHLTLFIENGR ILDYPARPLKTGLLEIAKIHKGD FRIT\ANQNLIIAGVPESEKAKIE KIAKESGLMNAVSPQRENSMA CVSFPTCPLAMAEAERFLPSFID NIDNLMAKHGVSDEHIVMRVT GCPNGCGRAMLAEVGLVGKAP GRYNLHLGGNRIGTRIPQITRRI EHRANDARTHRKVAEAFTRFA LFRPAPYQFIKRRQDFRLVMFSI YMPVPS

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10773	41141	A	10835	248	830	HHYRKMNIQQSKWLIVTVCDG KLNWLLSGSKVCCTWMLCVQ/ SEPELAKAWIFANLLAAFLIDDI IQPSLDFPPRRAEITIAADGTISA LNPGDPANTVAPVGRLKLVKA TGSEVQRGDDGIFRLSAETQAT RGPVLQADPTLRVMSGVLEGS NVNAVAAMSDMIASARRFEMQ MKVISSVDDNAGRANQLLSMS
10774	41142	B	10836	328	481	
10775	41143	A	10837	14	675	FRKLQVCWLPRPHLRPWWTCK PRWFGSCLRVFL/LERVI/GDV/ WGLRLWSALGVAFFG/WAFITS LQAKRGWMRIVPIILLAAALVS VRPLQDWAFGATHTAQTQTHL NFTQIQTVDELNQALVEAQGKP VMLDLYADWCVACKEFEKYTF SDPQVQKALADTVLLQANVTA NDAQDVALLKHLNVLGLPTILF FDGQGQEHPQARVTGFMDAET FSAHLRDRQP
10776	41144	A	10838	1	1413	GMALTYTALGLVVAAAGLQFQ AALQHPYVLIG\LAIVFTLLAMS MFGLFTLQLPSSLQTRLTLMSN RQQGGSPG/GAILLYIAQSGNM WLGGGTLYLYALGMGLPLMLI TVFGNRLLPKSGPWMEQVKTA FGFVILALPVNIAPGSLDKALNQ YAAHSGFTLSVDASLTRGKQSN GLHGDYDVESGLQQLLDGSGL QVKPLGNNSWTLEPAPAPKED ALTVVGDWLGDARENDVFEH AGARDVIRREDFAKTGATTMR EVLNRIPGVSAPENNGTGSHDL AMNFGIRGLNPRLASRSTVLMD GIPRPLRPLRSAAAFTGSRFARQ HGCHCTWYAVVVRCVTDTQS VGGVVNFVTRAIPQDFGIEAGIL MSDLKHGSLVGACLGRLGPGA VLYLAVAVLGVRVRRGVVLVC PLGGTGLGYSCQGGAFQFAAS CFLGRYGVVQGVIHVCFGPRSV FLDDCLRFDLPCLVWLSCPR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10777	41145	A	10839	1	908	LLKPFHVIAIATGRSLAVFCMG RLRTICSHATPPASAI/LLYI/AQS GTWGGGGTLYLYALGMGLPL MLITVFGTRLLPKSGPWMEQV KTAFGYVILALPVFLLERVIGD VWGLRLWSALGVAFFGWAFIT SLQAKRGWMRIVQIILLAAALV SVRPLQDWAFGATHTGQTQTH LNFTQIKTVDELNQALVEAKGK PVMLDLYADWCVACKEFEKYT FSDPQVQKALADTVLLQANVT ANDAQDVPTSAPFISPPNALVAI IVQLRFGDFYNRVSKGSRPTVF GRTLKARRITLSEKSILKAKIH
10778	41146	A	10840	3	808	SSGGHGRRAAGRLQHPLLRVH VPVVDTSCVPSCSRLQWHHLPL CPGQLQHGHFHGPWCFPPSG*G *GQGGRLPGSAVQERGCARYP GPHEVVCHVPLLPPAALLPLQR L*QLCRGL*PPLPLGQ/PTASGV ETIATSSCSCCHSVHTWWASWP SAWSTC*TTLRGWEPRTPPSRIL GSCGPHCRGDVDRGHVHPGE* AFQSLVPCQGTPKGPMAPP*VG RGVSP/PGTRVEAALSCESPPHA RQSMCFNLHTHSIDPKQSRRPY SDNVGKE
10779	41147	A	10841	2	646	CSWQPAVPTQPQPAGPSAPRQG LPGHSRGAQPALVSPHKGLTPV PGTPA\PASTPPAPAGGEGLPSP AAGAPPAHCPG/HPPAPATAAP VPGLCGPCPSLPACPQTR/PPTH VNTKKRV/PG/VRPAARRPWPP GCTWRGARTVTFLHQLNPGVN CQMLTVGRSGIRPTCTIASCSV NKLHPQMHPATQPHHRMALSP SHSEGPSHCWGLSLGDISPIPR
10780	41148	A	10842	3	550	

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10781	41149	A	10843	2	1132	LCLVMILYTRRRWCKRRRVPQ PQKSASAEAANEIHYIPSVLIGG HGRESLRNARVQGHNSSGTLSI RETPILDGYEYDITDLRHHLQR ECMNGGEDFASQVTRTLDSLQ GCNEKSGMDLTPGGDGRKARL MNKYKDNIIATSPVDSNHQQAT LLSHTSSSQRKRINNKARGMHV *H*GEGDSGTEAENDPQLTFYT DPSRSRRRSRGRNDRGGRNKTT LTLISITSCVIGLVCSSHVNCPLV VKITLHVPEHLIADGEPVLLRM GSQLDASDWLNPAQVVLFSQQ NSSGPWAMDLCARRLLDPCEH QCDPETGRREHRAAGNCQRDH ARAHSVWLGSPPYHDTSLRWS PMYTTMESAPHAFPPSVTADAE
10782	41150	A	10844	3	3935	HASGPGLKMALAGLCALLACC WGPAAVLATAAGDVDPSKELE CKLKSITVSALPFLRENDLSIMH SPSASEPKLLFSVRNDFPGEMV VVDDLENTELPYFVLEISGNTE DIPLVRWRQQWLENGTLLFHIH HQDGAPSLPGQDPTEEPQHESA EEELRILHISVMGGMIALLLSIL CLVMILYTRRRWCKRRRVPQP QKSASAEAANEIHYIPSVLIGGH GRESLRNARVQGHNSSGTLSIR ETPILDGYEYDIT
10783	41151	A	10845	184	357	ALQGWSKNLH\PEDIQLGKTPP P*QVAQEGGWSRRVGSDTWIL EEQPGSTTRRVSVGM
10784	41152	A	10846	226	609	VILSSFDLIKHGILLEISDSIQFRG CKRSRIPELGGLEELW*PGDCR QPRP\WRA\GRHLQPGSLGSLVS KHQLRGSRKTL/YSAFRKCHLL SVWEGKPLKI*RGDQVADSSQK KQLAADAHTPYRGGDI

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10785	41153	A	10847	20	1317	SSHQKQMLAPCFLGSLQNWQH HTAGKGK/WVLGTCAFGEQLA ASGHMKETRADRSKKLFRHYT VGSYDSFDTSRGGRVRKPYAGF FPDLQDICDEQPRPLHSTLRPAC GGIQPGKQQPMPFAKTDTCASD KHVEKKLERLIHQAVSDAPEPS RVVKGIFIGGLPCARLWVVPYL MGHVQEVTMAEGYERASQATF REQMQEVPCCLQRSTGSSMKT GNKIRRVTDNVLTRSGPLINDIL SVAVDSSVSVLIWMHLFSSHPL GIVRYWGCMGISCKLLLLTRVC YLITPLDLERFPFPNTEQVTFPE RRVSVFLLPLSWCLDTRLPREP GCRSRRDSFTHRVFYSVTPTSG DVPGSHPFCDKPVRRGDDPYIR NDRGTLYSTLQFISTCVQVVGV YGHLPGFKSDAAQAVPRLLSQ KRDQNHKEEEITDGDERPK
10786	41154	A	10848	1930	5781	RAKSPANIIMTGSNSHITILTLN VNGLNSPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNLTQSR
10787	41155	A	10849	1	3654	
10788	41156	A	10850	1	5127	
10789	41157	A	10851	209	3816	QGRPTFRFRKYREHHKDTPREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTEIQITIREYYKHLYANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPITGSEIEAITNSLPTK KSPGPDGFTAEFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASII LIPKPGRDTTKKGNFRPISLMNI DAKIL
10790	41158	A	10852	1	3663	

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10791	41159	A	10853	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQ
10792	41160	A	10854	1	3354	
10793	41161	A	10855	1	5073	
10794	41162	A	10856	1	3235	
10795	41163	B	10857	1	3300	
10796	41164	A	10858	1	2563	MKAEIKMFFETNENKDTTNQN LWDAFKAEEVESLNRPITGAEI GAIINSLPTKKSPGPDGFTAEFY QRYKEELVPFLLKLFQSIEKEEI LPNSFYEASIILIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFFPGMQG WFNIRKSINVIQHINRAKDKNH MIISIDAEKAFDKIQQPFMLKTL NKLGIDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNILLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTSNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGKDS LFNKWCWENWLAIWRKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITIQDIGMGKDFMS RTPKAMATKAKIDKWDLIKLK SFCTAKETTIRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKKHMKKCSSSLAIREMQI KTTMRYHLTPVRMAIIKKSGNN
10797	41165	B	10859	1	3420	
10798	41166	B	10860	1	4019	

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10799	41167	A	10861	1	1825	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFFSAPHHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTQNHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYHNLWDTFKAVCRGK FIPLNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQI DAIKNDKGDITTDPTEIQTTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPITGAE IVAIINSLPTKKSPGPDGFTAKF YQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIILIPKPGRDTTK KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIPGM QGWFNIRKSINVIQHINRAKDK NHMIISIDAEKAFDKIQQPFMLK TLNKL\GIKYLGIHLTRDVKDLF KENYKPLLKEIKEDRNKWKNIP CSWVGRINIVKMAILPKNILITL QLLLVLPELSTLIPLWLPALAGQ
10800	41168	A	10862	1	4449	
10801	41169	A	10863	824	3693	AWKGTTDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YT/FFSAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNNLLL NDYWVHNEMNAEIKMFFETNE NKDTTYQNLWDAFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLQKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
10802	41170	A	10864	1	3297	
10803	41171	A	10865	1	4791	
10804	41172	A	10866	3	3316	
10805	41173	B	10867	1	3415	
10806	41174	B	10868	1	4753	
10807	41175	B	10869	1	3384	
10808	41176	A	10870	1	3345	
10809	41177	B	10871	1	3772	
10810	41178	A	10872	1	3720	
10811	41179	A	10873	1	3894	

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10812	41180	A	10874	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELKEIETQ
10813	41181	A	10875	1	3780	
10814	41182	A	10876	1	3852	
10815	41183	A	10877	1	3345	
10816	41184	A	10878	965	4362	TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEYTFFSAPHHTYSKI DHIVGSKALLSKCERTEIITNYL SDHSAMKLELRIKNLTQNCSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTNQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLKELEKQEQTHSKA SRRQEITKIRAELKEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREKNQIDT
10817	41185	A	10879	1	3921	
10818	41186	A	10880	1	3988	MTGSNSHITILTLNINGLNSAIK RHRLASWIKSQDPSVCCIQETH LMCRDTHRLKIKGWRKIYQAN GKQKKAGVAILVSDKTDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDIYRTLHPKSTEYTFFSAPHH TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRIKNLTQS RSTTWKLNNL
10819	41187	A	10881	2	462	YFTDRLRARLAGTPL/IMFGTIA RSGVRIVSREPLNRRAILIIALSL AVGLGVSQQPLILQFAPEWLKN LLSSGIAAGGITAIVFSLAGHPA LATNAQPMEAFLLHQTTFFQNL IRVKEAICSDQFNTTMFRGLQG NSACTKCNPRCLNELTPTE
10820	41188	B	10882	16	163	

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10821	41189	A	10883	2	1509	RDEVNGCIRLVYDMYSTFGFEK IVVKLSTRPEKRIGSDEMWDRA EADLAVALEENNIPFEYQLGEG AFYGPKIEFTLYDCLDRAWQC GTVQLDFSLPSRLSASYVGEDN ERKVPVMIHRAILGSMERFI\GIL SEEFAGFFPTWLAPVQVVIMNI TDSQSEYVNELTQKLSNAGIRV KADLRNEKIGFKNRSGELSHLP PINQSKPRNFPSAALPQVPQPTH LSQRPRASPKPPPPDPERVELSL EEHREMLEGFYEEISKGRKPTLI LRTQLSVRVNAILASLESVKPL YTMALGLLVKYPDSALGQLRIE STVDGSRLYITGNGVLFQHVKF HAFLLYLGYTPQAAREVRIMQF CHTLREFALEYRTCRERVLQQQ QKQATYRERNKTRGRMITETE KFSGVAGEAPSNPSVPVAVSSG PGRGDADSHASMKSLLTSRPED TTHNRRSRDRHGPRGCQVCSA QPSLLRAVPVADMRALMTGKD CPPCPGKRLRGAELGPL
10822	41190	A	10884	296	757	ISRFRRRALSPKAESSLSSILPRE KRSPSRTWILTPRRLFSLAISSKS AGNTLSSRIFK*KA*ACK*RGR VSTRCRIFLALFIVTIKHRLMMR STASNRQYSISIWTILPCWSARC FSIKIAGIPAEPPRYLLISPGILTG LKINFFTTVSFW
10823	41191	A	10885	1	519	MGLPWQVGMGAIFWGAIGLLL LTIFRVRYWMIANIPVSLRVGIT SGIGLFIGMMGLKNAGVIVANP ETLVSIGNLTSHSVLLGILGFFII AILASRNIHAAVLVSIVVTTLLG WMLGDVHYNGIVSAPPSVMTV VGHVDLAGPIGNSLV/GCPYFAI LRRFSDGSGGLGRNQI
10824	41192	B	10886	1	3489	
10825	41193	A	10887	817	1528	WGSRDNRDEIRNTLVLDTLRLQ RVCAQRAFLVLFVLGKVTFEEL NFTFILVIQNVRGDTVEEPTVVR DNHRTARELQQGVFQRAQGFD IQVVGWFVEQQHVAANLSRCR LVNTPTQQVRFSTATFRVIWRV TPTAGKLSGGFLFKMYGLPAA AIAI\GTLLNQKTARKWAVL*SP PALTSFLTGITEPIEFSFMFVAPI LYIIHAILAALFMWKFVPETKR KTLEELEALSNRIAAE
10826	41194	C	10888	1	573	

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10827	41195	A	10889	2321	2554	WRKRCVKVRNLSPLCLPDRKL TLPCCSIAIRNCIAKLPVS*LWV ALWGWVTGRLRLNLIFTLTRK RQKLSSSQGSRW
10828	41196	A	10890	1	4350	
10829	41197	A	10891	137	686	KLLELRSKREAGMLERSSSRMV TCSQWAATRNPVVALPIYGFIE RCLVPFGLLHIWNVPFQMQIGE YTNAAGQVFHGDIPRYMAGDP TAGKLSGGFLFKMYGLPASAIA IWHFVKPETRAKVGGIMIFAAL TSFLTGITEPIEFSFMFVAPILYII HAILAG\WHSQSVFFWGCVTVR RSRTV
10830	41198	A	10892	3	3831	SIGMMGLKNAGVIVANPETLVS IGNLTSHSVLLGILGFFIIAIL/AS RNIHAAVLVSIVVTTLLGWML GDVHYNGIVF\APPSVMTVVGH VDLAGSFNLGLAGVIFSFMLVN LFDSSGTLIGVTDKAG\LADEK GKFPRMKQALYVDSISSVTGSFI GTFSVTAYIESSSGVSVGGRTG LTAVVVGLLFLLVIFLSPLAGM VPGYAAAGALIYVGVLMTSSL ARVNWQDLTESVPAFITAVMM PFSFSITEGIAL
10831	41199	A	10893	6	146	
10832	41200	C	10894	1	1197	
10833	41201	A	10895	1	763	MCSEKVAMCCDDDDDDDDDD DDDDDDDDDYSCSHGFWDFSY TWNTSIPQGHLGMGSPIKGLVE IRDKLGDRTQRVYIQRITGNGL EFENPCKQFRGLTRMYIRRLTR LSVQWYMVALERPVLQKYRY RGSKAHETSHSMSTVTSSNEKQ DNTRIDTQGATNR/VATLRHRE TVLANEVAPYAATDNVLAAST DVGDVSWKLPVAQCFSPCFAV GTPLHTWQ/SGLLQECQQEHQQ VTDTQPYHCPIPKNVTPSPLK
10834	41202	A	10896	2	412	LFEFTLDVKVRESPIL\FRDESM RTACSPDGLCSNGFGLELKCPF TSRDFMKFRLGGFEAIKSAYMA QVQYSMWVTGKDAWFFANYD PRMKREGIHHVVVERDPQYMS DFNEMVPEFIEKMDEALAEIGL TVRELGI

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10835	41203	A	10897	3	663	ARGKKPPRRGKEDFWDLSIATR VSVNPIKFPVEA*PFLKP\LQQV S\GPLGGRLPLPIPGNLLLQVAD GTLSLTGTDLEMEMVARVALV QPHEPGATTVPARKFFDICRGL PEGAEIAVQLEGERMLVRSGRS RFSLSTLPAADFPNLDDWQSEV EFTLPQATMKRLIEATQFSMAH QDVRYYLNGMLFETEGEELRT VATDGHRLAVCSMPIGQSLPSH
10836	41204	A	10898	377	1077	WRGQRCLASVFPRHPGAEGRG RPVFRAETIFL**SRRGLAR/TGR RKLPVKLKAADFPNLDDWQSE VEFTLPQATMKRLIEATQFSMA HQDVRYYLNGMLFETEGEELR TVATDGHRLAVCSMPIGQSLPS HSVIVPRKGVIELMRMLDGGD NPLRVQIGSNNIRAHVGDFIFTS KLVDGRFPDYRRVLPKNPDKH LEAGCDLLKQAFARAAILSNEK FRGVRLYVSESQLKSRQ
10837	41205	A	10899	591	871	VRGFPSGAEQLYG*SVSLLILLP NLSNSG/RTGFPVAPLPYSKSPS DFMSLLISTVPGSQL*QPIQRAE LVCTTCSPIVSAPTGQAPTQGAF SH
10838	41206	B	10900	1	1765	
10839	41207	A	10901	1	1177	MKSLIIVNPADCIGCRTCEVAC VVAHPSEQELNADVFLPRLKV QRLDSIKRFWEQMMRIVTAAV MASTLAVSSLSHAAEVGSGDN WHPGEELTQRSTQSHMFDGISL TEHQRQQMRDLMQQARHEQPP VNVSELETMHFPGMLFETEGEE LRTVATDGHRLAVCSMPIGQSL PSHSVIVPRKGVIELMRMLDGG DNPLRVQIGSNNIRAHVGDFIFT SKLVDGRFPDYRRVLPKNPDK HLEAGCDLLKQAFARAA\ILSN EKFRGVRLYVSENQLKITANNP DQEEAEEILDVPYSGAEMEIGF NVSYVMDVLNALKCENVRMM LTDSVSSVQIEDAASQS\AAYV GMPMRLEGSPPLGNPEFQKISSP CALYIALCSKARHHTGRYLGLC
10840	41208	A	10902	527	925	

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10841	41209	A	10903	1	1514	MAFGLFWLIWILMSTITRGIDG MSLALFTEMTPPPNTEGGGLAN ALAGSGLLILWATVFGTPLGIM AGIYLAEYGRKSWLAEVIRFIN DILLSAPSIVVGLFVYTIVVAQM EHFSGWAGVIALALLQVPIVIRT TENMLKLVPYSLREAAYALGT PKWKMISAITLKSAVVGNMTRI L\LRMAPIVVKTAPLLFTALSNQ FWSTDMMQPIANLPVTIFKFAM SPFAEWQQLAWAGVRNLNFYY GKFHALKNINLDIAKNQVCVC YNQCTESLVNGLYANAAHLVS VGQRSTGNSSVIKARQGSSIRP MIVKYSALCLCRMRSERFIRRT KHRKFDRLQCTCRPDKRSASG NLAFVISLRPVPLVAVVFALFA AFPMFSDVSIQLRHFIFANFLPA TGDVIQRYIEQFVANSNKMTAV GACGLIVTALLLMYSIDSALNTI WRSKRARPKIYSFAVYWMILTL GPLLAGASLAISSYLLSKQWAI DIDSVNRLGAIILTALITGDT
10842	41210	A	10904	900	1250	WYACDQCQTCLPDHAPECAVA *AKTCCTAIETGTYRQSGRERK QSAMVL*RVRVLL**RRETACH VRAGLL*S*GTALGGHYRRLQQ *NSTGRHAGSGGTPLRQRSSVV SSGVADG
10843	41211	A	10905	626	850	LRFCLVFNILSRYSLISTVQKFSP AMLNGTLPLENILH*LRNITAIM NLVIFHGLSA*SVCYIPGRGSV MSDRV
10844	41212	A	10906	307	858	
10845	41213	A	10907	698	1115	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPHSGTRGRRAR FSVRATYAAGRLATIPGYRGGP LGLMCGQPNRKPTDGANERLT MIRAATAMSE
10846	41214	B	10908	1	721	
10847	41215	A	10909	1	2615	
10848	41216	B	10910	1	1164	
10849	41217	B	10911	1	1930	
10850	41218	A	10912	689	1033	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPH\DGPEHSVFM PSR*APMTR*KIYSSPPYRSSQR AHRHA

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10851	41219	A	10913	393	686	NPSQLWEAAPPQWKWIQGAGK VSCQLSRAADQLGRQHHISDPC FSIVPLIL*FAAYFPINPAVLKLA PVALYADAIRYNARTPLQGSLL PLTRLVWA
10852	41220	A	10914	1313	2370	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPHRANPDANVV SEDVLRESVGKSVVNLIHGVRD MAAIRQLKATHTDSVSSEQVD NVRRMLLAMVDDFRCVVIKLA ERIAHLREVKDAPEDERVLAAK ECTNIYAPLANRLGIGQLKWEL EDYCFRYLHPTEYKRIAKLLHE RRLDREHYIEEFVGHLRAEMK AEGVKAEVYGRPKHIYSIWRK MQKKNLAFDELFDVRAVRIVA ERLQDCYAALGIVHTHYRHLP DEFDDYVANPKPNGYQSIHTV VLGPGGKTVEIQIRTKQMHEDA ELGVAAHWEI
10853	41221	B	10915	1	1556	
10854	41222	A	10916	1566	1947	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPH/ECAGLSLAT GISAAAGL*WARRSFIQRDSRD PRYRAPIRIHPLPGANHLRQ
10855	41223	B	10917	1	1571	
10856	41224	A	10918	2024	2589	QDMQNLLVLRETSVKPEYPGL KVPEAFR/RIQGRKGEPGEGAY VYRSAFSVFQKPRFSCALGGAI AASWAGGGAPSPCGRRAELPW GPGPVGVAQTVCPERPRRERRL RGEREEEAADKVMARRWRKSR RRKRKEMEERMSPEETEGTNF DFAGEAVGQAERKGPAFSAAE ESFHEEEKRRRKEQSDLTF
10857	41225	B	10919	690	2724	
10858	41226	A	10920	3892	4338	

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10859	41227	A	10921	2573	3473	ANGARLALPPLGTFQGRQLRRR RPRWRRRRPGEASGPVMRLRG PRPGASAQPWDGGSQVAR*WC PFPSPQGWDGGSQGGQGDGAR FRTHRAKVQQDGDGR*DEADG VHRHAPLQGRLVLVQVGVADE REDDAGNEGLQHLQQPGYGGH IASDLAGPGPGPGHFGGVSHTR DAGEEGGGDGVVPRTAVGQEL DIGGGVDDGGREAEEGRIAGEG DGEVAPRQGEAGLEPAQLHDE DDQGHGEAEAPGEHGPVAHGP RPGAHASHQREGHAGRHQLQQ AKETQGLCQGPRGPHDHGGPQ
10860	41228	A	10922	819	1274	NPLPRLQLRRQLHLPSVRNCCQ TRRCGR*HRQRLRQ*ARRKLVR SVYFGSCLRQLLREEWK*Y*RV *VLGWYSAVSTSSLPFDYCFLP NSDGYRRVVDPGSLSGHPFLYQ RYGWQHDDVHQPDLGLGPPGS LHPDPACFRCVLRNCGNLLA
10861	41229	A	10923	720	3546	RDGRKPLQPDAARNCGGSQSQ RSGSRKRRGDRRI/TLMSLKTRK ANRWA*SFRRKMAAISTP/RTDI ACAKYRYETLHADRVLYYIDS RQHQHLMQAWAIVRKAGYVP ESVPLEHHMFGMMLGKDGKPF KTRAGGTVKLADLLDEALERA RRLVAERTRYSAKSWKTVFRL VIGEQMIDVLGPEKRRRRTTQE KIAIVQQSFEPGMTVSLVARQH GVAASQLFLWRKQYQEGSLTA VAAGEQVVPASELAAAMKQ
10862	41230	A	10924	764	1227	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPHNPTLEWFLS HCHIHKYPSKSTLIHQGEKAET LYYIGKGSVAVLIKDEEGKEMI LSYLNQGDTIGDLGLFEEGQER SAW
10863	41231	A	10925	2467	2653	WLPFGLSHHNSPHPTSWGAN\G GFCQLLSMSVLIMHSGTLGAH WDFSPVIGLEANRGVGDGS

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10864	41232	A	10926	1	860	MSHQLTFADSEFSSKRRQTRKE IFLSRMEQILPWQNMVEVIEPFY PKAGNGRRPYPLETMLRIHCM QHWYNLSDGAMEDALYEIASM RLFARLSLDSALPDRTTIMNFR HLLEQHQLARQLFKTINRWLAL GVMMTQGTLFDATIIEAPSSTK NKEQQRDPEMHQTKKGNQWH FGMKAHIGVDAKSGLTHSLVT TAANEHDLNQLGNLLHGEKQF VSAMPATKEPQREELAEVDVD LLIAERPGKVKTLK/TESAQ/GT KRPSTSNT*KPASVPGWSTRFA SSSGSSAS
10865	41233	B	10927	754	910	
10866	41234	A	10928	2395	3454	
10867	41235	A	10929	1	1377	MSCMTPASDGTFISIDDEEAKQ FRESVVEWLMTNHPHDCPVCE EGGNCHLQDMTVMTGHSFRRY RFTKRTHRNQDLGPFISHEMNR CIACYRCVRYYKDYADGTDLG VYGAHDNVYFGRPEDGTLESE FSGNLVEICPTGVFTDKTHSER YNRKWDMQFAPSICQQCSIGCN ISPGERYGELRRIENRYNGTVN HYFLCDRGRFGYGYVNLKDRP RQPVQRRGDDFITLNAEQAMQ GAADILRQSKKVIGIGSPRASVE SNFALRELVGEENFYTGIAHGE QERLQLALKVLREGGIYTPALR EIESYDAVLVLGEDVTQTGARV ALAVRQAVKGKAREMAAAQK VADWQIAAILNIGQ\HPLFVT/N VDDTRLDDIAAWTYRAPVEDQ ARLGFAIAHALDNSAPAVDGIE PELQSKIDVIVQALAVFRLVIGE QMIDVLGPEKRRRRTTQEKIAN
10868	41236	A	10930	19	586	IAALLKDKHPAMLLLAATKRG KALAARLSVQLNAALVNDATA VDIVDGHICAEHRMYGGFAQE KINSPLAIITLAPGVQEPCTSDTS HQCPTETVPYV/APRHEILCRER RA\KAASSVDLSKAKRVVGVG RGLAAQDDLKMVHELAAVLN AEVGCSRPI\AEGENWMERHAQ HKSWNPLSWAPLGSQAHP

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10869	41237	A	10931	1	1364	MLRILCLALCSLLTGTRADPGA LLRLGMDIMNREVQSAMDESH ILEKMAAEAGKKQPGMKPIKGI TNLKVKDVQLPVITLNFVPGVG IFQCVSTGMTVTGKSFMGGNM EIIVALNITATNRLLRDEETGLP VFKSEGCEVILVNVKTNLPSNM LPKMVNKFLDSTLHKVLPGLM CPAIDAVLVYVNRKWTNLSDP MPVGQMGTVKYVLMSAPATT ASYIQLDFSPVVQQQKGKTIKL ADAGEALTFP/RGVMPKA/PPQL LVPATFLSAELALLQKSFHVNI QDTMIGELPPQTTKTLARFIPEV AVAYPKSKPLTTQIKIKKPPKV AMKTGKSLLHLHSTLEMFAAR WRRKAPMSLFLLEEHFNLKGQ HSLHENQLQMATSLDRLLSLSR KSSSIGNFNERELTGFITSYLEE AYIPVVNDVLQVGLPLPDFLAM NYNLAELDIVELGGIMEPADI
10870	41238	A	10932	111	415	VSALSLLLHRAPRCRRPSLPPLQ DAGLHGWEHGVQRGRGPAAH RDPV*EGWHHSGHLAQGHSEG *PCGDSETPAGREGKTAGHRTG RCGCRQEQTEGAQQD
10871	41239	A	10933	2	219	FLGGEGVIFPRGWWGAAMRFV STGSRHTTP*GSEKSAGPHTQW HQNSK*ATSETRLHSCASEGIVP AGCRPY

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10872	41240	A	10934	1	2358	VPMVVVPPVGAKGNTPATGTT QGKKAEGTQNQSKKAEGAPNQ GRKAEGTPNQGKKTEGTPNQG KKAEGTPNQGKKA\EGTPNQG KKAEGAHNQGKKVDTTPNQG KKVEGAPTQGRKAEGAQNQA KKVEGAQNQGKKAEGAQNQG KKAEGAQNQGKKAEGAQNQG KKAEGGQNQGKKTEEAQKQG KKAEGAQIQGKKNEGAQTQGK KAEGAQNQGKKNEGAQTQGK KAEGAQTQGKKADGAQNQGK KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKADGAQNQGK KAEGAQNQGKKAEGAQNQGT KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGK KVEGAQNQGKKAEGAQNQGK KAEGAQNQGKKAEGAQNQGQ KGEGAQNQGKKTEGAQGKKA ERSPNQGKK\GEGAPIQGKKAD SVANQGTKVEGITNQGKKAEG SPSEGKKAEGSPNQGKKADAA ANQGKKTESAFVQGKNTDVAQ SPEAPKQEAPAKKKSGSKKKGE PGPPDADGPLYLPYKTLVSTVG SMVFNEGEAQRLIEILSEKAGII QDTWHKATQKGDPVAILKRQL
10873	41241	A	10935	967	1574	SLKCLIISLSPVHSYPGKRPEVSF SPINSGQPPNYEMLKEEHEVAV LGVAYNPAPPTSTVIHIRNETSV PDHV/VLVPVQHSLHEP\CCLGF IAFAYSVKSRHRKMVGDLTGA Q/ALCLHRQVPEHLGPDFGHPH DHSAHHHPSVDLPSLPSSFLLLF LFLFLPALQLLFLSFSLVFFFFFS FFPLFQRLELWGWGEWDHHST
10874	41242	A	10936	3	370	RVATIVDIWEKSISGKKNSQNL FVNPCCLGFIAFAYSVKSRDRK MVGDLTGAQA/LCLHRQVPEH LSPDCGHPHDHSAHHHPGVDL PSLSIDQEASSRPGARALQDGA WASVFPSVQWEQQGW

1470

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10875	41243	A	10937	76	614	PDRRWSSLDTMNHTGQTFFSPV NSGQPPNYEMLKEEHEVAVLG APHNPAPPTSTVIHIRSETSVPD HV/VLVPVQHPLHEP\CCLGFIA FAYSVKSRDRKMVGDVTGAQ/ ALCLHRQVPEHLGPDSGHPHD HSAHRHPSADLPGLWIDQEASL RPGALPMTCIPRTPTSIPRPAPR GQELCP
10876	41244	B	10938	695	1011	
10877	41245	A	10939	410	5501	EAKTHKSVVMTDPLLDSQPASS TGEMDGLCPELLLIPPPLSNRGI LGPVQSPCPSRDPAPIPTEPGCL LVEATATEEGPGNMEIIVETVA GTLTPGAPGETPAPKLPPGEREP SQEAGTPLPGQETAEEENVEKE EKSDTQKDSQKAVDKGQGAQR LEGDVVSGTESLFKTHMCPECK RCFKKRTHLVEHLHLHFPDPSL QCPNCQKFFTSKSKLKTHLLRE LGEKAHHCPLCHYSAVERNAL NRHMASMHEDIS
10878	41246	A	10940	446	1704	GGPDMDARAPAVGGSCHQHGP SGAPGP/CIGRMES/EVGVRDHA IPEGARCNRFRKETTEGPLHCSR CGLLCPSPASLRGHTRKQHPRL ECGACQEAFPSRLALDEHRRQQ HFSHRCQLCDFAARERVGLVK HYLEQHEETSAAVAASDGDGD AGQPPLHCPFCDFTCRHQLVLD HHVKGHGGTRLYKCTDCAYST KNRQKITWHSRIHTGEKPYHCH LCPYACADPSRLKYHMRIHKEE RKYLCPECGYKCKWVNQLKY HMTKHTGLKPYQCPECEYCTN P\ADALRVHQETRHREARAFMC EQCGKAFKTRFLLRTHLRKHSE AKPYVCNVCHRAFRWAAGLR HHALTHTDRHPFFCRLCNYKA KQKFQVVKHVRRHHPDQADPN QGVGKDPTTPTVHLHDVQLED PSPPAPAAPHTGPEG

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10879	41247	A	10941	1	944	MSILLTSIARQSRDKRTRLGHK QRILAGLGSNHPIRRNLQGLRR FALVDRQLVVQNVVTRWCRM VYQSAANVFIQHRPISHDERVQ QRGTAITMMVQQAQWAERGK SGLSGVAIGPAVDTSALQAQLR ETLPPHMVPVVLLQLPQLPLSA NGKLDRKALPLPELKAQAPGR APKAGSETIIAAAFSSLLGCDVQ DADADFFALGGHSLLAMKLAA QLSRQVARQVTPGQVMVASTV AKLATIIDAEEDSTRRM/WIRNH SAVA*R*WPDAVLFPSCVRFCL AVQRALALSRSTMVDYRHSVT APQWPHADGGKPG
10880	41248	A	10942	1	939	MRTILTIDIQLRYPRRPGAFGTH TFLKCAFSNKQRRFTVKRFAFL AARYPASQEMPPVRHGHAVAA AIPCGNVPANGNTPARYKGQC GLCSSTLQDALRDFIQVAHTCEI PLMPACFGLADDKLWRWLNE KLPCSLMLLPTLPPSVLGIRLQN QLQRKIVLFGGVWMPGDEVKK VTCKNGVVNEIWTRNHADIPLR PRFAVLASGSFFSGGLVAERNG IREPILGLDVLQTATRGEWYKG DFFAPQPWQQFGVTTDETLRPS QAGQTIENLFAIC\SMLGGFDPI AQGCGGGVCAVSALHAAQQIA QRAGGQQ
10881	41249	A	10943	25	479	
10882	41250	A	10944	2	453	APSRTSGSSVGLQGSYVLDVDG REFGCERVKG*FLVHRAGHL/L TLWLFSSQINKMEWWSRLVSS DPEINTKKINPENSKVSPGWLG ELQQEGEGPRCFQSFTDSCHCL PS\LSDLDSETRSMVEKMMYDQ RQKSMGLPTSDEQKKQEILKK

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10883	41251	A	10945	3	1110	RDPQERRERGTRVQSSGTWIGA GAMGGEQEEERFDGMLLAMA HQHEGGVQELVNTFFSFLRRKT DFFIGGEEGMAEKLITQTFSHH NQLAQKTRREKIARQEAERREK AERAARLAKEAKSETSGPQIKE LTDEKAEKLQLEIDQKKDAENP EAQLKNGSLDSPGKQDTEEDEE EDEKDKGKLKPNLGNGADLAQ *RLNPDPCRELDLAVPF\CVNFR LKGKDMVVDIQ/RRQHLGVGL KGQPAIIDGELYNEVKVEES\SW LIEDG\KVVTVHLEKINKMEW WSRLVS\SDPEINTKK\INPENSK LSDLDSETR\SMVEKMM\YDQ\ RQKSMGLPTSDEQKK\QEILK\K FM\DQHPEMGFFPKAKFPTNPC
10884	41252	A	10946	50	426	
10885	41253	A	10947	1	942	QVWKQNCFKHYSNETDNSTTQ LVGLQTLQVVVPSLILCEHCMN FSSPHVWCCLVQAVPGGQGQTI MQVPVSGTQGLQQVSNI*KY*A VYQRRGFKE*IITTYQTQQIIIQQ PQTAVTAGQTQVIPLALSHRSK TDLEESDN*VRYFPVNADGTIL QQGKCTHKLP*DFLGQLFCPLD N*HLSSSGQGTVTVTLPVAGNV VNSGGMVMVRKCIFQLCL*NF LEHAT*CLLKFEPLYVNAKQYH RILKRRQARAKLEAEGKIPKER RVCITLGRI*ERRIAGFYF*NYLL YPKEKDSPHMQVGRHIHFILLFI TLY
10886	41254	A	10948	24	378	
10887	41255	A	10949	15	658	QRPNAAQTQPSRGCQLSAPARA GRFHPQSCRPSRVGCKGHVCIP GDRSLALWPPRLGCGE*TSSAL DSQGILVSNFPHEGS/PTPQQSG LKTGRILLNHGRRRLKVSQSEG RFLEVGWKQRGPTAHRTHSNR TRRRHALSTGGDTGRARNARS GGGRSPRSSLPAASSTPGVCWS PRMSQARQPPSCRRGVPRRPEM LRSLSPSCQICVCVRFRH

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10888	41256	A	10950	1171	1639	PMALWADGRARHKVGTECEC GMHPGLKCSGRTLGSQTMLAT TPCDSPT*I/SNKNGLRSV/SYR* CLINALWLFSISPHILVRCGTESS *LLPSLVPSWLP*LVRVR\PLPT GWC*IPSCLKP\PPTWSSHHSPQ RLP*NPATLVCLQNGTARSHSS TPV
10889	41257	A	10951	2	357	HERLLNPGRETDWATCYSETAS CSVA*ATVQ*HDHGSL*PQTPG LKWFSHFSLPSSWDYRHVPPCP ETGPCPVTQDGVQWSYHGSL*P QTPRLKQSYHVSLPSSWDYRW EHPVAGKQA
10890	41258	A	10952	15	578	IQTTPKGRRTKPCHRQKRTIVTP RQSTPRSNRGKDTRSKQRDETT E*TTRAQDTNKEGATQDRTETA RRTQSNMEKEKPNQHNRKRKD RDSRKDKGHERETKNTERNRT KRREKRKDNKHNEAKSQRQTR KKKETKETATRKREEPSNSCSM HPFQISWLHSVGDNGRRDQLLC QGFHLYYLMCFPQ
10891	41259	A	10953	2	369	DIDPTGLQSQGSPKGQDPPLMF SEDYQKSLLEQYHLGLDQKLR KYVVGELIWNFADFMTNQCQP KTTPSVILFLPSCEEPQANKATL VCLMNN/FYPGILMVTWKADG TLITQSVEKTTPSKQS
10892	41260	A	10954	1	417	FGTGPSASPRTSFRHQCGH*PH WTAVTVDSQGAGQPKTTPSVIL FLPSCEEPQANKATLVCLMNNF IPGILMVTWKADGTLITQSVEK TT/PSKQSNNKYVASSYLSLTPE \SWRSRRSYSCQVMQEGSTVEK SVAPAECS
10893	41261	A	10955	113	767	GPMRPGTGQGGLEAPGEPGPN LRQRWPLLLLGLAVVTHGLLR PTAASQSRALGPGAPGGSSRSS LRSRWGRFLLQRGSWTGPRCW PRGFQSKHNSVTHVFGSGTQLT VLSQPQ/ALTPSVILFLPSCEEP\ QANKA\TLVCLMNDFYPGILTV TWKADGTPITH\GVEKTTPSKQ SNNKYVASS/YTLSLTPEQWRS RRSYSCQVMQEGSTVEKS\VAP

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10894	41262	A	10956	1	344	GSAAGQVQQQQQRRHQQGKV TVKYDRKELRKRLVLEEWIVE QLGQLYGCEEEEMPEVEIDIDD LLDADSDEERASKLQEALVDC YKPTEEFIKELLSRIRGMREN*A PPPKKSV
10895	41263	A	10957	3	349	TMNNMRGQILLLFLLIWLWNR YGQLVGSSEKHKIASQLELIQS QFHYCVTLDKLLNFSEPVHVK QEQLLSVCSEKEVTEVKVLALV NHVGSKCCFLIFCSGPS*PKFSV SQVFSD
10896	41264	A	10958	998	1383	
10897	41265	A	10959	39	402	TDHIMREYKLVVLGSGGVGKS ALTVQFVQGIFVEKYDPTIEDS YRKQVEVDCQQCMLEILDTAG TEQFTAMRDLYMKNGQGFALV YSITGQSTFNDLQDLREQILRG* RTREDV\PMILVGN
10898	41266	A	10960	25	739	YKKNFDISLLSVKCETCTHMLT SSSL*C*NLICRSLFLIDFNL*AG FVI*VGFTAQSTFNDLQDLREQI LRVKDTEDVSIFSLCKMLCHLS VAK*KSACFQNLARQWCNCAF LESSAKSKINVNEVTYNCWAA QTSAFLVCFKLTARLLALSITNV SSCTGWGVQRSHQDQGNSKHA ASSVWKVGFGIVRLGTGTCLSS LERGYMCMEKEMFDPYTPSRV LKPRSEALELFGPLKSLT
10899	41267	A	10961	946	1424	YFRFLCVIFCSFLLRCLVSRVLL YPMLIAEIPRVQGRGGPSWPGL GGRLLKELSRLLTFLKVRKLSIL SGWREVPLGQPSLTEPP/PPAPP HPGPGSWLASASAPHLSQPPAA GPAGQPPSPGSPVPGGCSLALP VTSVLCLEPPALKPAAASAPVV AVH
10900	41268	A	10962	1	148	TALQEFGTRSGIPALGCPPPDP* PPPGSCPPPEPQLLSVGEPSRCS CSP
10901	41269	A	10963	10	233	LGAARRAQLLESWPRA\PPPAR LHACHLQP/LPRTPKVHTS*PTQ QQGGFSLCLKKKNVPVSVEMIC SSARLKLTE
10902	41270	A	10964	1	331	RPLLLSTLCWELRAALSYWRA GRAPPPPARLHAGPASGFWVLT PSGGEEGEPRTHLWGGGGRRG GGRKKKD*GGQGRGAGGFATF SPPANAPRLHTSLTNSSARWIFL CV

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10903	41271	A	10965	4	1023	FPRAGEKPYTCEESGRAFNQS* TLTTHMTIHAG*KPYKCEECGK AFYRF'SYLTKHMIIHTGETFYK CEECGRGFNWSSTLTKHNRIHT GEKPYKCEQCGKALNESSNLT AHKIIHTGEKPYKCEECGKAFN RSPKLTAHKVIHSGEKPYKCEE CGKAFSQSSILTTHKRIHTGEKP YKCEECGKAFNRSSNLTKHKII HTGEKSYKCEECGICRTPKMAV FSQCHQVLKITNIHYPSSIATIVH GDRAQSHVDICTLGDKASGAII GTAFYTTQCEQRAYNETAVSR YTISRPPSHHGGDSETTEFSPAI GRCNGVHKSWGSNRCSDRWRS
10904	41272	A	10966	1	290	
10905	41273	A	10967	1	1508	MSWAARPPFLPQRHAAGQCGP VGVRKEMHCGVASRWRRRRP WLDPAAAAAAAVAGGEQQTP EPEPGEAGRDGMGDSGRGECP SRRAGEPVTALSATPPPPPFPVIS SSMGSPGLPPPAPPGFSGPVSSP QVRGCDQLTAWPLSFSCFPCNP VLGVRGLHCPPPPGGPGAGKRL CAICGDRSSGMWLRG*TERESL GHVSSPVG*DLTYSCRDNKDCT VDKRQRNRCQYCRYQKCLATG MKREGKDPPCPGVLDHMPFSLI PLRPPEEMPVDRILEAELAVEQ KSDQGVEGPGGTGGSGSSVSV GVNPLSFVMGVGGGSLGLWAK RIPHFSSLPLDDQVILLRAGQ*P WIPLTS*HLTPL*LPDLFLATGL HVHRNSAHSAGVGAIFDRSVA LG*AGM*IEGVGL*AGPCLRAII LFNPGKRRITFVSQGQGNLGAS SSPMETYCKQKYPEQQGR*DG AGGH*GSLGGGECYEDVFLFFF KLIGDTPIDTFLMEMLEAPHQL
10906	41274	A	10968	945	1131	MICTVAISYVLFVDVYISLLSAT CSPKPQGSAVFQHD*VSPGI*NG SERCCSRDRHRQFLW
10907	41275	A	10969	37	332	AEGIRTIQGTENIFCKVVWGRQ VSLSQTNTLEGQSNDHGCQLR KRTFISTFTAHYSRFFLQRF/VFP YTGFEKCQSTAW*KPRYLLSHS VKGKRNLHPA
10908	41276	A	10970	137	283	
10909	41277	B	10971	1	624	

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10910	41278	A	10972	3	618	KTQDPAKAPNTPDILEIEFKKG VPVKVTNVKDGTTHQTSLELF MYLNEVA\AQHGVGRIDLGDN R\FIGMKGRGIYYTPTGTILYHA HLHIEAFTMDREVRTIIQGLGLK FAELVYTGFWHSPECELCRHCI AKSQERVEGKVQVSVLKGQVY ILGRESPLSLYNEELVSMNVQG DYEPTDATGFININSLRLKEYHR LQSKVTAK
10911	41279	B	10973	1	1102	
10912	41280	A	10974	748	1396	LYLQRPFFQIRSSLQVLGHRQIF PQSPRCLHLAPPPLMRHSHRSPT WY*FSPRRTQQSRPVSAQPLGS CGGIQPAPPPVTQPSQLSPPRGS R*LGSDGAGTQPRHVQNPCPLT CVHM*SPPPPCLNLQARCPQSL RAKVVPAVEQRARVGHVESPG SHCWLEREPEVGSGPQQGQRPL PAGAAD*CLGAFWQTHLDLGD SLISCSHDLQGWQLSQA
10913	41281	A	10975	1	846	
10914	41282	A	10976	2	851	WNSAELGRGGPGAGGAGVIGM MRTQCLLGLRTFVAFAAKLWS FFIYLLRRQIRTVIQYQTVRYDI LPLSPVSRNRLAQVKRKILVLD LDETLIHSHHDGVLRPTVRPGT PPDFILKVVIDKHPVRFF\VHKR PHVDFFLEVVSQWYELVVFTAS MEIYG\SAVAD\KLDNSRSILKR RYYRQHCTLELG\SYIKD/LSLV VHSDLS\GIVIL\DNSPGA\YRSH PGYGGR\DNAIPIKSWVSVTPS\ DTALLNLLPMLDALRFTADVRS \VLSRNLHQHRLWVTACFPLPP
10915	41283	A	10977	25	153	
10916	41284	A	10978	1	741	MMSFDSMSHIQVMLLQEVPSS YPASKKNEA/PQTSGGGPGTPR KGLGE/PAVVPMSPAVGT/PALT QCHGPHAEDDLEEPILTTDPVA RDCPLDLLMDGKTGAIISSLLHS NCLPAPFCQCSHAVKWQLKTV HSCCPLGEVQPQRRCVIATAKE KGIGVKHHCNIHSDNVNSIITAT VAAHQQQQLPQNGNNSGIKNN QNSSENTVTNNSKNISNHIICRN SSKNSKSSSSSSSNNNKNSSNTI NSNNKAR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10917	41285	A	10979	1	669	MMSFDSMSHIQVMLLQEVPSS YPASKKNEA/PQTSGGGPGTPR KGLGE/PAVVPMSPAVGT/PALT QCHGPHDEDDLEEPILTTDPVA RDLTMPTAASQHLQKQCLEHH HYFHSYNINSDITVSRNNISSIIT TPVHHCNIHSDNVNSIITATVAA HQQQQLPQNGNNSGIKNNQNS SENTVTNNSKNISNHIICRNSSK NSKSSSSSSSNNNKNSSNTINSN NKAR
10918	41286	A	10980	3	980	IESPGPFPPGLQRPVPHRGEFCL RCTSSEALPCFYSWTVTFSPWT VAAAQGQPRPGPASRTLLLATQ SEIAAAELGPGSWGGPSSCPSE QSSHGPPASS*AAPLQTGRRLRS RAS*RSGAPSVAALPAPLSRPQE RHPSVSASRSGHPPGPCPSPPPP AARPVQPSPCRAPPGSAAGRAR APHA*AAPGSWLSSAGAAARR WPFQTAKGSGS*DRPGRPGPDA PAAPPGWHRAPPSGSSSGAGTG RHPQPFGRPRRRTPAPYAAPCA FVATLVFS*LLIFGGAFSFPALS HCPTSA*LKRLLSEPAPIAFPFG LHPGTLLSRASE
10919	41287	A	10981	1	5229	
10920	41288	A	10982	1	7044	
10921	41289	A	10983	1	3228	
10922	41290	A	10984	10	209	TLSGGEPQRLEAERRARLQDEE RRRQQQLE*MRKREAEDRARQ EEERRRQEEERTKRDAEEKVM
10923	41291	A	10985	293	363	
10924	41292	A	10986	3	434	
10925	41293	A	10987	3	1536	
10926	41294	A	10988	315	993	VPVAPIFHFSHFSPAPTVFTQSR QDSMQCILRQHCHLILISRSSSL VPAGLRGAMAFALAIRDTASY ARQMMFTTTLLICPELLALLLS LSHSRSLLLHGYHGPS*YALFFS LSFSLVTWVGAKPGRYQSLIFV VVVGCTFQNQEPLREEDSDFIL TEGDLTLTYGDSTVTANGSSSS HTASTSLEGSRRTKSSSEEVLER DLGMGDQKVSSRGTRLVFPLE
10927	41295	A	10989	3	320	

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10928	41296	A	10990	3	582	GPPTPRRPRPLPSSLPSRRSRDPP RIPLCA*FPQTRKQIARSEPD*T WASQSSTSIPRIWRFVHA*KFST APLTATPPPGKMCSAGCRETVK TT*PPLRGGPAPFLLPSRAVARG TRPGFRSALSFRRPGNRSRGVN LIKLGLRSPPPPYPGFGGSYTPE NSQPLPSLLLHPLEKCALRDAE RQLKPPDHHLMVAWLIPDVWN GEGEPSPSHTRHSLRASSSNYV LRAPEGNLLARRLPRETAINLQ PKACYKTLSHPESFSHFYNQFC PRRHQWLPAQPPGHFFLG
10929	41297	A	10991	3	338	NSPSRPRSSQRGVAGRRSEAGP VAVP*GGPKKGRGC*GNGRWG QRPRWMLRASGSGESTTPACSA ENRHAS*RKKRKRPGQVSWEE TEETRSGHSQPRGHAEPLLHRP QRR
10930	41298	A	10992	3	226	TILSS*SSSSSSSPSPSPSPSPSPSP SPSPSPSPSPSPSPSPSSSFFLRWS PALFPRSLSFSLFPGTGTPFSCP
10931	41299	A	10993	24	489	KEYLVRTK*QKGKGENPLVKIT FRPPPGLRTYPSAPWSARSTYG RAAAVWRPHSPSAPRRGTHPW PAGHRGQRASGEGVGTHTHAH MSSVCACSTHTCWSRNCKDPR EDRGRGLTVLLEAAVCNSCLLL VLKTPRNPQLPILYTDSDTKSST GNP
10932	41300	A	10994	1	1491	
10933	41301	A	10995	140	308	RNVIKLKGWSRPSKQQDNPTLR PGPPSPAGGFQQLLMRMRRPLA GGGKSWGIAHFYKPLQRERRA GAECGLARQVRAEVTKWIGVN RRPRKRKRMEKEEVFEKLLPD QLGLLLEHLLEQKTLSPRTLQS LQRTYHLQDQDAEVRHRWCEL IVKHKFTKAYKSVERFLQEDQA MGVYLYGELMVSEDARQQQL ARRCFERTKEQMDRSSAQVVA EMLF*RGQDRFSLKKCDKVKG MVKTQQATGQPDSPPRPALTG RRVPATADADEKAFGGWRKIL GYRTFL

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10934	41302	A	10996	219	688	RRMHAYVSLDPLERPPFFFFFLF FFFFFFFLRRSFALVAQAGVHW RDLGSPQPPPPRFK*FSCLSLPSS WNYRHAPPRPANFVFLVETGL QLPTSGDLPASASQSVGITGVS HCAWPGNWLLKETRCGSSVGR QITGPITPDAWVDPGIPDRYLQ
10935	41303	A	10997	3	298	FFFFFLRQSFALVAQAGVQWRD LCSPQPPPPRFK*FSCLSLPSSW NYRHGPPHPANF*FLVEMEFH HVGQACLKLLPSGDPPALASQS AGITGVSHRA
10936	41304	A	10998	2	438	APSVRSGNERDLARDEEAQETQ VRGCHASGG\CTPAATAGASPP AWAGRRGTGQRLRSQPRQTGR QPPRVQPLAPPPGAPAPLPNPQ NCRRKTRSHPRFWAGTLAPGPC PGLWCLPGLVQVDVLAAGRCD HLSCLPPLCPQAFLL
10937	41305	A	10999	2856	3044	GAATGEGGCCRLPGHPALAST A*AIPCRGPRVQETSPPPVLGW DPGSRAMSRALVFAWVGAG
10938	41306	A	11000	1	908	GLGDPGVPVLRSGGLGPPADLK GDQAVAE*LHEASGVTEHHPS AQPGPGGEAAEPAHLIV*EPEG GSPGHPGGGPGHPG*SEGPAGG KPGPAGGGSAQGCRRSSEPSGT *SGRSPR*GPHGHPDCRTHPAR EGAQVHSRSPLPGGAPVRRGCS QGPEQRLQQEDFLRVQQLSAA GPLRPQLYPQVWLCPDEHQLLE QYPRSYFSERIDVFKPCGVQQG CPVLDRASSKISPEDAAGSVVR LRSLWAASGLQQGASGLATFL QLLTCGVLWPDEELVHLLLDE VVASAALRCPDPVPMEPTCG

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10939	41307	A	11001	218	990	VLQLLKAMRLELFLPPGGFMV LLASGVKLQTFATQVPSWLHP VDPSPGLEVELPASPVQCAHTP QPLGGRWDWVPWSRGQRSSG RLGPHGSPWRRWEAQAWQPA GPKPCPVGS*GPVRNRGQRRW AGTAGDPVHPPQPLAQVLSPSL PGADRAGQLLRVQGPPSPCPPG TPAGPQGRCAAPVPTGVSPSTP PCKLREQAPALASPERGSHSAA VG*RAPQVLPKW*PELMFRWV RSFFLLVGSWLTSGVKLHPFVV SVTALKGDASGVIPSSRWVHGL AGLRCEAADLRDSGAQLASPS GSLTRTGGGAACQSRAVCPHSS AFGWSMGLGAMEQGAALIGEA RASREPMEEVGGSGMAACRSQ ALPRGQLRPSEKSRAAPVGWH CWGPSTPSAATGPGAKPLIARG RQGRPAAQSAGPAKPMPTRNSS WPARAVRSPGSHWRLSLHTSL QAERAGSGLGQPRKGLPQCSSG LKGSSSAAKVVAQAEEAQRAS EGCEDYLARCHLSIRKMRRRN
10940	41308	A	11002	3	644	EPPGPTGPPSPQSPWHPGLPGR WSSTHVVFTHLHLAGPGWSCD HRWMGKQLPVSLSASGVQGVP RFRSQDMYQSSRNKFPSGAAH VPQEWAVPWKNQGNTHQSSRP SESGCCAQAEGSNQCHQRQEA AGPSRLSLPDGGRRLETPRHPN GPWYWNNSPQRLN*WRRGDPS WPEPQGKPHTGGARVPACQRR EICLSPFRGPRRRQKENIYEYL
10941	41309	A	11003	202	438	FHGHPAPGEMRGWPRVTKRSP AQSGKT\HFPPGSPGPPDTSTESI FRRAWKAPGFPGRGRTADPET ARCGAWDEIVEPV
10942	41310	A	11004	520	1094	GPLSQCPPLPRLLPPLGVYSKGR APHADTHSPGHRRTHAHAQPA AAAATATR*QRRRRLPPRRTPF RRPAARPDRRVPAHSSAVLPRP GKPGAFQALRKMDSVDVSGGP GEPGGKLGFARLRRAPPDRLPG CPSSHSFQTQSLSFMAHNVDEP LESATSLLGLLRRSWFCFTWQK QTVYWSTGRIRHSGEK
10943	41311	A	11005	1	138	SISLMNIDVKILNKILANQIQQHI RKLIHHD*VGFIPCLRILVIYI

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10944	41312	A	11006	65	297	NQRLPQPFLPTTPPPPATRAT*D EEKSPYPGPGSDKKCPTLQLPSP PTPSAGGFPPLGESGSPGGLVK AQIMEGISM
10945	41313	B	11007	322	6900	
10946	41314	A	11008	3	215	
10947	41315	A	11009	1	234	
10948	41316	A	11010	149	300	
10949	41317	B	11011	28	162	
10950	41318	A	11012	700	861	RRKCIPGRRNSKHKGPDGAGRP *VCREQQEGQCAWTGYPGAQG PDPYCGKGPYS
10951	41319	A	11013	291	744	LKRTKCDQLLKTSFLDLGRGPI LKWLCTSKWGHQQIIIRA*GTE YKTTSFFFFFETASRLCHPGWE CSGAISAHS*FLLPGSCHSPASA S*VAVTTDTREHAQLIFF*HFSR DGFHVVARWLDLLTCDLPLSL QVLGYRNYIIIVRQLPSR
10952	41320	A	11014	139	414	SFKTAPPGFFFSF*LHLILMLKFT PGAIKLVFL\QFLLGISFFFLGKP PSSWFRNESCSVFRKESSQSWQ GRAHVWG*SDPWSSGRSRRAH L
10953	41321	A	11015	5	565	VHTTEATCTTTGAKPCPWPSKL ATRQDHSVLSTSNPRGPTPHKS GSPETAGALSSGDAGSRGEGPR TVSSERSSPGKGGSTLLGTTA*G PGPAHFASAVLGPSSKSLQAAS *EVDSFPSSLLKTAVSVLASTVR LSVSFMPPFITVSVTSSVISASSS PSELASMATLPGASG*AARAVN FELDEE
10954	41322	A	11016	188	515	SQTVSIVGELPIPRKRCEIGIWD AQKR/CPRLTGPWATISVPTISK KATGN/PQHPNHPRARYQINAE *WKVHF*TNTDRPSHECPCTLV VHRTLDQLRHKSSTSGGKTHG
10955	41323	A	11017	80	397	SVQRSVDHL*DHP*TSVDWELY LDGSSFANPCKVTLKTTTSPAS VTPEADWSMHSQSMRNSLRDS FSLKFGLIIIHDFLTPTFNPLENP CGFLTRFCCVPNQISS
10956	41324	A	11018	104	392	PSQFHLKLLHLMLALLYPVGTC QVKDSSLLQKSTSVPPDSPQTG H\SKLGPFNPGRFR*RPQCQPGV LPPDVELSCHSWSNVLWTTAA KTPIFCSY

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10957	41325	A	11019	125	1404	NLALGMAMWN\RPCQRLPQQP LVAEPTAEGEPHLPTGRELTEA NRFAYAALCGISLSQLFPEPEHS SFCTEFMAGLVKWLELSEAVLP TMTAFASGLGGEGTDVSVQTL LKDPILKDDPTVITQDLLSFSLK DGHYDARARVLVCHMTSLLQV PLEELDVLEEMFLESLKEIKEEE SEMAEASRKKKENRRKWKRYL LIGLATVGGGTVIGVTGGLAAP LVAAGAATIIGSAGAAALGSAA GIAIMTSLFGAAGAGLTGYKM KKRVGAIEEFTFLPLTEGRQLHI TIAVTGWLASGKYRTFSAPWA ALAHSREQYCLAWEAKYLMEL GNALETILSGLANMVAQEALK YTVLSGIVAALTWPASLLSVAN VIDNPWGVCLHRSAEVGKHLA HILLSRQQGRRPVTLIGFSLGAR VIYFCLQEMAQEK
10958	41326	A	11020	3	1693	CQRLPQQPLVAEPTAEGEPHLP TGRELTEANRFAYAALCGISLS QLFPEPEHR*VLLSCPLGTPVGL HSDAHYGQRLAVAVHVEGTLP FTSSTFAAASVFQKARPWQHPG EQMAFSGKPFLVAAVTSAGGS GAPSVGCTELISTSVLGYHTAL EMAGLVQWLELSEAVLPTMTA FASGLGGEGADVFVQILLKDPI LKDDPTVITQVHPTPGVKDGKL IF*ARVLVCHMTSLLQVPLEEL DVLEEMFLESLKEIKEEESE*ES PATKTEGGGEDKDRKHPLMGD KMTESKTDLWIYEMGNAGVLL FRRYLWLQPKKKENRRKWKR YLLIGLATVGGGTVIGESS*RCA PLVAAGAATIIGSAGAAALGSA AGIAIMTSLFGAAGAGLTGKVQ KE*VGAIEEFTFLPLTEGRQLHI TIAVTGWLASGKYREDQEDQA ALAHSREQYCLAWEAKYLMEL GNALETILSGLANMVAQEALK YTVLSGKCPHLPWPASLLSVAN VIDNPWGVCLHRSAEVGKHLA HILLSRQQVPGNGCVIGFSLGA RVIYFCLQEMAQEKGEHGLL
10959	41327	A	11021	208	324	VSLLKAADNWLVNSYPFCNSV SSEFFFR*IRDFFLFWIH
10960	41328	A	11022	1265	1459	
10961	41329	C	11023	188	730	

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10962	41330	A	11024	64	228	QHLLRRWGRSGLLLNDR*VSN EIKMEINKFIELNNNSDTIYQTL WDTANTVLKFM
10963	41331	A	11025	1	648	
10964	41332	A	11026	26	613	VGAGGRGWRFAAAVRRAAGG GLRPGPAPGPRAGGGGPRGAH LALLRRAGALRAGKEYGKADA RWVYFDPTIVSVEILAVALDVS LALFLIYAIVKEKYYRHFLQITL CVCELYGCWMTFLPEWAHPEA PNLQQPATGWLYWLGFTLFFF* RCVGFLIPRNWLLWAVHGPRTS RKWHQKGNQFQWKEVFSGTF
10965	41333	A	11027	2	252	ARGRAGVAGGPR*AAELPGLP RDPFPASRPLRRSDCLGGLIRHK PPDPGAGARVEGEALPSWSPGG ALEEGVT*PGTRGPPWE
10966	41334	A	11028	3	637	RDQVRRGQGGEPARIQCPRRRL GEGPGAPNRLGPPARDPRCSPW PRADSPRDPNRLSSPQLPRPAYL GPACFP*PSWGVSRSLPSLAPW RPHRLPDSQRFPNGGSRSRATS GSWTWKSKECREWRPSGSRGT RGSSGSGAGSSGSSAGVGRRAG HGRWHLR*GPLFPAAPASATCP LWHGWKGASLDLGLQPWATF YPRVTGARGGRTLGP
10967	41335	A	11029	158	462	
10968	41336	A	11030	339	866	QICHSPPGNKAHSHLLPYQTPV PSSQYPPSPSRTLQLPFPTPWNP CQWPSRGSCGPSAVGTGPPFPT GIPSVP*APSARG*HHSSACGCH PGCAGPQPARSPHGPAPASGCH TVSGCCHALLQSCLAPGRPSPA GTWPHPPPGGLPSAPGTEPCTA FEGFQPPCWLSQHPLSPCL
10969	41337	A	11031	621	944	TPQGGTAPSGGRHPWASASPHR LPPL*CSARPGCH/SSRMRSPGT RPSGPL\QDCHPPPRPQTPHAGS HHTSAPQAPAGTF**RQRVAPG SSCWHLPQSWSCSAWLGGC
10970	41338	A	11032	3	257	AGRASKGG*NPSKAVQGSVPG AEGSPPEGGCGQGPAGLGLPGA RQDCSRA*QHPPGPGGGQEVY LDISLAPGSTGIQGLEAKHL
10971	41339	A	11033	94	227	SSYVFKSILTAFGMTWMRLETII LSEVTQG*KTKHQMFSLICGS

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10972	41340	A	11034	404	894	FVYFFRGELCKISSTLGFKGTGQ GLQPSKVS**VPSRPAGNGRPA YPETSQPPPGPSGG*HWLAGW Q*GGPEPGWTCIWP*GS*GTEIG SPSQPGPEPAGVPSPRDAGSAA TGCHTGLAGVVWPPRLCHRRV TDGRKSMKRCLSRSYCTSSVRA SGGGAGRIT
10973	41341	A	11035	1	408	
10974	41342	A	11036	68	204	SFLWHPLGLHFHTHH***NYKS SSK*MVRIRVTFSKFIFVRNNYC
10975	41343	A	11037	5	188	PQCRLHLRQGLALSPKLECSSAI TAHCSLELPGSSNPPSASRF*GS RSVAQAGVQQCYHSSLQPRTP GVKQSSLSFPFLRLQPKVSSATL PVRLQE
10976	41344	A	11038	1	263	
10977	41345	A	11039	2	283	
10978	41346	A	11040	1	1965	MAAENEASQESALGAYSPVDY MSITSFPRLPEDEPAPAAPLRGR KDEDAFLGDPDTGEAR*PRPCP ALGSPRSSFFCVKHPGSPLRETR KDPFSAAAAECSCRQDGLTVIV TACLTFATGVTVALVMQIYFG DPQVRGTNGEGEETGEWGVG* CLRNCGKGSSVDAAVAAALCL GIVAPHSSGLGG*GAVEVGVPQ AYFLPPGL*ASCAARALREETL QRSWETKVGTLVRRESSGESLF IALLLTQALIC*VLAQDGFNVT HDLGQWGLGIWERHEVDGEG* NL*DLEPPPLPGSLLHRPDLAEV LDVLGTSGPAAFYAGGNLTLE MVAEVSARVVRVGACPKVPIA GHPRPHFFGVYRGDLSPGSQGP PSGEASQSMATSFWPFNLTSLV SREQALHWVAEVRLTRLPFPGF KDIRSGEIGYCHRADDMLRWV LGRTWGLQRQRWVWGKGQEK SSYELDGAPTAAQVLIMGPDDF IVAMVRYASSDSEPGTRDPLNQ EGVGAG*RFSWPNRTANHSAPS LVGFASLLSWGP*GL*VGGAM AWLPLCGTYLALGANGAARGL SGLTQVRFTPWLAFFSREPSCG LDCRCLS*QSNLLQVDSECRAE TSWGGHRDR*RKDSSQGCPWV HGSRRTNNFIIAVKDPRSPDAA

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10979	41347	A	11041	1	363	SSMTTVHATTATQKTVGETLA* LLQNIIPVSTSVAEAMGKVIPEP DKRLTGMAFCVPTHNMLVVAL ICHLQKAAKYDGMRRCFNATT GITFNGHFVRLLSWDEFGSSNR VVDLMVHTASKE
10980	41348	A	11042	162	303	CLLLKSCSQEAAAALALPALGL VFDVFL*IYFVRTKYLRVGFRN FF
10981	41349	C	11043	56	118	
10982	41350	C	11044	345	410	
10983	41351	C	11045	7	439	
10984	41352	A	11046	2	80	
10985	41353	B	11047	205	5326	
10986	41354	A	11048	1	813	
10987	41355	A	11049	1	1454	
10988	41356	A	11050	2	1624	
10989	41357	A	11051	1	1185	
10990	41358	A	11052	1	2149	MKEKMLRAAREKGRVTHKGK PIRLTADLSAETPQARREWGPIF NILKEKNFQPRISYPDKLSFISEG EIKYFTDKQMLRDFVTTRPVLK ELLKEALNMERNNWYQPLQKH AKNMPNSIILIPKPGRDTTKKEN FRPISLMNIDAKILNKILANRIQ QHIKKLIHHDQVGFIPGMQGWF NIHKSINVIQHINRTIDKNHMIIS IDAEKAFDKIQQLFMLKTLNKL GIDGTYLKIRIKYLGIQLTREVK DLFKENYKPLLNEIKEDTNKW KNIPCSWVGRINIMKMAILPKVI YRFNAISNKLPMTFFTELEKTTL NFIWNQKRARIAKSILSQKNKA GGITLPDFKQYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYTYLIFDKPEKNKQWGKDSLF NKWCWENWLAVCRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEEILGITIQDTGMGKDFMSKT PKAMATKAKIDKWDQIKLKSF CTAKETTIRVNRQPTKWEKIFA TYSSDKGLIFRIYNELKQIYKKK TNNPIKKWAKDMNRPFSKEDIY AAKKYMKKCSPSLAIREMQIKT TMRYHLTPVRMAIIKKSGNNR QTESQIMSELPITIASKRIKYLGI QLTKDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWIGRINIVK\M AILPKPTNVHVTNLAAQDTTAL EAAQISLEGHPQEKEISVTAMPL
10991	41359	A	11053	1	2031	

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10992	41360	A	11054	1	1188	
10993	41361	C	11055	1	353	
10994	41362	B	11056	151	1608	
10995	41363	A	11057	1	373	
10996	41364	B	11058	1	488	
10997	41365	A	11059	1	1257	
10998	41366	A	11060	2	3527	
10999	41367	A	11061	1	2373	
11000	41368	A	11062	1	1755	
11001	41369	A	11063	1	1599	
11002	41370	B	11064	220	1286	
11003	41371	A	11065	1	1826	
11004	41372	A	11066	1	1645	MDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSKVSGYRIN VQES\QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRIN\ILKMAILPKNW KKTTLKFIWNHKRACIAKSILS QRNKAGGITLPDFELYYKATVT KTAWYWYQNRDIDQWNRTEP SEITPHIYNHMIFDKPDKNKKW GNDSLFDKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNV RPKTIKTLEESLGNTIQDIGIGK DFMSKTSKAMTTKAKIDKWDL IKLKSFCTAKETTIRVNRQPTE WENIFAIYSSDKGLISRIYKELK QIYKKKTNNPIKKWAKDMNRH FSKEDIYAAKKHMKKCSSSLAI REMQIKTTMRYHLTPVRMAIIK KSGNNRTRENYFKIHMESKKSQ NSQGNRKEKEQSWRHHATRLQ TIVQGYTVAKTACYWYKNRPT DQSNRTENQEIRLHTYNHLIFD KPDKSNGETTPYSINGARITG
11005	41373	A	11067	1961	2588	KLAQDRDALSPPLLFNIVLEVL ARAIRQEKEIKGIQLGKEEVKLS LFADDMIVYLENPIVSAQNLLK LISNFSKVSGYKINVQKSQAFL YTNNRQTESQTMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLNEIK\EDTNKWKNIPCSWV GRINIVKMA\ILPKVN\YRFNAIP IKLPMTVFTELEKNYFKVHMGT KKEPASPSQS
11006	41374	A	11068	2	278	
11007	41375	A	11069	3	274	

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11008	41376	A	11070	261	1382	LELSFPPAGQRGVLSGDPQNLC TCPSGSWHVPRCWAVERQRPN LPRTVTQLVAEDGSRVYVVGT AHFSDDSKRDVVKVSAATRHIP DTGWCKLLPGSRDGLVRFPTY RVSMLKMDESTLLREAQELSLE KLQQAVRQVRSRGQGSGSGSG SKPPHITEQLGMAPGGEFREAF KEVGTG*GRGWPQGCGSQAVT FKRAIAALSFWQKVRLAWGLC FLSDPIR*GCPRDPGRPAGWSV GMAEMIGEFPDLHRTIVSERDV YLTYMLRQAARRLELPRASDG DGRPQAWDPL*G*GPRGHVPGI EKNWSTDLNIQEIMT*VPAPPC KPHPTSPQVAAFFGLLGYSLYW MGRRTASLVLSLPAAQYCLQR
11009	41377	A	11071	3	506	KDCQF*VGPEQKKALYKVHAPI QAALQLGPYE*ADQKRTCVRF GRHTCETAAFTFWKSLGLDKV TKPRSSSSQLLALAIRSSPGSTT DACLLDSFSGKSRISSWFGS
11010	41378	A	11072	2	374	IRRESTHLQQALGTTPQDRLTC TGHSAQPPACSASPLPPGPP*SS AWPLPPSTRLARQKQAAATAQ P*PLTTQTLGPWSSASTWTSAH KQPGAAAQEWTSTAGSRQLLA GASGSSPSSCSVWTN
11011	41379	A	11073	3	553	
11012	41380	A	11074	239	547	GHHFQMNVVCRCSVWMLSLEP HPVGQIHSC**ERAKLCGKEFN RMHNLMGHMHLHSDSKPFKCL YCPSKFTLKGNLTRHMKVKHG VMERGLHSQVSRPSLEA
11013	41381	A	11075	1	267	MAISMVTTRSTTIRTTAAGCHY ENDMAHNHSDRGGLPLKVVLT TPFLTPPGKGGGAAGALERRTE EGDRDAGGAAQEGGLTPTSVP PSS*HTLWLRTVDPEASTSPSTP RHPYPNRGGGGRALEPHPRR*V *AGCHYENDMAHNHSDRGGLP LKVVLTTPFLTPPGKGGGAAGA LERRTEEGDRDAGGAAQEGGL TPTSVPPSS
11014	41382	A	11076	1	1707	
11015	41383	A	11077	1	1407	

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11016	41384	A	11078	1	1275	MVKGSIQQEELTILKIYAPNTG APRFIKQVLSDLQRDLDSHTIM TGDFNTPLSTSDRSTRQKVNKD IQELNSALHQADLIDIYRTLHPK STEYTFFSAPHRTYSIIDLIGGSK ALLSKCKRIEITTNCLSDHSAIK LELRIKKLTQNRSTTWQLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTIQKISESRSWFF EKINKIDRLLARLIKKKREKNQI DAIKNDQGDITTLERVVLEEPD TLHLLNYTPRKVLYRWNRQSS TSVIETNKTSVELSLPFDEDYIIE IKPFSDGGDGSSSEQIRIPKIS/NK KTK*PNPWRQK*G**LAVADA YARGSGASTSNACTLSAISTI
11017	41385	A	11079	1	426	MLHTKQHLSMGTEDMDDKLH FSDCSAASLVSLSTTTGGHVLT NMSADIARYLPVLYRWNRQSS TSVIETNKTSVELSLPFDEDYIIE IKPFSDGGDGSSSEQIRIPKISNA *ARGSGASTPNACALSAISRIMI SLTARSSL
11018	41386	A	11080	3	620	DRTLAEAPHTAPARSGHRGWC PRPHRRRRNRGRQLLAPGRGA DPGAGEAATVQWRLLRGQPAA ALHVQQGAGDAANAGLQRGA HADSHDRAVPAGHAPGPVAAA GRGHDGQVPAALG*AGGPVGL RRPEPPLQTRGKGRLAPATQQV GQARRLPTGRGQLLLRRPQPAA HHGPRPRLGGRGRGGSHKSPPH GIWPRLAGWRATLE
11019	41387	A	11081	335	640	PLGVLWSLWKSLVHSDAGAGE L*EVITGSTWPNP*QCCLVPNV DDEEEGEEQDDDDDEEEEGL*D IDEEGDEDEGEEEEDDDDVEEG EEDEGEDDWKFAKE
11020	41388	A	11082	2	204	

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11021	41389	A	11083	3	1471	SKDTKRDVDSKSPGMPLFEAEE GVLSRTQIFPTTIKVIDPEFLEEP PALAFLYKDLYEEAVGEKKKE EETASEGDSVNSEASFPSRNSDT DDGTGIYFEKYILKDDILHDTSL TQKDQGQGLEEKRVGKDDSYQ PIAAEGEIWGKFGTICREKSLEE PKGVYGEGRISRPCGDRW*RSD AEESSHHRGRQSGYPENKLCGF LLKTPHHVLERADEAGSHGNE VGNASPEVNLNVPVQVSFPEEE FASGATHVQETSLEEPKILVPPE PSEERLRNSPVQDEYEFTESLH NEVVPQDILSEELSSESTPEDVL SQGKESFEHISENEFASEAEQST PAEQKELGSERKEEDQLSSEVV TEKAQKELKKSQIDTYCYTCKC PISATDKVFGTHKDHEVSTLDT AISAVKTVIRDSDKTKSGEGAY GREMKSPHKFPEGKIHNDKEH DRIVQEFLAETGPKVTRFNEQC RFRPRIYVYENNQTQIMVEEPQ
11022	41390	B	11084	148	235	
11023	41391	A	11085	30	420	VSGTRGPSPCLGTSWASGAWR PPLGGLPPSAGANGPGRVRSAA GCSLVAGCKVLGSWVSGFAGR SHVACAGSSGESVRARCPGTA* AAGGPGPQAFQAAY*QGSRMH RAPPRPNRQVQTWWEEGAGTG
11024	41392	A	11086	2	73	ERLRMPGVAKGRPR*GNPRRG RG
11025	41393	B	11087	1	1412	
11026	41394	A	11088	39	427	PPYWGHFHSSAAASAALKGKD GGSSRSLVPPAQ*HSHSPSKTHC VHTPSRSCAQGLTHTLTQSPPSL KIAQSPSFDARAHARLRIWQIPS APRVPPLSASLSPTRTAGSVRFE SQSTKTSRSHRFLPRT
11027	41395	B	11089	1	813	
11028	41396	A	11090	3	365	RTPSSKGCGRPPRGMGAQGSA GCGRRSPRRSRQARRWSHPC* PPSSPPWPRPARSPPGCSHRAAL SSPSPPSSFLARHSARPRLALAL GPPPWCSSGCASSAPFDLQHPE QSQNQDARG
11029	41397	C	11091	295	412	
11030	41398	A	11092	21	164	GAVTENDFYDLVRTIGGDLVE KVDLIDKFVHPK*VKSFLILPLTI SV

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11031	41399	A	11093	1	1373	GISTMVGSALRRGAHAYVYLV SKASHISRGHQHQAWGSRPPAA ECATQRAPGSVVELLGKSYPQD DHSNLTRKVLTRVGRNLHNQQ HHPLWLIKERVKEHFYKQYVG RFGTPLFSVYDNLSPVVTTWQN FDSLLIPADHPSRKKGDNYYLN RTHMLRAHTSAHQWDLLHAG LDAFLVVGDVYRRDQIDSQHY PIFHQLEAVRLFSKHELFAGIKD GESLQLFEQSSRSAHKQETHTM EAVKLVEFDLKQTLTRLMAHL FGDELEIRWVDCYFPFTHPSFE MEINFHGE\WLEVLGCGVMEQ QLVNSAGAQDRIGWAFGLGLE RLAMILYDIPDIRLFWCED\ERF LKQFCVSNINQKVKFQPLSKYP AVINDISFWLPSENYAE\NDF*Y LVRTIGSDLVERVDLIDKFVLPK THKTSHSYRIMYR\HMEPTLSQ\ REVRHI/HIQALQEAAVQLLGV
11032	41400	A	11094	8	119	
11033	41401	A	11095	2	475	QAGPSGGIPEGIAITGDDSSMHA IAPEDLPVGQDVEAEDSDTGDL DPVLTVFRRGVEREFFSNWYKT AWSFSKLAQKGLLSS*PSSLSSS SSSSDKAVTAGTELFASSLSSSS DPRRSISSSSLLFVAPLPVVSSTL AGPYLPTAFFTPGRLAFSFS
11034	41402	B	11096	677	696	
11035	41403	A	11097	1	357	STMIEAHVDVRTTDGYFFLLFC VGFTKKHNNLIPKTSYA*HQQY ICLPHQDDRVTHQNPSLPDGSIA RVLSIYYLYISRREMNSIISQGL QKVHIHIVIPGSLMNQELLDDLI TVFFKA
11036	41404	B	11098	1	541	
11037	41405	A	11099	14	671	PAPWRLGKNKRLTKGGKKGA\ KKKGVNPFSKKEWY\D\VKAPA MFNIRNIGKTLVT\RTQGTKIAS DGLK/GVRVFEVSLADLQNDEV AFRK\FKLIT\EDVQGKNCLTN\F HGMDLY/TRDKMCSMVKK\WQ TMIEAHVDVKTTDGYLLRLFC VGFTKKRNNQIRKTSYA\QHQQ \VRQIREGRWM\EIMDPRRWQD QMDLEEVGHELIAGSIWKRHR KGLPIYLSSP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11038	41406	A	11100	1	217	RQGLTLSFRLECPGVISAHCSLN LPGSSKPPASAPQVAGTTGVYH HAS*FFIFFVEMGFHHVAQPGL CNFVF
11039	41407	A	11101	2	442	LDVQIQEAQRTPGKFIAKRYSP RHFVIRLSKLKTKERILRAVRQ KHQVTYKGKPIRLAADFSTETL QARRDRGPIFSLLKQNNYQPRI LYPEKLSIIYEGKIQSFSDKQML REFAIRKPPLQELLKGSLNLETN PGNT*KQNFFKA
11040	41408	A	11102	2	545	EPRPGEKTAHVYGPDCLCGSCV QLSFSGAFFSTRWVSYEQANCK GEQFVFEKGEYAHWDWWTSS QRT/DLSSLRPIKVDSQEHKIILY ENPNFTGKKMEIIDDD\VPSFHA \HGYQEKVSSVWLRSGTWVGY *YPGYRGLQYLLEKGDYKDSS DFGARHPQVQSVRCIHDMQGH QCGAFHPSK
11041	41409	A	11103	2	389	EIIDDDVPSFHAHGYQEKVSSV WVRSGM*VHCQPWLTLPQELR LWGPRSGETLALTSAPVSKTCD FGARHPQVQSVRCIHDMQGHQ CGAFHPLGTQEEEEAGQKEQM EQVPFWLARGDICELSGKKSV
11042	41410	A	11104	1	446	MEEEELEFVEELEAVLQLTPEV QLAIEQVFPSQDPLDRADFNAV EYINTLFPTEQLPMPSAHGGVSS CGNAGGPVSFATRENARCGIW GSGGVCDGVFGA/GAAGWGGV *GGGALGWMLSGRRIVLRSAIF TSPVSRAGSPERGWSCDC
11043	41411	A	11105	1	210	SSDGRHLAFDQGSPG*VLGHVG KQRAVDVQPSVAVRVRQPLLL LSTIMGSGLLGWEQGIDILNSIEI CSI
11044	41412	A	11106	2	287	AAESPGRSTRTDGAGLTRSLPR GSRCAGAWVAAGGLSWARGG GRQEAGWRNDG*GGTGARGG AGSRAAAHARGAAGHRASVSK PGPSRSSRFQCC
11045	41413	A	11107	150	389	GEEIAWLGAARPGKPTPSRIPL* PSLFPWRPHKFPERSVFAGSQP ASQSPPLRPPPPSHPEGSCLGSR LPPPGYLLPLR
11046	41414	C	11108	43	213	
11047	41415	A	11109	3	246	SSFPAPAREGALAPCRCLAGISV TLQGNP*GRCHHHHHHHHHH HRCYDSQESGKLPRPGPKAELE GPPAWLLVGPGAHP

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11048	41416	A	11113	1	726	
11049	41417	A	11114	2	251	LSCGRSLHQGSVTSCKTINALT LTVDTWRGCAW*GCACTFHCR SATNMIRAYVYFSTISVLSLQEI RLSLRAILADLRLSICF
11050	41418	A	11115	1	1041	
11051	41419	A	11116	1	398	MGPNSTLENLLKGATSVFYNR DQEEAQKKERKLRGRTKALAA ALQ/SWQSPGAPRCIH*LLSVW QARVF*RGMPRQQDEATSTLSI QWQKPVETELSPDMEVTGFRA SLTDERVHLPEVLPQEYTEQRR QGHL
11052	41420	A	11117	5	137	
11053	41421	A	11118	5	272	
11054	41422	A	11119	2	211	WNQPRCPSTVNWIMKIWYIYT MEHYAAIKRNMIMSFAATWME LEAIFLSKMPQ*QKNKYCVFLH ACLES
11055	41423	B	11120	1	1560	
11056	41424	A	11121	1	588	
11057	41425	A	11122	80	574	EPAAQGNVLVDLLC*MKNRNR WLPNELSQVLHVTQSQFSKTG MSAKHTAFAMRMSPAQMTDIV VGLSTGQSPFMVLMQQGGHSA MQETRIASLPVTAIPAGMKIPCV TAGSACMVGPSVRVNEWFSAY GMAGMAYSRVSTFVRGLSPRY LTTREAPGCGSSAGH
11058	41426	A	11123	48	131	
11059	41427	A	11124	1	1195	
11060	41428	A	11125	2	1028	
11061	41429	A	11126	1	1008	NMMEQVLDIPSL*VISKDNANV TIDAVCFIQVIDAPRAAYEVSNL ELAIINLTMTNIRTVLGSMELDE MLSQRDSINSRLLRIVDEATNPL ALKIAARMIEDGELDKRIAQRY SGWNSELGQQILKGQMSLADL AKYAQEHHLSPVHHQVAEWM RARNGQLFRLRSNHLTLLVEQN NFYARGAKIYPDIHIDRSLKKCP SDLFAANARCGICQQSDERCLR YQPRRERGLYRIDITYPGKSYTT TALPSRFVWFVTGKAQSTQAS ALSYIDSLLYHHLDLYGQRLGH LDDGTDSWNHVPTLNGQCTLV LIHEYVDTRGPEIKTILVISWWN ILVFH

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11062	41430	A	11127	3	333	DIGIGEENRKRWLRTGKCSFLP KEREWMDRLMSWGLVDTFRH ANPQTADRFSWFDYRSKGFDD NRGLRIDLLLASQPLAECCV*T GIDYEIRSMEKPSDHAPVWATF RR
11063	41431	A	11128	2	136	YCKLACLQVDSRGSQVFALDV AARHR*QFAMPESDAVAMLKH LS
11064	41432	A	11129	3	431	GVFGRVSEKQRPAAPAAGERPL PRPRPLPCGAAARTGPFAAQAA *RAAAAPRSERRRHHGAEEGH QRCIYRHAADRALGEAARRTG YALRPAGEPELAAAARRR*RAP DPGPRVPRHLGLLATRACPPGG AHCSPERGAISW
11065	41433	A	11130	64	2436	RRQGLEGWWAIGLEGLTGKAL AWLFTVPGVRGLQWSPRFFLTR LRTLLCKVLGVLFSVAGGKKG PTCILQILKGQRRQEA*CISGWA ERVWASGQA*WEVWLHWAKS RNWFLFWKQHVHALRVRLDTT LFSLEEGSSFWNQGLTWKVVR RTFSESINHTPRITLGVPYSVHSF QLPGLLNFGEFKVCFVLSPRIFN LTHENFLSSEGPEIGGLLGATFN CLNKRLAKYRMRNVHPKPKLV RYLHSRLPPEPAAAP*AWCGPR HLSCRQMSSSSQIGNDSFQLQV TPVHLLPLSHTTRKNPEMYDLP LLFFNPQESAILQLFHQDGECLH CSPIVGDWCHLGHSQACPSFSV PSGLFVPSLLCGAAFGRLVANV LKRYSVCVRVCAHVHVCARVR VYACVWVRMTISLTVILIESTN EITYGLPIMVTLMVSTLPPGPCQ AQGHVRPTGPIFRSLLEWETEV EMDK*GHDFAHVLVSECISSEA *GMLLFCGGPDRSLFSTFRAVW SLSRLLDSVIAAGKQ*A*RT*SV GYSLLCPDLKGDPSAVSILRTT VHHAFPVVTENRGNEKEFMKG NQLISNNIKFKVKKTA*EERQV RDKRSRLTRLSALELRNMCDE HIASEEPAEKEDLLQQMLERR* EPGGAPTARRATQRWGEPLAQ MFPLTFHGLILRSQLVTLLVRG VCYSESQSVSLSEAEISQARPDE
11066	41434	A	11133	3	80	

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11067	41435	A	11134	2	958	LKCELS\DQGLAPAIQTVRLTHE SLTALEIPNALLQTIQDLILDLR VRCVMATLQHTAEEIKRLAEK EDWIVDNEGLTSLPCQFEQCIV CSLQSLKGVLECKPGEASVFQQ PKTQEEVCQLSINITQVFIYCLE QLSTKPDADIDTTHLSGDVSSP DLFGSIHEDFSLTSEQRLLIVLS NCCYLERHTFLNIAEHFEKHNF QGIE*ITQVSMASLKELDQRLFE NYIELKADPIVGSLEP*IYAGYF DCKDCLPPTGVRNYLKEALVNI IAVHAEVFTISKELVPRVLSKGI EAVSERAQSTDAVCFILQQKWS
11068	41436	A	11135	52	1053	MDEEERVYRACYILCISLLSSPG NPGLHSPMLDLDNDTRPSVLG HLSLFLIQKYNHSILFFSPLAWR YKTPHRVAFVEKLTKLVLSQLP YF*IISNMFYFVFLIFKTAEKSNP INHI*TRLCLFLVF*KMIQEVMH SLVKLTRGALLPLSIRDGEAKQ YGGWEVALRSHSAHFCLDVFV RRLTHESLTALEIPNDLLQTIQD LIFRPGSQL*PVSRIFIFSAGTFRF KNHLHDFTGFHTCLTGAPRGPV GGCASDDGQAAADTSQWLS*I* VLYL*LFLLASMFSLSVDVFSL AP*R*FSKHLFCF*EQRLLIVLSN CCYLERHTFLNISHGSP
11069	41437	A	11136	50	426	
11070	41438	A	11137	2	949	QQVWKQNCFKHYSNETDNSTT QLVGVQTLQVVVPSLILCEHCM NFSSPHVWCCMVQAVPGGQGQ TIMQVPVSGTQGLQQVSNI*KY *AVYQRRGFKE*IITTGQTQQIII QQPQTAVTAGQTQVIPLALSHR SKTDLEESDN*VRYQPVNADGT ILQQGKCTHKLP*DFLGQLFCPL DN*HTTSSGQGTVTVTLPVAGN VVNSGGMVMVRKCIFQLCL*N FLEHAT*CLLKEEPLYVNAKQY HRILKRRQARAKLEAEGKIPKE RRVCITLGRI*ERRIAGFYF*NY LFSPKEKDSPHMQVGRHIHFILL FITLY
11071	41439	B	11138	26	80	

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11072	41440	A	11139	203	797	HRHIARHLFPRTTPTP*LSWQGS *TPRWKGVRAVVTQPRKERRA ESEQFQATKPRSQL*LQPPTPSL VSSCQLKTTAASRPLT*PSKSVY PSAPFHPWLPC/SKPERSVSPES NDSISEELNHFKPIVCSPCTPPK RLPDGRVLSPLIIKSTP/PQPKQK PAEADFL*GQSTDPQKVGTDLS GAADQKDPFKSHSYLSGS
11073	41441	A	11140	33	379	EATSNFKQPPSLPFWCLKSRTSL KPRQSKVCSSSFPVI*GKTGNEL ALQIP*FKSSCGPRFPD***PAGR /SAPSLGPPPSQSCAHQ*EHWVQ VCIKHGITNAEPPAEHLKVLVR E
11074	41442	A	11141	248	622	SESSGRFWLCGLGPGTSPLLSL KFPHLLPASRGRSPPSPRPRVPR GKATQVVWAWGYRCVDEDPA RCLGTPGRTD/PHCGQGLLCPL GKSCSTSQPLSQGDGRGTSWDR SHACSPGGHPHRCIGCM
11075	41443	C	11142	1	1311	
11076	41444	A	11143	452	1286	
11077	41445	A	11144	2	299	GLPLAHGLLGRFGMDRIYEGQ VEMTGD*CDVESIDGQPGAFTC YLDVGLARTITGNKVFGALKG AVDKGCSVPHSTR*FPACDSAE FALGIPYFVQPNI
11078	41446	B	11145	49	832	
11079	41447	A	11146	1	1074	
11080	41448	A	11147	1	360	
11081	41449	A	11148	1	1155	
11082	41450	A	11149	75	266	
11083	41451	A	11150	2	222	
11084	41452	A	11151	1	549	
11085	41453	C	11152	453	665	
11086	41454	A	11153	1	1962	
11087	41455	A	11154	1	295	ASTAGVSYYVAQAGLKLLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFM YFAGTWMKLETIILSKLSQGQK TKHRMFSLVGGN
11088	41456	A	11155	1	363	
11089	41457	B	11156	1	375	
11090	41458	A	11157	1	197	
11091	41459	C	11158	1	270	
11092	41460	C	11159	1	146	
11093	41461	C	11160	1	268	
11094	41462	C	11161	1	301	
11095	41463	A	11162	1	289	
11096	41464	B	11163	19	240	

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11097	41465	A	11164	2	253	
11098	41466	B	11165	1	978	
11099	41467	B	11166	1	316	
11100	41468	A	11167	191	319	
11101	41469	A	11168	608	763	
11102	41470	A	11169	274	437	
11103	41471	A	11170	1	417	
11104	41472	C	11171	1	792	
11105	41473	A	11172	3	449	IYLTKELKDLYKEKCKTLLKEIT DDTNKWKHIPSSWMGRINIVK MTTLPKAIYKFNAIPFRIPPSFFT ALEDTILKFIWNQKR/CPHSQCK IKQKEQIWRHHTT*FQAIL*GHS HQNS/IGTWMKLENIILSKLLQG QKTKHCMFSLIGGN
11106	41474	A	11173	1	441	
11107	41475	B	11174	1	597	
11108	41476	A	11175	5	265	
11109	41477	A	11176	3	280	SIYPNTCTRMFIVALLTIAKTWN QAICPTMIDWIKKMWHIYSME YYAAIKNDEFMSFVGTWMKLE TIIFSKLSQGQK\TKHRMFSLIGG ELEQ
11110	41478	A	11177	590	747	KAYQPEKAQDQVDSQPNSTRG TWMKLETIILSKLTQEQK\TKHC IFSLISGS
11111	41479	A	11178	3	274	FYYKDTCTHMFIVALFTIAKTW NQPKCPSVIDW/IMKNMWHIYT MEYYAAIKNDEFMSFSGTWMK LETIILSKLTQE\QKTKHCMFSLI SGS
11112	41480	A	11179	1940	2061	
11113	41481	A	11180	493	743	KATRSVNC/WWDHL*RPFWGS PH
11114	41482	B	11181	1	1248	
11115	41483	B	11182	50	8445	
11116	41484	A	11183	40	125	
11117	41485	B	11184	1	1896	
11118	41486	A	11185	1	624	
11119	41487	A	11186	1	357	
11120	41488	A	11187	1	304	
11121	41489	A	11188	681	834	
11122	41490	A	11189	3	2128	
11123	41491	A	11190	175	402	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11124	41492	A	11191	46	790	NPGAVKMPAYHSSIMDPDTKLI GNM/AHLLPIRSQFKGPAPRET\ KDT\DIVDEAIFLPSGPNVFF\KN YEIKNE\ADRTLIYITLYISECLK KLQK\CQFPKAQGGGKEMFYA GESTNFSHFLGEPGF\PTLTAILC PNPANK\QEDE\VMRALFTNQP KGKRLGLRLCEKSFSDP\QNG*T PAKWVDLAFVKRQF\MNKSLS GPWTVEGSPGQPTVSRGPGAAF FQQDVTQSFCLYLVKFYRDERR ACLYLKNS
11125	41493	A	11192	1	828	
11126	41494	A	11193	1	525	
11127	41495	A	11194	43	1826	THVRLAGARASPRAPRLRPRKP RPQGLPCLPGLRRARLEGGARG RADEMFLLPLPAAGRVVVRRL AVVRSGSRSLSTADMTKGLVL GIYSKEKEDDVP\QFTSAGENFD KSLAGKLRETLNISGPPLKAGK TRTFYGLHQDFPSVVLVGLGK KAAGIDEQENWHEGKENIRAA VAAGCRQIQDLELSSVEVDPCG DAQAAAEGAVLGLYEYDDLK QKKKMAVSAKLYGSGDQEAW QKGVLFASGQNLARQLMETPA NEMTPTRFAEIIEKNLKSASSKT EVHIRPKSWIEEQAMGSFLSVA KGSDEPPVFLEIHYKGSPNANE PPLVFVGKGITFDSGGISIKASA NMDLMRADMGGAATICSAIVS AAKLNLPINIIGLAPLCENMPSG KANKPGDVVRAKNGKTIQVDN TDA\EGRLILADALCYAHTFNP KVILNAATLTGAMDVALGSGA TGVFTNSSWLWNKLFEASIETG DRVWRMPLFEHYTRQVVDCQL AD\VNNIGKYRSAGACTAAAFL KEFVTHPKWAHLDIAGVMTNK DEVPQSTGKA*LGRPTRTLI\EF L\LRFSQDNCLVQILKNVFHSVL NWTVELKKVFE
11128	41496	A	11195	1	273	

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11129	41497	A	11196	2996	8256	LPTRRSWAVFFKGGESGAHTLR RKARKKRKKQVKGGSPKKGEE AKKVEAPRLPKLAAPGGGAGA KGGAGGTSDMRLWSWVLHLG LLSAALGCGLAERPRRARRDPR AGRPPRPAAGPATCATRGPRPP RLAAAAAAGRAWEAVRVPR RRQQREARGATEEPSPPSRALY FSGRGEQLRVLRADLELPRDAF TLQVWLRAEGGQRSPAVITGL YDKCSYISRDRGWVVGIHTISD QDNKDPRYFFSLKTDRARQV
11130	41498	A	11197	75	266	
11131	41499	B	11198	1	363	
11132	41500	A	11199	1	649	PRIRHEVIEEVIRMMLEIINSCLT NSLHHNPNLVYALLYKRDLFE Q\FRTHPSFQDIMQNIDLVISFFS SRLLQAGAELSVERVLEI\SQG\ ALRCPKDRLKEISQKLKFKYVE EEQPRGVF*SPYVWSLVLQLQQ SALYWEFHRTFQLFHPWDSRLR GRDASSPPGTPSSQGRPFQSSFIS GVTEVGQTGYLVYLLLKEDCT SVFSSHTLIWRIGC
11133	41501	A	11200	108	210	
11134	41502	A	11201	53	259	
11135	41503	A	11202	1	2679	
11136	41504	A	11203	1	675	
11137	41505	A	11204	834	1077	KGLWTVPPSFGDTVSGPPVPTG GSAGHTVPPPPR*CRRQPPPSPP WRRLFLPQLRSRSSQPPAGPAR HLPPPAARPECFCA
11138	41506	A	11205	1	681	
11139	41507	A	11206	1777	1940	VPILPQPLLLHPIILLS*VPILPQP/ PAPPPYNPFITSPPHTWSGLQFH SVTSPPPPAQQFTLKRVAEAKGI VK
11140	41508	A	11207	3	547	
11141	41509	A	11208	1	578	
11142	41510	A	11209	194	379	
11143	41511	A	11210	1	927	
11144	41512	B	11211	1	916	
11145	41513	A	11212	1	441	RRKLQKQALGPEQNLETLLNL ATSVFYNRDQEEQVQKEKRDQ RKAAALVMALRQTNLGGSERT EHEAGQSPGKACYQCGLLGHF KKDCPMRNKLPPR/RVSTMLRQ SLEGALPQRMKVPWVRSPQPD DPTTGLRVPGASASSCHHPH
11146	41514	A	11213	164	359	
11147	41515	C	11214	157	189	

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11148	41516	A	11215	13	399	VEAFPTGSEKATAVISSLLSDIIP QSRLPTSIPSDNRRAFISQISQAV FQALSIP*NLYIPYGPPSSRKH/T LTKLSHQLKKDWTILLPLSLLRI QACPRNATGYSPFKVLYRHSFL LRPSLIPDTRPT
11149	41517	A	11216	2	152	WYGEIMGDVSQGCFER*WAMF LRAASSGIRGGVGT*SGRH*AE GRFYGDFRGNRAASVFSR
11150	41518	A	11217	1	1143	
11151	41519	A	11218	28	453	
11152	41520	A	11219	275	1128	DISTPSLATDHMPITIPLNLIT/TY PTQRQYPIPPHALKGLKPVITDL LQHRLLKPINSPYNSPILPVQKP DKSYRLVQDLRLTNQIVLPIHP VVPNLYTLLSSIPSSTTHYSVLH LKDAFFTIPLHPSSQPLFAVTWT DPDTQQSQQLTWAVLPQGFRD SPHYFSQALSHDLLSFHPSASHL IQYIDDLLLCSPSFESSQQDTLL LLQHLFSKGYQSDDRPAFTSQI TQAVSQALGIQWNLHIPYHPQS SGKVEWTNGLLKLLLLLLTANI DDTSYLQIPHKGLQ
11153	41521	A	11220	1	606	
11154	41522	A	11221	713	835	LSQWRSDNGPAFISQITQAVSQ APGIQ*NLYIPYHPQSSGK
11155	41523	A	11222	1	1133	AEALPVQFYFHLSDIRGMLLHE PDLQKGIKAVSQEDPQWSYQA DSPGIARRDYMVSRLVEGLKK AAYKAVNYDKLKKTTQVTIVP GPDFNLASHIIPDTTPDPHDCYL SDTPGIHSISHISFFAIPHPDHTW FIDGSSTTPNRHTPAKAGYAIVP STSIIEAAALPPSATSRQAKLIAL TRTLTLAKELCVNIYTDSKYAF HILHHHAVIWAERGFLTKQGW SNINASLIKTLLKATLLPKEAGV IHCKGHQKASDPIAQGNTYAD KIAKEAASGPTSVPHGQFFSFSL VTPTYSPTKTSTYPSLLTQGKW FLDQGKYLLPASKAHSILPSFH NLFHVGYKPLAHLLEYLISFLS WKSILKEITSQ*SICYSTTPQG
11156	41524	B	11223	1	1156	
11157	41525	A	11224	1	4991	
11158	41526	A	11225	3	590	
11159	41527	A	11226	203	1772	
11160	41528	A	11227	1	1669	
11161	41529	A	11228	1473	1604	
11162	41530	A	11229	82	159	

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11163	41531	A	11230	1	1323	
11164	41532	A	11231	377	631	LLKGKLTNRKDIHTKTPSVRHH HRRPKPGRDTTKKIILNQYPW* TSMQKSSIKYWQTESSSTSKSLS TMIKLASSLGCKNWKKL
11165	41533	C	11232	1	1677	
11166	41534	A	11233	753	966	FVFLWSLMMVTYRWGFGVDV LSVC*FSFQQS\EPQLQVCWSLL EVHS*PCLPGYQQRRNSCWPRG SCDVVIT
11167	41535	A	11234	1253	1459	LSDSPKLK*RKKC*GQPERKVG LPTKGSPSD*QQISWQKLCKPE ESGGQYSTFLKKRIFNPEFHIQQ
11168	41536	B	11235	1	924	
11169	41537	A	11236	299	436	
11170	41538	A	11237	259	536	FQKEWYQLLLVPLV/EIWL*IHL VLDFF*LVNY*LLPQFQSMLLV SSEIQLLPGLVLGECMCQGIYPF LLDFLWSLMMVTYRWGFGVD VLCVC
11171	41539	B	11238	79	1587	
11172	41540	A	11239	1608	1763	
11173	41541	A	11240	1	2001	
11174	41542	B	11241	1	741	
11175	41543	B	11242	1	1368	
11176	41544	C	11243	1	3924	
11177	41545	A	11244	470	619	KVTRGWGSPHQDAG*SPCQSH QDQTP*GILKEHQEKARRK*RQ LCVLQL
11178	41546	B	11245	1	3546	
11179	41547	A	11246	363	476	
11180	41548	A	11247	1	759	
11181	41549	C	11248	376	986	
11182	41550	A	11249	556	821	MSIRSTWRRAEFNSWVSFLTFR LVDLSLVFDDGDVQVGFWCGC PSCLLVFLL/ISQDPQLQVCWSL QEVHSRPCSPGYQQQRLQYSEY
11183	41551	A	11250	119	340	
11184	41552	B	11251	1	942	
11185	41553	A	11252	436	732	LHIWPFLLPCKAQNQVHCSKFC PLGRFPFMAVLQGCPRKGL*CC SCPLLGGIWISCRIICAFRTYLRP IMYIPLPFADGMLLCTAHSMAR CFGYCSLVV
11186	41554	C	11253	1	1878	
11187	41555	A	11254	720	1535	ILPEVQGGAGTI*LSLFLIE*PLF LSPA*LPWPELPTLC*IGVVRDG TPVLCQFSKGMLPVFAHSV

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11188	41556	A	11255	2	1059	WLLAASPLWLCRIRP/LILAAFM GWQSRSALGTQSQESGKGSPD QVLVPQDCGPWLGSVELVSVP GSQAGEEPILSENKGRVTQMKI PEERSGSNICCSAIFAVLQPPLLI PRQTRSGVDLQQNPTDLQLRVL TVRRKTNKEKGHPHQNPTCTSP ASKTKGALRFIKQVLRDLERAL DSHTIMGDFNTPLSTLDRSTRQ KVNKDIQELNSALHQVDLIDIY RTLHPKSTEYTVFSAPHHTYSKI DHTVGSKALLSKCKRIEILTNCL SDHSAIKLELRIKKLTQNHSTTL KLNNLLLNDYWVHKETKAEIK MVFEIDENKDTIYQNLWDTFK AVCRGKFIALKAHKRKQERVT
11189	41557	A	11256	82	159	
11190	41558	A	11257	820	1358	HTDGFLVWMPFLFVSFPSNSQD RQLQVCWRLLEVHSRPCFPGY QQRWLQNNRY/SVNRKCCCLIV PLEVLSQRSTHQHVGEWLCLL GRKFPAGMEACTAMLCSSSVL EAATLSFSVQHRACTGGS*KPQ QGRVYPSEGREHNGAAAFGPF CSSECPASCPDPGTQPCAPGTYI PFFSCQT
11191	41559	A	11258	2435	3261	QVRGYRCRFVTWVNCMSLRFG VQRIPSPSLTGTQPPVGAD*HLT RPGTPLR*NFQRNDQAVTFAVH \HIH\FVQPLLLIPMQTGSGVDLR QTPTDLQLRVLTVRRKTNKQK GHPHRNPICMSPSSKTKARQAN IQIQEIQRTPQRYSSRRATPRHII VRFTKVEMKEKKLRAAREKGR VTHKGKPIRLTVDLLAETLQAR REWGPIFNILKEKNFQPRISYPA KLNFISEEEIKSFTDKQMLRDFV TTRPALQELLKEALNMERNNQ YQPLQNHAKL

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11192	41560	A	11260	1439	2544	VSSTTKEKALSVPPRWCILQKK NPPNHQPVSLPEVFLPQILKFSG PPHWRRIEDEYKVMRLNIGDM KTKKKMLEKYEQLEIRHQQKS RT*KAVCCIT*LSRHIILLGQAPL VQQSM*QPESHHQVNPPETSYG IHQTPKLS*IGIK*RPWIM/MSEV KGYKVGNFFFAKAPNRAPPLL KPRQTGSGVDLQQTPADLQLR VLTVRRNTNKQKGHPHQNPICT SPSSKTKEVENLEKRLDKWLTR LTNVEKSLNDLMELKTMAREL HDEGTSFSSQFDQLEERVPVME DQMNEMKQEEKFREKRMKRN EQSLQEIRDYVKRPNLRLIGVPE SDGENGTKLENTLQDIIQENFPS LARQANIQIQEIQRMPQR
11193	41561	A	11261	2772	3111	QSGPSAAGLLEFAGGPLQTLFA WVSAAEVGKCKGSGSSLS*PK KGVMDGTWKIGSLPPEYCAFPT G*KNGAP/LRLYPTPGSEGPTPT ESP*/FASTAVGDQTARQQRGW GRGARH
11194	41562	A	11262	248	597	DRCPAAWDRHPAGIQSSRREPS KATWTLRSKLSVQDGRRDSSL RLNCKVAARLGAGHPPMLRLG LRC*YPGKQGLEWTSSKLQQTC H*GS*LLKGKLTNRKDIHSKTPS VRHYHQR
11195	41563	B	11263	1	2250	
11196	41564	A	11264	1298	1681	GVSVPLLWGASQLGYLGVMDP LAEAVCPFSDLQLHSGRTSTVF KAALGQSGAHCPERCVSAQS* AD*RALREHKQ*FGSTLCGPVM VVAMELGSSTMVELVSSPANS VKVFLFLHIFSSTCCFLTFS
11197	41565	A	11265	1272	1497	SGLLPIKVAFTKPQFLFILLRIWL *RGYVFCSWKVTTPREQPQCIT DGYQIFIFMQKTLSCLSILGKRT MSLMQ
11198	41566	A	11266	1	1071	
11199	41567	A	11267	788	1286	
11200	41568	A	11268	3	455	
11201	41569	A	11269	1	711	
11202	41570	A	11270	225	525	GGGENFSYPWYLLVGCGWFSS SPIVPDVPPFSLLLPAQKKKPAP PK\PEPKPKKAPAKKGEKVPKG KKGKADAGKEGNNPAENGDA KTAQAQKAEGAGDAK

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11203	41571	A	11271	914	1261	TAKPKTNWCCRAPTSRLASTFA TMPFKKAECVGDAHPATVKDE PQRISARLS\AKPAPPKPEPKPK KAPAKKGEKVPKGKKGKAD\A GKEG\NNPAEN\GDAKTDQAQK A\EGA\GDAK
11204	41572	A	11272	3	359	
11205	41573	A	11273	440	642	WKAEREEIEPR/PKKAPAKKGE KVPKGKKGKAEAGQDGDNPTE NGDAKTDQGQKAEGAGDAKR TVSHQN
11206	41574	A	11274	499	723	
11207	41575	A	11275	147	459	STYVPLPSPPSSMPKRKAEGHA MGDKAKVKDEPQRRFARLS\A KPAPPKPEPKPKKAPAKKGEKV PKGKKGKAD\AGKEGE*PLQKN GDAKTDQAQKA\EGA\GDAK
11208	41576	B	11276	179	400	
11209	41577	A	11277	24	601	
11210	41578	A	11278	266	441	
11211	41579	A	11279	17	570	HQPKKDLTGFVKWPRYIRLQR QRAILYKRLKVHLAINQFTQAL ARQTATQLLKLAHKYRPETKQ EKKQRLLARAEKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIAHDVGPIELVVFLPA LCRKMGVPYCQ\IKGKARLG\R LVHRK\TCTTCRFTQ\VNS\EDK GALAK\LVEAIRTNYNDRYDEI R\RHWGGNVLGPKSVARIAKL\ EKAKAKELAH*TGGSYQDQLQ
11212	41580	A	11280	175	289	RPCVKESGKPHLKSSTMWTTL KLLRI*PRRTTCSPRLS
11213	41581	A	11281	205	361	
11214	41582	A	11282	144	396	CLEVLHKILFFEMESHSVTQAG VQWRDLGSLQPLPPG\SSNSPTS ASQVAGIRSMRQKGRANFFVFL VEMGFHHVGQADLELLTL
11215	41583	A	11283	241	550	
11216	41584	A	11284	2	106	
11217	41585	A	11285	2	447	PPLSRLLCPRHPHSGWPEGYSPE HLRCGLRSGTLRSRQALHCQVS SNP*PPSLWF*GCGNVL*ELCLF VLPVSVNLYQVLLSEIWEFHRT

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11218	41586	A	11286	1	2172	PAGRCRTAWAVAAQQLMLSA ALRTLKHVLYYSRQCLMVSRN LGSVGYDPNEKTFDKILVANRG EIACRVIRTCKKMGIKTVAIHSD VDASSVHVKMADEAVCVGPAP TSKSYLNMDAIMEAIKKTRAQ AVHPGYGFLSENKEFARCLAAE DVVFIGPDTHAIQAMGDKIESK LLAKKAEVNTIPGFDGVVKDA EEAVRIAREIGYPVMIKASAGG GGKGMRIAWDDEETRDGFRLS SQEAASSFGDDRLLIEKFIDNPR HIEIQVLGDKHGNALWLNEREC SIQRRNQKVVEEAPSIFLDAETR RAMGEQAVALARAVKYSSAGT VEFLVDSKKNFYFLEMNTRLQ VEHPVTECITGLDLVQEMIRVA KGYPLRHKQADIRINGWAVEC RVYAEDPYKSFGLPSIGRLSQY QEPLHLPGVRVDSGIQPGSDISI YYDPMISKLITYGSDRTEALKR MADALDNYVIRGVTHNIALLR EVIIN\SRFGKRNLNT*FL\SKGF PEAFKGHLLTKS\EKTQFLAIAS\ SLFV\AFQLRAQHFQENSRMPVI KPDIANWELSVKLHDKVHTVV ASNNGSVFSVEVDGSKLNVTST W\NL\ASPLLSVSVDEHSEGLFQ CLSREAGGNMSIQFLGTVYKV NILTRLAAELNKFMLEKVTEDT SSVLRSPMPGVVVAVSVKPGD AVAEGQEICVIEAMKMQNSMT
11219	41587	A	11287	62	2600	
11220	41588	C	11288	277	508	
11221	41589	B	11289	94	1440	
11222	41590	A	11290	57	237	FLHAENKAHRPGISLCGLRAQP RQPASRHAW*SMRSEQRPWLT ASGRSSGQTRSSRSLG

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11223	41591	A	11291	3	1968	EFDYSEDKSSWDNQQENPPPTK KIGKKPVAKMPLRRPKMKKTP EKLDNTPASPPRSPAEPNDIPIA KGTYTFDIDKWDDPNFNPFSST SKMQESPKLPQQSYNFDPDTCD ESVDPFKTSSKTPSSPSKSPASFE IPASAMEANGVDGDGLNKPAK KKKTPLKTDTFRVKKSPKRSPL SDPPSQDPTPAATPETPPVISAV VHATDEEKLAVTNQKWTCMT VDLEADKQDYPQPSDLSTFVNE TKFSSPTEELDYRNSYEIEYME KIGSSLPQDDDAPKKQALYLMF DTSQESPVKSSPVRMSESPTPCS GS\SFEETEALVNTAAKNQHPV PRGLAPNQESHLQVPEKSSQKE LEAMGLGTPSEAIEITAPEGSFA SADALLSRLAHPVSLCG\ALDY LEPDLAEKNPPLFAQKLQREA\ VHPTDVSI\SKTALYSRIRTTEVE KPAGLLFQQPDL\DSALQIARAE II\TKEREVSEWKDKYEESR\RE VMEMRKIVAEYEKTIAQMIEDE QREKSVSHQTVQQLVLEKEQA LADLNSVEKSLADLFRRYEKM KEVLEGFRKNEEVLKRCAQEY LSRVKKEEQRYQALKVHAEEK LDRANAEIAQVRGKAQQEQAA HQASLRKEQLRVDALERTLEQ KNKEIEELTKICDELIAKMGKS
11224	41592	A	11292	63	2203	
11225	41593	A	11293	27	586	
11226	41594	A	11294	89	288	
11227	41595	A	11295	1	522	HERFETTYFKKFP\GYYVTGDG CQRDQDGYYWITGRIDDMLNV SGHLLSTAEVESALVEH*RLLQ EA\AVVGHPHPCEGVNASYCFV TLCDGHTFSPKLTEELKKA\VM RKRLAPFATPDYIQNAPGLPKT\ RSGKIMRRVLRKI\AQNDHDLG DMSTVADPS\VISHLFSHRCLTI
11228	41596	A	11296	2	569	
11229	41597	B	11297	1	990	
11230	41598	A	11298	1	252	
11231	41599	A	11299	39	174	RHIYSSNEVH*KEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEEEEIPLSSL

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11232	41600	A	11300	16	379	ILDTSPMRWTQKNFSMILAQPE QQCKTLSQNKNKDRRIKKKEE KKKKKKKKKKKKKKKKKKKK KKKKK*EKEKEKEKEKKKEKE EEKKK/QEEEEEEEEEEEEEEE EEEEEEEEEEERRRR
11233	41601	A	11301	1	249	
11234	41602	A	11302	1	353	
11235	41603	A	11303	1	847	
11236	41604	A	11304	3	224	QEKKRRKEKKK\KEEEEEEEE EEEEEEEEEEEKKKKKKKKKK KKKKKKKKKKKKKKKKKKKK KKKKKKKKKGRKTDLAVDPV
11237	41605	A	11305	1	417	
11238	41606	A	11306	1	1314	
11239	41607	B	11307	1	133	
11240	41608	A	11308	45	266	
11241	41609	A	11309	35	313	FLQMEDTYIVTKLLLLLRFAWL YLDLVFVLI*YRKKRRKKKRKK KEKEKEKEKKKKKKKKKKKKK KKKKKKKKKKKRKKEMALQS CSLWYLYA
11242	41610	C	11310	240	391	
11243	41611	A	11311	1	579	
11244	41612	A	11312	141	410	PEPILTMESKGMWQLFELTL/H NSKVNTLSKELHSEFSEVMNEI WASDQIRSAVLISSKPGCFIAGA DINMLAACKDPSRSNTAITRKH RE
11245	41613	A	11313	1	358	KWFTPMEFEIKGGYA*SKNWR LSVRCGGWPLRRLMEEGSLPNP SRIYYRNKLRILKSQNNSSVDPC MRNLDECEVCRDGWELFCCDT CSRVFHDDCHIPPVESEKMKES AGSQQCCQES
11246	41614	A	11314	1	921	
11247	41615	A	11315	108	2765	

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11248	41616	A	11316	98	2418	AKLMAQQGQQGQMASGDSNL NFRMVAEIQNVEGQNLQEQVC PEPIFRFFRENKVEIASAITRPFP FLMGLRDRSFISEQMYEHFQEA FRNLVPVTRVMYCVLSELEKTF GWSHLEALFSRINLMAYPDLNE IYRSFQNVCYEHSPLQMNNVN DLEDRPRLLPYGKQENSNACHE MDDIAVPQEALSSSARCEPGFS SESCEQLALPKAGGGDAEDAPS LLPVSCKLAIQIDEGESEEMPKL LPYDTEETFDLKTPQVTNEGEP EKGLCLLPGEGEEGSDDCSEMC DGEERQEASSSLARRGSVSSEL ENHPMNEEGESEELASSLLYDN VPGAEQSAYENEKCSCVMCFS EEVPGSPEARTESDQACGTMDT VDIANNSTLGKPKRKRRKKRG HGWSRMRMRRQKNSQQNDNS KADGQVVSSEKKANVNLKDLS KIRGRKRGKPGTRFTQSDRAAQ KRVRSRASRKHKDETVDFKAP LLPVTCGGVKGILHKKKLQQGI LVKCIQTEDGKWFTPTEFEIKG GHARSKNWRLSVRCGGWPLR WLMENGFLPDPPRIRYRKKKRI LKSQNNSSVDPCMRNLDECEV CRDGGELFCCDTCSRVFHEDCH IPPVEAERTPWNCIFCRMKESPG SQQCCQESEVLERQMCPEEQLK CEFLLLKVYCCSESSFFAKIPYY YYIREACQGLKEPMWLDKIKK
11249	41617	A	11317	1	1210	
11250	41618	A	11318	1	743	MRYKKEQPLFLPKYDLGADAA ILQPQEEDCGSTQVRGGHHRTK TEETGLLVTSLNQGIKPHDSVT KLLSPQRSSVLFLLLITSGVHTD SSKAVLESRRSLGYEASFLEYF QSFYKLFPVDRLYAWHCSDHR NTTVTAINTDRPGLLTLSLTVTI GQGSKKAPSGFSHISPAPTVKQ QPILCDDRDFSPSSFPSTNTPSQF ATNEVLTTGPPPGAG/CCQYSTI TRKTGPNCQAGGCPGGARPAK
11251	41619	A	11319	314	486	
11252	41620	A	11320	3	122	
11253	41621	A	11321	1	289	
11254	41622	A	11322	1	399	
11255	41623	A	11323	3	259	

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11256	41624	A	11324	1	369	MPATWEAEARESHKREFETHL/ VQHSETPSEKEEE\EEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEEGEEEEEEEEEEEEEEEEEEE GEEEEEEEEEEEEEEDEEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEEEEGEEEEEEEEEEEEEEEEE EEGEEEEEEEEEEEEEEEDEEEEE
11257	41625	B	11325	1	441	
11258	41626	A	11326	1	267	
11259	41627	B	11327	1	234	
11260	41628	A	11328	1	383	MVRPFLYKKIKEEEEEEEEEEE EEEEGEEEEEEEEEEEEEEEEEE EGEEEEEEEEEEEEEEEEEEDKD DEEER/EKKEEEEEEEEEEEEEE EEEEEEEEEEEEEEEKKHSL*DPD LGEKENKGQRKRKLARGTSQP SLSPGGSDPLGA
11261	41629	A	11329	305	625	VAPGDRHAFPLAPSGLSPELTLP QTQCCAQATVQGLEGTRSWSQ SGTSSLSPWSHTSLRRRRKEEG EEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEE/IEEGEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEEEEAKTQ
11262	41630	A	11330	294	501	AFDKQPRGRGRVVKEEVLKKK KKEEEKEEEGEEEEEEEEEEEE E/EEDEEEEEEEEEEEEEEEEEE EEEEEEEE
11263	41631	C	11331	618	966	
11264	41632	B	11332	1	332	
11265	41633	A	11333	1	705	
11266	41634	A	11334	1	417	
11267	41635	A	11335	1	639	
11268	41636	A	11336	2	2347	LMLVVIFNGTERIEDLRKPPSFD AILGGGLRVLFFQNEAHPPFAS WRNNEEARTDRPSQQLRSLNG KWRLMRYFLLTHLCETLVKVK DAEDQLGARVGYIELDLNSGKI LESFRPEERFPMMSTFKGLLCG AVLSRIDAGQEQLGRRIHYSQN DLGEYSPVTEKHLTDGMTVRE LCSAAITMSDNTAANLLLTTIG GPNELTAFLHNMGDHVTRLDR SEPELNEAIPNDERDTRCLGQW QQRSQTINWPTTTLAP
11269	41637	A	11337	56	243	YSCLMFPQDGE*LEKEEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEN

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11270	41638	A	11338	1	503	MKHQHFALLVPEKFLIAQSTAS RVDRRQIWRDVSSERGEISQCL KVGTSLNSTDVSAVEAVRATV LGSGTLTPTVLRSNAGPYTRIST VPACLLGQEEEEEEEEEEEEEE EEEEEEE\EEEEEEEK/EEEE/EEE EEEEEEEEEEEEEEEEEEEEEEE EEGEEEERRKS
11271	41639	A	11339	1	651	
11272	41640	A	11340	1	2184	MNIDANIPNKILENRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRTKDKNCMIISIDAEK AFDKIQQCFMLETLNKLGIGGT YLKIIRAIYDKPTANIILNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGVQLGKE EVKLSLFADDMIVYLENPIVSA QHLLKLISNFSKVSGYKINVQK SQAFLYTNNRQTENQIMSELPF TIASKRIKYRGIQLTRDLKDLFK ENDKPLLKEIKED/DKEMEEHS MLMGRKNQYRENSHAAQELE KNYFKVHMEPKKSPHYQVNPK PKEQSGRHHVT*LQTILQGYSN QNSMVLVPKQTYRSMEQNRSL RNNATYLQLSDL*QTQEKQAM GKGFPI**MVLGKLASHM*KPE TGSLPYTLYKNQFKVD*RLKR* T*NHKNQRRKPRHYHSGHRHG QGLHV*NTKINGNKNQN*QMG SN*TKELLHSKRNYRQSDQATY KMGENFHNLLIRQRANIQNVQ* TQTNLQEKNKQPHQKVGEGHE QTLLKRRHLCSQKTHEK\NSPSL AIREMQIKTTMRYHLTPVRMAI IKKSGNSRKHIQKKEEEEEEEA EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEE EEEKCSLKHTEAPCVKGIETIFW NKFSLCDITKSYLSGVQKLEER AHKVKLALKFKKEIKMALHGG
11273	41641	A	11341	1	870	
11274	41642	A	11342	2	259	GSTISCARCAELRGSASRFRPLP AAAMKWMFKEDHSLEHRCVE SAKIRAKYPDRVP\LTMGQLYE KEKDEDGFLCVAYSGENTFGF

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11275	41643	A	11343	1	461	GCRCRCRRRCCCARCAELRGS ASRFRPLPAAAMKWMFKEDR W\LEHRCVESAK\IRAKYPDRVP VIVEK/VSQGSQIVDIDKRKY\L VPSDITV\AQFMWIIRKRIQLPSE KA\IFLFVDKTVPQSSLTMGQLY EKEK\DEDGFLYVA\YSGRGTLF
11276	41644	A	11344	1	966	
11277	41645	A	11345	1	1037	RPPFPVPGVQKCPLPTRGGLHIG RWLRDRAGPPEAQDGTGGRSR SRRRPPALPNSRPSPVASGREM VVLSVPAEVT\VILLDI\EGTTT\P IAFVKG/DILFPYIERKMLK\EYL QTHW\EEEEFQ\QDVSLFEGNK A\EEDAHLDG\AVPIPGKHLGIG V\DD\LQQMI\QAVVDNVCWQM SLDRKTTALK\QLQGH\MWRAA FTAGRMK\AEFFADVVPA\VR\K WREAG\MKVYIYSSGSVEAQKL LFGHSTEGDILELV\DGHF\DTKI GHKRRRVKVTRK\IADSI\GCST\ NKHFVFWTDVTSRRASAGLRE AGCCTLAVV\VRPG\NAGINR*L RKTYYSLITSFQWNYYLPSST
11278	41646	A	11346	346	858	
11279	41647	A	11347	1	234	
11280	41648	A	11348	1	1696	
11281	41649	A	11349	1	234	
11282	41650	A	11350	1	1696	
11283	41651	A	11351	1	211	
11284	41652	A	11352	1	417	
11285	41653	A	11353	1	1458	
11286	41654	A	11354	219	329	
11287	41655	A	11355	132	451	
11288	41656	A	11356	1	996	
11289	41657	A	11357	1	867	MARLWGALSLWPLWAAVPWG GAAAVGVRACSSTAAPDGVEG PALRRSYWRHLRRLVLGPPEPP FSHVCQVGDPVLRGVAAPVER AQLGGPELQRLTQRLVQVMRR RRCVGLSAPQLGVPRQVLALEL PEALCRECPPRQRALRQMEPFP LRVFVNPSLRVLDSRLVTFPEG CESVAGFLACVPRFQAVQISGL DPNGEQVVWQASGWAARIIQH EMDHLQGCLFIDKMDSRTFTN VYWMKVND*SFATGAEDSGY QDANTFTLSWANLTWHQLGW LAYDRKLDCQGMAD
11290	41658	A	11358	3	226	
11291	41659	A	11359	1	756	

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11292	41660	A	11360	35	142	
11293	41661	C	11361	151	484	
11294	41662	A	11362	1	1245	
11295	41663	A	11363	2	1464	CQAKFIMNRLKK/NERQKVQDI KEVKQNIHLIRASFAGKGKQLE EKMQPLEPEAIMLSELMQEQKT KCRMFSLISGKHGVHMDSKTG ATDSGAYLRVEEIQTTIREYYK HLYANKLENLEEMDKFLDKYT LPRLNQEEVESLNRPITGAEILAI ISSLPTKKSPGPDGFTAEFYLRY KEELVPFLLKLSQSIEREGILPNS FYEASIILIPKPGRDTTKKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNL RKSINVIQHINRAKDKNHMIISI HEEKAFDKIQQPFMLKTLNKLG IDGTYLKIIRAIYDKPTANIILNG QKLEAFPLKTGTRQGCPLSPLL FNIVLEVLARAIRQEKEIKGIHL GKEEVTLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASRRIKYLGIQLTRDMKD LFKENYKPLLSEIVTVF
11296	41664	A	11364	41	559	
11297	41665	C	11365	63	370	
11298	41666	A	11366	3	211	
11299	41667	A	11367	47	358	PDMGLEDEQKMLTESGDPEEE EEEEEELVIGLRLSVHTGNLGRP GM*NFPLLLSIQN*MGDPHSAIS GGQCGSASWPSARIPLQQVREQ CRASWKKCVK\ARERLEL\CDE R*SSRSHTEEDCT\EELFDF\LH A\RDHC\VAHKLL*QLAFCTDPP TTSERAMPSQLEEMCKRPGSG
11300	41668	A	11368	1	2082	

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11301	41669	A	11369	1	2013	MKHLKRWWSAGGGLLHLTLL LSLAGLRVDLDLYLLLPPPTLL QDELLFLGGPASSAYALSPFSAS GGWGRAGHLHPKGRELDPAAP PEGQLLREVRALGVPFVPRTSV DAWLVHSVAAGSADEAHGLL GAAAASSTGGAGASVDGGSQA VQGGGGDPRAARSGPLDAGEE EKAPAEPTAQVPDAGGCASEE NGVLREKHEAVDHSSQHEENE ERVSAQKENSLQQNDDDENKI AEKPDWEAEKTTESRNEGISLG DIPLPGSISDGMNSSAHYHVNFS QAISQDVNLHEAILLCPNNTFR RDPTARTSQSQEPFLQLNSHTT NPEQTLPGTNLTGFLSPVDNHM RNLTSQDLLYDLDINIFDEINLM SLATEDNFD\PIDVSHLFDEPDS DSGLTLDSSHNNTSDIKSNSSHS VCDEGAIGYCTDHE\SSSHHDL EGAVGGYYPEPSKLCHLDQSDS DFHGDLTFQHVFHNHTYHLQP TAP\ESTS\EPFPW\PGGRSQEGL RE*DTLKDTDRNLSRDEQRAK ALHIPF\SVDEIVGMPVDSFNSM LSRYYLTDLQVSLIRDIRRRGK NKVAAQNCRKRKLDIILNLEDD VCNLQAKKETLKREQAQCNKA ININMKQKLHDLYHDIFSRLRDD QGRPVNPNHYALQCTHDGSILI VPKELVASGHKKETQKGKRK
11302	41670	A	11370	3	255	
11303	41671	A	11371	1	1611	
11304	41672	A	11372	109	207	MLCLQRFYMIFVDFQSRPQF*L KSCQHIISCHQ
11305	41673	A	11373	1	666	
11306	41674	A	11374	1	1254	

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11307	41675	A	11375	33	1458	KLPLKAKMGKEKTHINIVVIGH VDSGKSTTTGHLIYKCGGIDKR TIEKFEKEAAEMGKGSFKYAW VLDKLKAERERGITIDISLWKFE TSKYYVTIIDAPGHRDFIKNMIT GTSQADCAVLIVAAGVGEFEA GISKNGQTREHALLAYTLGVK QLIVGVNKMDSTEPPYSQKRYE EIVKEVSTYIKKIGYNPDTVAFV PISGWNGDNMLEPSANMPWFK GWKVTRKDGNASGTTLLEALD CILPPTRPTDKPLRLPLQDVYKI GGIGTVPVGRVETGVLKPGM\V VT\FAPDNVTTEV*SVEMHHEA LSEALPGDN/VGAFNVKNVSVK DVRRGNVAGDSKNDPPMEAA GFTAQVIILNHPGQISAGYAP\V LDCHT\AHIACKF\AELKKKI\DR RF\GKKLED\GPK\FWKSGDAAI VDMVP\GKP\MCVESFSDYPPL GPFAVHDMRQT\VAGGAHQKQ VDKK\AAGA\GKVTK\SAQKAQ
11308	41676	A	11376	1	880	
11309	41677	A	11377	1304	2340	KETEAQRKRLRRNEPEEQEIRT RKTRSPQTPDQQTYKKGRNER LCGISQPTKEPTRGGFCRFRNPP SNRIFACWGKPAWTACCNSLR ARRMLMERNARAAGSRKRMG RMDCWARVLDI\NLAAEAKSEP EKKAGVKRICKRRCTGSSFDL\ DY*LFNGDYYDRMYSYP\ARVP PPPPIARAVVP\SKRQRVSGNTS RRGKSGFNSKSGQRGSSKSGKL KGDD\LQAIKE\ELT\QIKRKSGF LFLGKTWEKIEKEQSKQAVEM KK**SQKEEQSSQLR*KKDET*C *RLEVLKGGA\EDSA\EEGDLLD DDDNEDRGDDQLELIKDDEKE\ AEEEEDDRD\SANGR\DDSLST

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11310	41678	A	11378	80	1141	ETQNRISSPSPSCEIFLIFSYIFRL CEKPYHQTRSASNVTNKTDPRS MNS\RVFIGNLNTLVVKKSDVE AIFSKYGKI\VGCSVHKGFALSF SMLMKRNARAAVAG\EDGRMI AGQVLDINLAAEPKVNRGKAG VKRSAAEMYG/SQ*QNTLLRPL YFSSSFDLDYDFQRDYYDRMY SYPARVPPPPPIARAVVPSKRQR VSGNTSRRGK\SGFNSKEWNSG VSSKFWKR*KGDDLQ\AIKEEL T\QIKQKVDSL\LENLEKIEKEQS KQAVEMKNDKSEEE\QSSSS\LK KDET\NLKMESEGGCRLTLPEE GDP\LD**YDE**RSGGNDPAGS *SKDDEK\EAEE\GEDDRD\SAN G\EDDS
11311	41679	A	11379	1	1134	
11312	41680	A	11380	1	642	
11313	41681	A	11381	397	898	
11314	41682	A	11382	1	663	
11315	41683	A	11383	44	398	ATMLGLNIISRKWFYKSSEKSL GLRGGLGRPLAFTLYSLLQAAL LCVNAIAVLHE/ERRISSKNICA GGTRTIGIGWIWEKEPGIKSQL MNLIRSVRTEMRVPLIIVNSIAI VLLLLFG
11316	41684	A	11384	3	754	GLYYRKCQLISKEDVTHDTRLF CLMLPPSTHLQVPI/GEHVYLKL PITGTEIVKPYTPVSGSLLSEFKE PVLPNNKYIYFLIKIYPTGLFTPE LDRLQIGDFVSVSSPEGNFKISK FQELEDLFLLAAGTGFTPMVKI LNYALTDIPSLRKVKLMFFNKT EDDIIWRSQLEKLAFKDKRLDV EFVLSAPISEWNGKQGHISPALL SEFWKRNLDKSKVLVCICGPVP FTEQGVRLLHDLNFSKNEIHSFT
11317	41685	A	11385	1	1785	
11318	41686	A	11386	95	369	
11319	41687	A	11387	511	728	
11320	41688	A	11388	1	100	
11321	41689	A	11389	1	777	

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11322	41690	A	11390	2	707	PNPKCR*VFPVFLFYRPI*PFPSS PA/SLIARPS*VPILPQPPLL/TPY NPPTTSPPHTRSGLQFSSATSSSP PAQQFPLREVAGAEGIVNAHVP FSLSDLSQISQHLGSFSSDPTKYI QEFRYLTLSYNLTWSDLNVILT STLSPDERERVFPVSQSH/V**P/ SGFMSQTSRKALEQFPERIPQW NYQANSPGKNFKN*NLALKPH NRN*STLPSTCTIIERKQPDGNA FLSYNYLPP
11323	41691	A	11391	2	339	LLLFRSLPAKLNQAPILPWPL/PP PPYNPSITSPVHTWFSLQFHSET SPPPPAQQFPLRAVAGTEGIVR MNGKEFFLQPNLTLITAGFKSQ TSRKALEQFPERIPNGTIRQIPQ
11324	41692	A	11392	1	993	
11325	41693	A	11393	3	1127	TKETRFIHGPKTPAPVTDWEGS LPLVFNHCRDASLIIHSRFKGVR PHRDTCLGPSPLAASPAFLGKG QAAHCQAELSPNSSSASTPPPY NPSITSPPHTRSGLQFSSATSSSP PAQQFPLREVAGAEGIVRVHVP FSLSDLSQISQCLGSFSSDPTKY TQEFQCLTLSYNLTWSDLNVIL TSTLSPDEWERVSSLAQSHADN \PGFTSQTSRKALEQFPE/TDPQ WNHQANSPGIARRDYMVSCLV EGLKKAAYKAVNYDKLKETTQ GEDENPAQVVARLAATLRRFT ALDPEGPEGRLILNMHFITQSAP DITKKLQKLESGPQTPQQELINL TFKVHNNGEETDAARSPWKPP GPSRTPSFRACFPCPHNFCGY
11326	41694	A	11394	1	312	
11327	41695	A	11395	1	244	MFADR*LFSTTHQS\IVPLYL\LF GA*AGVLATA\LSLLIRAELGQP GNLLGNDHIYNVIVTAHAFVIIF FIVIPIIGGFGN*LVPLIIGAPDM AFPRINNISF*LLPPSLLLLLAS\A IVE\AGAGTRLNKSYPP\LAGNY SHPWKPPVDLTIFSLHLAGVSSI LGAINFITTIINIKPPAITQYQTPL FV*STTHQSHRTTIPIYSAHELA SSPQPLSLLIRAELGQPGNLLGN DHIYNVIVTAHAFVIIFFIVIPIIG GFGN
11328	41696	A	11396	1	1287	
11329	41697	A	11397	3	583	

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11330	41698	A	11398	3	419	ILSISKLRTSLAGEGSVDTPKAS GVTRHIKGPGVAAEMSAFILPL PG*VSPGWEWAASAVLNGLRT TLALRRGVCLIRSRPGTLGLED GASPRTESLHTGTACKGAVDGS SEVDEKLKRIALDFLGLHGGDD PRSSWH
11331	41699	B	11399	1	1242	
11332	41700	C	11400	504	755	
11333	41701	A	11401	155	710	ETETTGEREGSLSNHPSNPTAA GLSLDTMKSHCPNHSSLLSTAA SPPKLWRCFKEEH\ELAVLGAP PKPLLPPTSHRDPTSASVYLRAP THVVWSLFKHPLS*TPCCMGF\I AFA\YSVKSRDRKIGCERDPGPI AYASTAK\CLN\IWALILGLLHD HSGSSSSPVLIVPGLWDRSGGIT GGQELCP
11334	41702	A	11402	1	1158	
11335	41703	A	11403	80	996	LKGKFLSMSG\ALDVLQMKEE DVLKFLAA\GTH\LGGTNLD\FH MEQYIYKRKSDGIYIIYLMRTW EKLL\LAARAIVAIENPADVSAI SSRNTGQRAVLKFAAATGATPI AGRFTPGTFTNHIQAAFRE\PR\L LVVTDPRADHQPLTEASYVNLP TIALCNTDSPLRYVDIAIPCNNK GAHSVGLMWWMLAREVLRM RGTISREHPWEVMPDLYFYRDP EEIEKEEQAAAEKAVTKEEFQG EWTAPAPEFTATQPEVADWSE GVQVPSVPIQQFPTEDWSAQPA TEDWSAAPTAQATEWVGATTD WS
11336	41704	A	11404	1	819	
11337	41705	A	11405	1	1032	
11338	41706	B	11406	63	344	
11339	41707	A	11407	49	281	FFKSTVCSFQKQFQTLPVPIGGS IMY*DISDHRGQR**NVGPCGH
11340	41708	A	11408	985	1213	TQCVTINY*GMKWGSFGYIVFH KDGCALIDKRFHTFCVSFKGSQ IQSSAAFLIPDVQVHQRLQKDF QGLMVPIVGS
11341	41709	A	11409	1	774	
11342	41710	A	11410	3	249	
11343	41711	A	11411	3	619	
11344	41712	A	11412	3	493	

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11345	41713	A	11413	3	292	DALPRWPSGSGDGGAVREAGQ QGTRLERPAAVLIRAADPGRRT QALA/GLPRG*PHPRMDPPESFQ ATGGTQQMTSTAPSWLTM*LR SVSGW*ELKD
11346	41714	B	11414	190	315	
11347	41715	A	11415	227	545	
11348	41716	A	11416	1	1896	
11349	41717	B	11417	52	1822	
11350	41718	A	11418	1	458	
11351	41719	C	11419	196	327	
11352	41720	A	11420	258	375	TRALSKFGSSRVEQS*AGYSGP GTP*EGGSGILGETVC
11353	41721	A	11421	3	854	
11354	41722	A	11422	1	434	MTVSKNKCHTKGGKKGTEKK VVASFSKIYWYNVKAPAMFSIR NIGKALVIGTHGTDFVSDGFKG GLIEIPDSIGKDKEKACRSIYPLH DVFVRKVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF
11355	41723	A	11423	1	642	
11356	41724	A	11424	260	534	
11357	41725	A	11425	1	438	
11358	41726	C	11426	391	750	
11359	41727	A	11427	786	926	AQGQRQETIQGGRSLSRTLYL* GRSGTSLSQKLAQLSSLTGDST
11360	41728	A	11428	488	649	VLQLLKVAHPELFIPPGGFVFSL TSGVKLHT*ALQLLKVAHPELL IPPGSWSH
11361	41729	A	11429	1	2028	
11362	41730	A	11430	1022	1417	SLMGTSTSSALGMHVPRAITRD VLSAPVIVSGNTAKFCTMLGHF LKKTRTERRDIQAP*SFISLPPKS TWEKLSSAAMVSTLR*GASDQ K/C*LLGGNDRVSLIVIQVEG\PL QDPGTLGRLLQSLTVKRISV
11363	41731	A	11431	1	535	
11364	41732	A	11432	3	1186	
11365	41733	A	11433	201	458	QVDGCIPELKV*F*KKRGRRGR RGRRRRRGRRREEGGGGGGG SFWRTHHTKPKDQHKKDTMG HFRSCAFQEGFVVHVPLLSSEK
11366	41734	A	11434	1392	1532	AQGQRQETIQGGRSLSRTLYL* GRSGTSLSQKLAQLSSLTGDST
11367	41735	A	11435	1253	2820	
11368	41736	A	11436	1504	1718	VIGIWALALGILARPQRGFHVV HLQDVGGAAA*AAKGLLRNVV R**VDQVQVSGAQGIAGVVVT VGGEEDF
11369	41737	B	11437	1	1383	

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11370	41738	A	11438	3	310	VHGRASSLGVG/TPIPKGHGQIK P/DRLKPPVYGACKLLDMELEM AFFVGPGNRLGEP/IPISKAHEPI FGMVLMNAWSARHIQKWEYV PLGPFLGKSFGTPVKSS
11371	41739	A	11439	1	1337	MSFIPVAEDSDFPIHNLPYGVFS TRGDPRPRIGVAIGDQILDLSIIK HLFTGPVLSKHQDVFNQPTLNS FMGLGQAAWKEARVFLQNLLS VSQARLRDDTELRKCAFISQAS ATMHLPATIGDYTDFYSSRQHA TNVGIMFRDKENALMPNWLHL PVGYHGRASSVVVSGTPIRRPM GQMKPDDSKPPVYGACKLLDM ELEMAFFVGPGNRLGEPIPISKA HEHIFGMVLMNDWSARDIQKW EYVPLGPFLGEEFWGHCLLPW VVPMDALMPFAVPNPKQGPRG PCRYLCHDEPYTFDINLSVN\LK G\EGMSQAAT\ICKVQILKYMY WT\MLQQAHSPTLSNGC\NL\RP GDLLGFLGPI\SGPGAQKNFGS\ MLELSWKGTKP\ID\LGNGQT\R KFLLD\GDEVIITAMATRDFKW YS\QGDGY\RIGFGQ\CAGKVLP ALLPIMRFFLLF
11372	41740	B	11440	100	383	
11373	41741	A	11441	1	263	MEYYAAIKKDEFMSFVRIWMK LETIILSKLSQGQKTKHRRFSLI DG/IHHRSFTRTENSSQRTGRKC WN**PTCGLARSWFGKTWSGN
11374	41742	A	11442	2	160	
11375	41743	A	11443	150	308	CLHR*GRGSPRPGPGGGSTGGA GPGAGPSLAPPLPAQNAEGLGG RRRGNKYL
11376	41744	A	11444	1	372	
11377	41745	A	11445	49	177	SQQGLYAKPTSSQAL*GDGQAS AEMGRILSYE*EHAVFGFSSL
11378	41746	B	11446	1	420	
11379	41747	C	11447	1	334	
11380	41748	C	11448	1	268	
11381	41749	C	11449	1	564	
11382	41750	A	11450	1	264	
11383	41751	A	11451	33	194	
11384	41752	C	11452	1	309	
11385	41753	A	11453	1	738	
11386	41754	A	11454	1	2028	

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11387	41755	A	11455	3	1008	LKDAVFSIRISPESQKLFAFQWE DPESGVTTQYTWTQLTQGFENS PTIFGEALARDLQKFPAKDLGCI LLLYMDDLLLGHSTAVRCAKG MDALLQHLEDCGYKVSKKKA QICRQQVTKWGDWERFEWEPL QQQAFCKLKEKFMSAPALGLP DLTKPFTLYVSEREKTAVGVLI QTVGPWPTPVAYLSKQLDGVS KGWPPCLRALAATALLAQEAD KLTLVQNLNIKAPHAVGTSAQ KPELIALTRALELSEGTWMKLE TIILSKLSQGQK/DQTLHVLTGIS RST*ACSCLASLQVGLETGSQL SLENPLRVGIQRRRCFTCAVDG EGFLLGVPMA
11388	41756	A	11456	677	879	KRRNHQILEIRSHLQSVEDNLK SGLGSTASL*MSWTQPRNGAE VGFLLILGYIKETPRNAETPSMV
11389	41757	A	11457	1	624	
11390	41758	A	11458	3	130	VEEEQGHSFRNAR*IISW*RNEN GLDRMDCSCRNGERDKGHG
11391	41759	A	11459	1	1477	MADPPWSSVQVNKYDSGLLSS VSAEPLASSASSHPGMSDNAPA SLESGSSSTPTNCSTSSAIPQPGA ATKPWRSKSLSVKHSATVSML SVKPPGPEAPRPTPEAMKPAPN NQKSMLEKLKLFNSKGGSKAG EGPGSRDTSCERLETLPSFEESE ELEAASRMLTTVGPASSSPKIAL KGIAQRTFSRALTNKKSSLKGN EKEKEKQQREKDKEKSKDLAK RASVTERLDLKEEPKEDPSGAA VPEMPKKSSKIASFIPKGGKLNS AKKEPMAPSHSGIPKPGMKSMP GKSPSAPAPSKEGERSRSGKLSS GLPQQKPQLDGRHSSSSSSLASS EGKGPGGTTLNHSISSQTVSGS VGTTQTTGSNTVSVQLPQPQQQ YNHPNTATVAPF*EGFHLP*HA *VITF*TANYASSDNDLNVGYT H*LTASEFFQSRLSSLGEVAGLH AHTC*A*LGSNIPFSVRLRPVPA ASAEDLRGHQGLIKDRAQVS
11392	41760	A	11460	1	327	LLLMGLKHNVLKLPRGPMVTL RESVWETLNFLK*SFV*LNMLIF KKSS*RLQ*VRFHFLCPRVLIVQ LPFMSENMRCLVFCSCVSLLRM MVSSFIHVPFFKVLSFFALG
11393	41761	B	11461	119	203	
11394	41762	B	11462	1	677	

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11395	41763	A	11463	2	74	
11396	41764	A	11464	1	1256	MSASQDSRSRDNGPDGMEPEC VIESNWNEIVDSFDDMNLSESL LRDIYAYGFEKPSAIQQQAILPC IRGYNVIAQARSGTGKMATFAI SILQQIELDLKATQALVLAPTRE LAQQIQKVVMALVDYMGASC HACVRGTNMRAEVQKLQMEA PHIIVGTPSRVFDMLYR\RYLAP\ KSIRMLVLNEADEMLSRGFKG QIY\DISKRLNSTTK\VVLLSAT MPFD\VLEVTKKFMRGPH/IRIL VKKEELPLEGIRHFYINVEPEE\F NLDTLC\DWYEP*PIT\QAVIFHQ PPGGKVDW/LSPEKMHARDST VPPMHGDMTKKE\RD\VIMREF RSGS*PEF*ITPLTLPGQRPLMC QPGFL*SFKLMTLPPPTRGKLLI HRNRSRVDRFGRKGVA\INMVT EED\KRTL\RDIETFY\NTSIEEMP
11397	41765	A	11465	1	402	KSRGRGLPYTMDAFMLGMGM LKYPNFVAT*ARGYPGFAPSYG YQFPGFPAAAYGPVAAAAVAA ARGSGSNPARPGGFPGANSPGP VADLYGPASQDSGVGNYISAAS PQPGSGFR/HTGIAGPLIATAFT NGYH
11398	41766	A	11466	226	486	
11399	41767	A	11467	2	432	
11400	41768	A	11468	1	834	
11401	41769	A	11469	205	570	
11402	41770	B	11470	61	939	
11403	41771	A	11471	96	269	
11404	41772	A	11472	123	593	VAVLEARLLSPVRASKMTKKR RNNGRAKKGRG\HVQPIRCTNC ARCVPKDKA\IKKFVIRNIVEAA A\VRDISEASVF\DAYVLPKL\YV KLHYCVSCAIHSNVVMESISVK ARKD\RTPPPRFRPGGCWPHVP PPKPNVRELEFFKDLKDRLISS WEEK
11405,	41773	A	11473	1	228	
11406	41774	C	11474	187	423	
11407	41775	A	11475	1	546	
11408	41776	A	11476	1	1254	
11409	41777	A	11477	1	1386	

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11410	41778	A	11478	1	1445	HLKAKMGKEKTHINIVVIGHVD SGKSTTTGHLIYKCGGIDKRTIE KFEKEAAEMGKGSFKYAWVL DKLKAERERGITIDISLWKFETS KYYVTIIDAPGHRDFIKNMITGT SQADCAVLIVAAGVGEFEAGIS KNGQTREHALLAYTLGVKQLI VGVNKMDSTEPPYSQKRYEEIV KEVSTYIKKIGYNPDTVAFVPIS GWNGDNMLEPSANMPWFKGW KVTRKDGNASGTTLLEALDCIL PPTRPTDKPL\ALPLQGVH\KLG GIGTVSSAPMET\GFSNPGMVV TFAPSPR*QRKVKSVE\MH\HEA L\NEALSGEQCGLSMSKKVSVK ECFVRGN\VAG*PAKNDPTQWE ASWLSLLQVIILEPSQAQISAGL CPLYWDC\HTGSHLHAKFAELK EKIDRR\SGKKV\EDGPKIL/RSL GDAAIVDMV\PG\RPMCVESFS DYPPLGRFAVRDMRQTVAVGV IKAVDKKAAGAGKV\TKSAQK
11411	41779	A	11479	1	996	

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11412	41780	A	11480	1	1875	MPSDLAKKKAAKKKEAAKAR QRPRKGHEENGDVVTEPQVAE KNEANGRETTEVDLLTKELEDF EMKKAAARAVTGVLASHPNST DVHIINLSLTFHGQELLSDTKLE LNSGRRYGLIGLNGIGKSMLLS AIGKREVPIPEHIDIYHLTREMP PSDKTPLHCVMEVDTERAMLE KEAERLAHEDAECEKLMELYE RLEELDADKAEMRASRILHGLG FTPAMQRKKLKDFSGGWRMR VALARALFIRPFMLLLDEPTNH LDLDACVWLEEELKTFKRILVL VSHSQDFLNGVCTNIIHMHNKK LKYYTGNYDQYVKTRLELEEN QMKRFHWEQDQIAHMKNYIAR FGHGSAKLARQAQSKEKTLQK MMASGLTERVVSDKTLSFYFPP CGKIPPPVIMVQNVSFKYTKDG PCIYNNLEFGIDLDTRVALVGP NGAGKSTLLKLLTGELLPTDG MIRKHSHVKIGRYHQHLQEQL DLDLSPLEYMMKCYPEIKEKEE MRKIIGRYGLTGKQQVSPIRNL SDGQKCRVCLAWLAWQNPHM LFLDEPTNHLDIETIDALADAIN EFEGGMMLVSHDFRLIQQVAQ EIWVCEKQTITKWPG\DIL\AYK EHLKSKLVD\EEPQLTKELPTTC
11413	41781	A	11481	194	418	YGLASVSPTQISSSSCNPWMFE GGTLVGGDWIGSHDSEGVLTR SGCLISVWHFSCAVSPATL*RRC LLLLRLPP
11414	41782	A	11482	1	675	
11415	41783	A	11483	1	1125	
11416	41784	A	11484	1	711	
11417	41785	A	11485	673	796	
11418	41786	A	11486	3	570	RLQEFGTRNRHLPVNSPKLTNT KGKRRGTR\YMF\SRPFRKHGV VPLATYMRIYKKGDIVDIKGM GTVQKGMPHKCYHGKTGRVY N\VTQHA/VMGIVVYKQA*GQR FLPKRI*CCVIEHI\KHS\KSRDSF \LK\RVKENDQKKKEAKE\KGT W\VQL\NRQLAPPREAHFVRT\N G\KEPGACWNPIPYEFHGHNR
11419	41787	A	11487	1	2091	
11420	41788	A	11488	1	2208	
11421	41789	A	11489	430	1032	

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11422	41790	A	11490	3	1158	EDQIDRLDFIRNQMNLLTLDVK KKIKEVTEEVANKVSCAMTDEI CRLSVLVDEFCSEFHPNPDVLKI YKSELNKHIEDGMGRNLADRC TDEVNALVLQTQQEIIENLKPLL PAGIQDKLHTLIPCKKFDLSYNL NYHKLCSDFQEDIVFRFSLGWS SLVHRFLGPRNAQRVLLGLSEPI FQLPRSLASTPTAPTTPATPDNA SQEELMITLVTGLASVTSRT\SM GIIIVGGVIWKTIGWKLLSVSLT MYGALYLYERLSWTTHAKERA FKQQFVNYATEKLRMIVSSTSA NCSHQVKQQIATTFARLCQQV DITQKQLEEEIARLPKEIDQLEKI QNNSKLLRNKAVQLENELENF TKQFLPSSNEGSVTIEIALVTLIG GNRNL
11423	41791	A	11491	132	381	SKAESVFPPTLPRQRPAAAAGP HWGAG*GQDEAGLHPGPEDRG FLRETPADPGLQAGLGQVHPPR SRADPPAPYQVPPRMGT
11424	41792	B	11492	129	470	

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11425	41793	A	11493	1	1955	FVSCQAPWSHPPAQLSPVGADA MTLTLSVLICLGLSVGPRTCVQ AGTLPKPTLWAEPASVIARGKP VTLWCQGPLETEEYRLDKEGLP WARKRQNPLEPGAKAKFHIPST VYDSAGRYRCYYETPAGWSEP SDPLELVATGFYAEPTLLALPSP VVASGGNVTLQCDTLDGLLTF VLVEEEQKLPRTLYSQKLPKGP SQALFPVGPVTPSCRWRFRCYY YYRKNPQVWSNPSDLLEILVPG VSRKPSLLIPQGSVVARGGSLTL QCRSDVGYDIFVLYKEGEHDL VQGSGQQPQAGLSQANFTLGP VSRSHGGQYRCYGAHNLSPRW SAPSDPLDILIAGLIPDIPALSVQ PGPKVASGENVTLLCQSWHQID TFFLTKEGAAHPPLCLKSKYQS YRHQAEFSMSPVTSAQGGTYR CYSAIRSYPYLLSSPSYPQELVV SGPSGDPSLSPTGSTPTPGPEDQ PLTPTGLDPQSGLGRHLGVVTG VSVAFVLLLFLLLFLLLRHRHQ SKHRTSAHFYRPAGAAGPEPKD QGLQKRASPVADIQEEILNAAV KDTQPKDGVEMDARAAASEAP \QDVTYAQLHSLTLRREATEPPP S\QEREPPAEPSIYAPLAIHLAHG GPRSHTQQKETQRLQKARELPP VDTNEPQPAWDP

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11426	41794	A	11494	22	1991	GLIPLQSAGSPEGDAMTPALTA LLCLGLSLGPRTRVQAGPFPKP TLWAEPGSVISWGSPVTIWCQG SLEAQEYQLDKEGSPEPLDRNN PLEPKNKARFSIPSMTQHHAGR YRCHYYSSAGWSEPSDPLELV MTGAYSKPTLSALPSPVVASGG NMTLRCGSQKRYHHFVLMKEG EHQLPRTLDSQQLHSGGFQALF PVGPVNPSHRWRFTCYYYYMN TPRVWSHPSDPLEILPSGVSRKP SLLTLQGPVLAPGQSLTLQCGS DVGYDRFVLYKEGERDFLQRP GQQPQAGLSQANFTLGPVSPSN GGQYRCYGAHNLSSEWSAPSD PLNILMAGQIYDTVSLSAQPGP TVASGENVTLLCQSWWQFDTF LLTKEGAAHPPLRLRSMYGAH KYQAEFPMSPVTSAHAGTYRC YGSRSSNPYLLSHPSEPLELVVS GHSGGSSLPPTGPPSTPGLGRYL EVLIGVSVAFVLLLFLLLFLLLR RQRHSKHRTSGLRLCPSSPRPE K\ADFQRPAGAAETEPKDRGLL RRSSPAADVQEENLYAAVKDT QSEDGVEIYTRQSPHDEDPQAV TYAEVKHSRPRREMASPPSPLS GEFLDTKDRQAEEDRQMDTEA AASEAPQDVTYAQLHSLTLRRE ATEPPPSQEGPSPAVPSIYATLAI
11427	41795	A	11495	1	1818	
11428	41796	A	11496	3	574	IRCSSVDPRVRPRVRGASGAAA YCCRHVSIPRDHTTHNQSRKW HRNGIKKPRSQRYESLKGVDPK FLRNMRFAKKHNTKGLKKMQ ANN\AKAMSARAEAIKALVKP KEVKPKIPKGGQPINLIRLAYIA HP\KLGKRARARI\AKGLKLCRP K\AKAKAKAKAKDQTKAQAA APASVPAQAPKRTQAPTKASE
11429	41797	B	11497	45	331	
11430	41798	A	11498	1	1779	
11431	41799	A	11499	1	837	

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11432	41800	A	11500	3	557	ERGYSFTTTAERDIVRDIKEKLC YVA\LDFEQEMATAASSSLEES YE\LPDGQVITIGNE\RFRCPEAL FQPSFLGMESCGIHETTF\NSIM K\CDVDIRKDLYANTVLSGGTT M\YPGFADRMQKEITALAPSTM KIKIIAPPERKYSVWIGGSIL\AS LSTF\QQMWISKQEYD\ESGPSI\ VHRKCF
11433	41801	A	11501	1	1188	
11434	41802	A	11502	1	684	
11435	41803	A	11503	1	1398	
11436	41804	A	11504	22	1239	
11437	41805	A	11505	837	971	
11438	41806	C	11506	1	3018	
11439	41807	A	11507	23	368	
11440	41808	A	11508	1	816	
11441	41809	A	11509	1	441	
11442	41810	A	11510	195	293	IKVSPSGRDPVRDN*ITW*FLPY CSSTTGSLH
11443	41811	A	11511	56	372	MELPASPALFARTPQPLGGRW DWAPWSRGWRSSRRLGPHRSP RRGSEAQAWRAAGPEPCPAGR QLRPVNIEWLFALILTHTFGTFQ VLA*TSQALI*NPRVLYPD
11444	41812	B	11512	108	326	
11445	41813	A	11513	3	326	GSKKKFH*HSRILERSRSWRTS YQGRPQEPSWLHPVDPHRGCR WSCLPVPCRAPSTPQPLGGRWD WAPWSRGRRLSGRLGPHRSPR NRGRLRHGGLQVPSRASQEGS
11446	41814	A	11514	3	619	VRDIHGSPTHHRPGGLRGKNGF VGEARDPRYRSGHCFRECRTQ ALVAFT*C*SCGFTEVKN*GLSC LPAGQGSGPAARHV*ASHPLHG LPCGPSLP/NRAPPPTPRRPVPST TQGLRNASARRGTGRQLHLQP WCGIH*VKPAGLLSLLHGQAC GDPATPSRERLSQPAVPTALGS RRRLLLGPAGSPGSSLPPSRQPP GGRRRPP
11447	41815	B	11515	1	1524	
11448	41816	A	11516	1	1365	
11449	41817	B	11517	1	654	
11450	41818	B	11518	1	795	

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11451	41819	A	11519	486	929	QKQEESWPEDTYPRALAAFPR GRARDLQPAMPEPPTLSMGSC APEPPRGAPPPAPRRRIPSTTQG LRSSGAGRRTCRQLHLQPRCRI HWVKPAGLLSLWLFQMHSASC WWNYHSGAWRMVALFSWLH* ECPSGESGAPILHFPFALP
11452	41820	A	11520	35	473	VLQLLRRHVWSCSFPPGVVVSL ALAVKLQTFVTQEPSWLHPVD PAPGLQVELPASPLQCTRTSQPL GGRWDWAPWSRGRRSSGRLGP HRSPWRG*EAQAWRAAGPEP/ WPRGKA/C*GPARNRAKRRFPH CTF*EEVTVCSPQKRGGD
11453	41821	A	11521	23	229	RSWNPQTLFVGMYNATAAWK PI*QFLKKLNMKLP*DPGREPLN QTG*KGKRGGQEAFLEKGISSR MSQ
11454	41822	B	11522	152	901	
11455	41823	A	11523	1	3063	
11456	41824	A	11524	242	263	VLQLIKAVWTQRTQEPSWLHP VDPALGLQVELPASPAPCACTP QPLG\PLLPGLPLWRHLRSPSVH HCTVGAPFWAGQGRSPLPQRR CALFLAGP
11457	41825	A	11525	1584	2082	QRAGSPHSPRSLSVPPLPGLPLW RHLRSPSAHRCTMGAPFWAGQ GHSRLPQLAGRRGGRGASGNR CCVQRLQASWSSRWAWAWRA PHSEQPAGPAGPGQ*GTWHPG QRLQRMYWVLQQCRLTGAVL DFSPGLSCLPAGQGSGPAARHA *AFHPLHGLLCGRSLPD
11458	41826	A	11526	1293	1558	CIQHCHHCCCYRCRASAAGAA SLQGSTHVRIQH\CTP\CPVLLTP SVRLRDVCTRSIWPLVVTGLPS AMNVSSWCSTSSPAFGVLVLWI
11459	41827	B	11527	179	1031	
11460	41828	A	11529	1	342	
11461	41829	A	11530	1	3081	
11462	41830	A	11531	1	371	
11463	41831	A	11532	1	501	
11464	41832	A	11533	1	836	
11465	41833	A	11534	88	573	
11466	41834	A	11535	1	675	
11467	41835	A	11536	1239	1556	FLSLPTFLFVIFSGEEELLVLALV FLSLFFFFFFLRWSFAVVAQAV\ VQWHNLSSLPFGFKQFSCLSLP SSWDYRCPPPRPANFCIFTRDG VSPCCPGWSRTSDLR

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11468	41836	A	11537	2	375	ASIEIDSLYEGIDFYTSITRARFE ELNADLFRGTLDPVEKALRDA KLDKSQIHDIVLVGGSTRIPKIQ KLLQDFYEAVAYGAAVQAAIL SGDKS\ENV\QDLLSL\DVT\PFP LGIETAGG\VMTVPH
11469	41837	A	11538	2	295	NRMGNHFIAEFKRKHKKDISEN KRAVRRLRTACERAKRTL/SSST QASIEIDSLYEGIDFYTSITRAPF EELNAWGISWWWSLPPPVGAS SGPTIEEVD
11470	41838	A	11539	1	1659	
11471	41839	A	11540	1	810	AGKPHCGGEFCTPNVHHFFR*F *ANPKRTII/ENKEALTPPPTV/C* RAKPTLSSAPRAVI/EIDSS*E/GI GLYTSITPPRFEELNADLFLAPL TPVEKALRNA\KLDKSQIHDIVL V\GGSTRIPKIQSFLQDFF\NGKE LNKSINPDEAVAYGAAVQAAIL SGDKSENVQDLLLLDVTPLSLG IETAGGVMTVLIKRNTTIPTKQT QTFTTYSD\NQPGVLIQVYEGER AMTKDNNLLGKFELTGMPGG MPGGFPGGGAPPSGGASSGPTI EEVD
11472	41840	B	11541	848	2399	
11473	41841	A	11542	1	876	
11474	41842	A	11543	16	1203	SIPHEPWPVSLLLFQEQVPGKK ELRKGLALLEAIISICGSLDKVL KEKRKLFIHSMGEGTINGLLDE LLQTRVLNQEEMEKVKRENAT VMDKTRALIDSVIPKGAQACQI CITYICEEDSYLAETLGLSADQT SGNYLNMQDSQGVLSSFPAPQ AVQDNPAMPTSSGSEGNVKLC SLEEAQRIW\EQKSAEIYPIMDK SS\RT\RVALIICNEEFDSIPRRTG AEVDITGMTMLLQNLGYSVDV KKNLTASDMTTELEAFAHRPE HKTSDSTFLVFMSHGIREGICG KKHSEQVPDILQLNAIFNMLNT KNCPSLKDKPKVIIQACRGDSP GVVWFKDSVGVSGNLSLPTTE EFEDDAIKKAHIEKDFIAFCSST PDNVSWRHPTMGSVFIGRLIEH
11475	41843	A	11544	2	654	
11476	41844	A	11545	3	291	LIPPLLRPLVQSGGIPEMGKFMK PGKVVLVLAGRYSGRKAVIV\R YSVDIPLDKTVVNKDVFRDPAL KRKARREAKVKFEERYKTGKN KWFFQKLRF

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11477	41845	A	11546	157	386	
11478	41846	A	11547	2	531	FWQESASGHLWLSGFLSGPFSL LSAEMGKFMKPGKVVLVLAGR YSGRKAVIVKNIDDGTSDRPYS HALVAGIDRYPRKVTAAMGKK KIAKRSKIKSFVKVYNYNHLMP T\RYSVDIPL\DKTVVNKDGFTD P\ALKRNARMEA\KVKFEERYK TGKNKWFF\QKLRVLDAFVLII KNYKE
11479	41847	A	11548	1	414	LGGLKGTWGETKPAMAAAEEE DGGPEGPNRERGGAGATKTLL YTGNHLFSPQWLETRPERQECP VCKAGISREKVVGEKSLLTFSL HFLRLKTPQICRLPV*LFLPP*GF QPFGDTGGFHFSFGVGAFPFGF FNSPSY
11480	41848	A	11549	1	654	
11481	41849	A	11550	3	663	RGQEVVSGLLGRVYVYLGGLK GTWGETKPAMASAEEE\SGAPN VPNRERGGAGRPKTPFECNICL ETAREAVVSVCGHLYCWPCLH QWLETR\PERQECP\VCKAGISR EKVVP\LYGRGS/QRSPQDPRIK NSPRPPGGRGPAPE\SRGGSQP\F GDTGGFHF\SFGVGAFPFGFFTT VF\NAHEPFRRGTGVDLG\QGH PSLQLGKEFPLPGFSAIFFLFWL
11482	41850	A	11551	3	369	
11483	41851	A	11552	375	851	
11484	41852	A	11553	1	927	
11485	41853	A	11554	104	845	

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11486	41854	A	11555	200	1496	ETIQAVVFMSLHFLYYCSEPTL DVKIAFCQGFDKQVDVSYIAKH YNMSKSKVDNQFYSVEVGDST FTVLKRYQNLKPIGSGAQGIVC AAYDAVLDRNVAIKKLSRPFQ NQTHAKRAYRELVLMKCVNH KNIISLLNVFTPQKTLEEFQDVY LVMELMDANLCQVIQMELDHE RMSYLLYQMLCGIKHLHSAGII HRDLKPSNIVVKSDCTLKILDF GLARTAGTSFMMTPYVVTRYY RAPEVILGMGYKENVDIWSVG CIMGEMVRHKILFPGRDYIDQW NKVIEQLGTPCPEFMKKLQPTV RNYVENRPKYAGLTFPKLFPDS LFPADSEHNKLKASQARDLLSK MLVIDPAKRISVDDALQHPYIN VWYDPAEVEAPPPQIYDKQLD EREHTIEEWKELIYKEVMDS\EE KT*KWC*LKGQPSP\SAQVQQ
11487	41855	B	11556	56	1564	
11488	41856	A	11557	1	970	
11489	41857	A	11558	1	903	
11490	41858	A	11559	237	479	PVGTNTECEIPFQPMETGHSSR VDASGYK*PCLLCSVYSRGKTA GECTLF*VHHFLSSLCPVNLGA NNQLHYIPWFSTDG
11491	41859	A	11560	1	477	
11492	41860	A	11561	125	1133	
11493	41861	A	11562	1	837	
11494	41862	A	11563	2	708	CQHYKFRYHQQGEGQEEPPLN PHGAARAEVYLRKCTFDMFNF LASQHRVLPEGATCDEEEDEVQ LRSTRRATSLELPMAMRFRHLK KTSKEAVGVYRSAIHGRGLFCK RNIDAGEMVIEYSGIVIRSVLTD MRKKFYDGKGIG\CYMFSMDD FDVVDATMHGNAARFINHSCE PNCFSGVIPGGGPENKIVIFGLR RILGGEEVNLRTKKFPIE\DAK\N KLPC\NCGAKRCRRFLN
11495	41863	A	11564	2	136	
11496	41864	A	11565	1	551	AILYAKRASVFVKLQKPNAAIR DCDRAIEINPDSAQPYKWRGKA H/RAQKIAEHRRKYERKREEREI KERIERVKKAREEHERAQREEE ARRQSGAQYGSFPGGFPGGMP GNFPGGIPGMGGGMPGMAGM PGLNEILSDPEVLAAMQDPEVM VAFQDVAQNPANMSKYQSNPK VMNLISKLSAKK

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11497	41865	A	11566	1	804	
11498	41866	A	11567	64	1215	PPSFAHHLPTMDPRKVNELRAF VKMCKQDPSVLYTEEMRFLRE WVESIGGKVPPATQKAISEENT KEEKPDSKKVEEDLKADEPSSE ESDLEIDKEGVIEPDTDAPQEM GDENAEITEEMMDQANDKKVA AIEALNDGELQKAIDLFTDAIKL NPRLAILYAKRASVFVKLQKPN AAIRDCDRAIEINPDSAQPYKW RGKAHRL\LGHWEEAAHDLAL ACKLDYDEDASAMLKEVQPRA QKIAEHRRKYERKREEREIKERI ERVKKAREEHERAQRE\EEARR QSG\AQYGSF\PGGFLGG\MPGN FP\GG\MPGMGGG\MPGMG\GM PGLNEILSDPEVLAAMQDPEVM VAFQDVAQNPA\NMSKYQSNP K\VMNLISKLSAKFGGQA
11499	41867	A	11568	1	265	VKAKIQDKEGIPPDQQRLIFAG KQLEDGRTLSDYNIQKESTLHL VLRLRGGIIEPSLRQLAQKYNC DKMICR/KKCGHTNNLRPKKK
11500	41868	A	11569	3	318	
11501	41869	A	11570	7	57	RFFNFLGGIP/P*SGPKGMTL/DQ TQGSKSKQIQWPALTFKPLVER NIPSSVTAVEFLVDKQLDFLTE DSAFQPYQVRNFRLLFKIKG*L NFIDIQTFFKQYSLNIISSNF*LC EKPNECSQLILLIG*TVY*FFNFL GGIPLNLGQKE
11502	41870	A	11571	1	2109	
11503	41871	A	11572	50	251	
11504	41872	A	11573	1	1922	
11505	41873	A	11574	2	479	
11506	41874	A	11575	1	909	LILTSVLLFQRHGYCTLGEAFN RLDFSSAIQDIRTFNYVVKLLQL IAKSQLTSLSGVAQKNYFNILD KIVQKVLDDHHNPRLIKDLLQD LSSTLCILIRGVGKSVLVGNINI WICRLETILAWQQQLQDLQMT KQVNNGLTLSDLPLHMLTNILY RFSDGWDIIT\LGQVTP\TLYML SEDRQLWKKLCQYHFAEKQFC RHLILSEKGHIEWEVGCNFATF RKHYPAKEQYGRQHCIFCRHCS ILFWKDSGHP\CTAADPDSCFTP \VSSQQFIALFQVLRAAPCHPY WRFVNPAVCAGLIVSVL
11507	41875	A	11576	1	1035	

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11508	41876	A	11577	63	606	FAKNERTQRGKRRG\TRYMFSR PF\RK\HGVVPLGPHICRJ\YRKG DIVDTQGNGVLFKKGMPHKCY PWPKLEGVLQLLPQHA\VAIVV NQPVLGQSFFPRE*IVRIEHI\KH SKSPR*ASLK/RVLKENDSEKER SPNEKGTWGSNLKRHLAPPQK KHTL*RTNGKEPEL\LEPIPYEFH GHNRC
11509	41877	A	11578	1	490	
11510	41878	A	11579	150	536	NCKISFLHFCYIFVKALKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQLKR/QGKNLVYISLVLRA L*G*DLTHHIIILFPFFFL**PAPP REAHFVRTNGKEPELL
11511	41879	A	11580	336	476	GMGTVQKGMPHKCYHGKTGR VYNVTQHAVGIVVNKQVK*VV LCG
11512	41880	A	11581	1	626	WAFRPEPPSSSKFAQNDGPQRG KRRGT\RYMF\SRPF*ENHGVVP LAHIFMR\IYK\KGDIVRHPRGM GYCSKKGMPPTSCYPWQKLGR V\YNVTPAMLFGIVCKQTKLKG NDSLPRG/ILMWRI*AHLRHF*G ARD/RASLKTCGRENGSRKKER KPKGGKVTWGFQLKRRHLGFP PQEEATFLLKEPIGGREP*ACLE PYFPYWISWGINRC
11513	41881	A	11582	499	723	
11514	41882	A	11583	96	411	PAPTSRCRRRRAPLPKKKAEGD AKGNKAKVKDEPQRRSARLS\A KPAPPKPEPKPKKAPAKKGEKV PKGKKGKAD\AGKEGE*PLQKN GDAKTDQAQKA\EGA\GDAK
11515	41883	A	11584	3	493	
11516	41884	A	11585	588	759	GEGCGWAEVGRCRPGPPDPAG PAGAAGP\GAARGGLFRGVLSP SSRCGGGSSSSRSGR
11517	41885	A	11586	213	626	
11518	41886	A	11587	1	645	
11519	41887	A	11588	1	739	
11520	41888	A	11589	327	676	NPNPSWNLAHVWDMDRK*EQ RGIQ/V**SNINKS*KEKMSMQC LEMPRNPDH*GRIDVSFQNLMR LTR*SQMGYLPWDLKQELETFS KLS*KQVMLSVVVTFVRNMLQ LRFLTSFSG
11521	41889	A	11590	11	328	

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11522	41890	A	11591	1	378	LFIVTVCPAFLRFSSAICDSFLIC PQVGGCVRRVLLVTVGVLLSIS LDMAATGVSLGSSWSLFLGIW LMIRFQVS*WYPNWLLILSWRN ISITSTPSYYFTYFPTFCYQISPPN QLFCFCLCSWFL
11523	41891	A	11592	1	780	
11524	41892	A	11593	1	1461	MVTLMGHAALCLHYVMQLGT TGGAWYFPRASSQAREMPQCP TLESQEGENSEEKGDSSKEDPK ETVALAFVRENPGAQNGLQNA QQQGKKKRKKKRIIISGKVLED FLALAMHFADEETGQKRCSLN QTIQLLITPDTGSIWHQAFLSSIV RRAAQQYGFREGGEDDDWTL YWTDYSVSLERVMEMKSYQKI NHFPGMSEICRKDLLARNMSR MLKMFPKDFRFFPRTWCLPADP AQLDLWSQTFWPRPRTAPDGT GADGLGLRLGSLGK/VSFWFPA CHGLG*PEASYTAS/MACGSLP/ WKLSTFSAYLEDHSYNVEQIW RDIEDVIIKTLISAHPIIRHNYHT CFPNHTLNSACFEILGFDILLDH KLKPWLLETEKMQTAGALFISP ALPSYSNFPLQVARREFQTSVV SRDIDTAAKFIGAGAATVGVAG SRAGIGTVFGSLIIGYARNPSLK QQLFSYAILGFALSEAMGLFCL MVAFLILFAM
11525	41893	A	11594	1	2301	
11526	41894	A	11595	3	381	
11527	41895	A	11596	1	729	
11528	41896	A	11597	1	1006	MVKVKARVNEFGYTGCLVTRA AFNSGKVDIVAINDPFIDLNYLA YMLQYDSTHGKFHGTIKAENG KLVINGNPITIFQE*DPTKIKWG DAGTEYVVESTSIFTAMEKVGA HLQRGAKRVMIFAPSTEAIMFM MKVNYEKYDNSLKIISNASCTT NCLAPLAKVIHDNSGIVERLMI TVHVITTTQKTVDGPCRKLRPD GHRALQNIIPASTSTAKAMVKV IPELNKKLTGMASHVPTAKVLV VDPTCHL/EKPAKYYDIKKMM KQASEDPIKGILGYTEHQIVSSD FNSDTQSSTFDAGAGITLNDHF VKLISWYDNEFGYSNRVVDLM AHMASKE
11529	41897	A	11598	3	508	
11530	41898	B	11599	1	5068	

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11531	41899	A	11600	58	659	PVATTCECIFIHLGEADVWIGN AA/WELYYLEQSIQHDSPMPSD KTTG*GDN*FYASS\GAGKFVS RAVFINLEPIVTDEVCTGTYHQ LFHPEQLITDKEDAAHNYAWG HHDIGKIIGCYSTNKTKCTIQFV DWCFTSLKVGINCQLPTVVPAG NLANIKRAACMLSNTIAIAEAW VCLGHKSDLSYANCSFVHQFFN KSIH
11532	41900	A	11601	511	1173	
11533	41901	A	11602	3	497	WCDGPQNRYALICQQC/YSHNG MALKEEFEYIAFRCAYCFFLNP ARKTRPQAPRLPEFSFEKRQVV EGSSSVGPLPSGSVLSSDNQFNE ESLEHDVLDDNTEQTDDKIPAT EQTNQVIEKASDSEEPEEKQET ENEEASVIETNSTVPGADSIPDP ELSGESLTAE
11534	41902	A	11603	2	764	
11535	41903	A	11604	1	444	
11536	41904	B	11605	44	1748	
11537	41905	B	11606	1	1134	
11538	41906	A	11607	1	549	
11539	41907	A	11608	212	548	
11540	41908	A	11609	1	905	ESVAAAARAFPFTAPKELERQQ RRRFRFHHLFLFPSLRTPCRVSV SLQPWLWKATEVMAMFEQMR ANVGKLLKGIDRYNPENLATLE R\YVETQ\AKENAYDLEPNLAV LKLYQFNPAFFQTTVTAQILLK ALTNLPHTDFTLCKCMIDQATI QERNGPIPDQIFVPSGTLLEDPA HFPGPFWQTPGNGRACQKAWD ENHWTLFGKVLT\GF*RLLVRK FIC\HVVGYHLPSHIDR\WLLAE MLGDL\SDKPAKRCWMSKIRLR EDDRRGQIF\ICS\QE*EHLNPRN\ IVEKIDFDSVSSIMASSQ
11541	41909	A	11610	186	209	QLWPN*LLSRNKEATLRYSQLP TCHSICY*MPAF*HTISDLSFNK NINCKSYHLRVFYKYV*IVCHF *VPKVYWTKYYQTSCRT*WR* SGVE*PPIISSSSSACCLLRRLPT EGTCPEIFWNPRLGISAECRDSC GPTSF
11542	41910	A	11611	2	2948	
11543	41911	B	11612	1	999	
11544	41912	A	11613	1	657	
11545	41913	A	11614	1	707	
11546	41914	A	11615	1	297	

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11547	41915	A	11616	1	1287	
11548	41916	A	11617	242	540	LTNEKKVQDQMDSQPNSTRGT RRSLYPFLLKLFQLIEKEGILPNS FYEASIILIPKPGRDTTTTKKEF* TNIPDEHRCKNPQ*NTSKPNPA AHPKAYPP
11549	41917	A	11618	193	916	
11550	41918	A	11619	1	2169	
11551	41919	A	11620	1	615	
11552	41920	A	11621	39	568	NSAWARRPLVLPLMSLVSPWK SSQHIF\RVLNPPNLDGRRKNSP LPITCHLRVWARRYAHVV\LRK AD\IDLTK\RAGEL\TEDEVERVI TILQ\NPRQYKIPD\WFLNRQKD VKDGKYSQVLANGLDNKLRED L\ERLKEDSAPIEGLRH\FWGLR\ VRGQHTQDQLGRRGRHRGASA GARR
11553	41921	A	11622	1	378	
11554	41922	A	11623	1	222	
11555	41923	A	11624	2	367	
11556	41924	A	11625	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLSAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
11557	41925	A	11626	1	633	
11558	41926	A	11627	164	714	IGVNRHLIQESPSWNLAGAPLE QIFQRKEQAAIFAILQPLLVISRQ TGSGVDPQQTPADLQK/SGSDS REQNKTENEFDELTEIGCRRWV ITNSSELKEHVVTQCKEAKNLE KMLQELLTRITSLEKNINDLME LKNTAQELREAYTIINSQTDQA EERISEIEDQLNEIKGEDNIREKT VKRNE
11559	41927	A	11628	504	936	TESSSININKKDDHAKTP\PKDH NSSPAREQNKTENEFDELTEIGC RRWVITNSSELKEHVVTQCKEA KNLEKMLQELLTRITSLEKNIN DLMELKNTAQELREAYTIINSQ TDQAEERISEIEDQLNEIKGEDN IREKTVKRIE

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11560	41928	A	11629	1949	3232	PGKQDLEWTSSKLQQTCRRGT LLVEGKLTNRKE*HQHQQKLR PHGNLIQRDHNCSPARE\QNWM ENEFDKLTEVGFRRWTITNSSK LKERVLTQCKEATNLAKRLEK LLTRITSLEKNKNDLMELKNTA QELREAYTSISGRINQAEQRTSE IEDQLNEIKRRGVSVCPQPSEDT PRSTARVPKGMVPFRPRVPLVT PPREKKEAPWLACLRTRALRILI DPPSQVWDIVSCDAENETKLEN TLQDIIQENFPNLARQAN\VQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEK\MLRAAREK\GQVT HKAKPIRLTADLSAENLQAR/R TEWGPIFNILKEKNF\QPRISYPA K\LSFISEGEIKYFTDKQMLRDF\ VTTRPALK\ELLKEALN\MERD N\RYQP\LQNHAKFVKTIEAREE TCINLMCQITS
11561	41929	A	11630	1	421	
11562	41930	A	11631	2	415	
11563	41931	A	11632	59	492	GHIGVRPSLHPVTSTTSGNVSPT LARAMASISELACVYLALILHD DEVIIMEVNINTLIKAASVNVE/ PFWPGLFGKALANVNIGSLICN VGAGGPALAAGAAPAGGPAPSI AAASAEEKKMEAKKEESEESD DDMGFGLFTKPVL
11564	41932	A	11633	100	527	PPRTGQRQPLHSARRHGPSVS\E LACI\YSALISARTDEVTVT\EDK INALIKSSPL*MLSPFWPWLCLQ RPLA\NVNIGSL\ICNVRGPVEPA ASQPGA\GPARKVLAPST\AAAP S*RRRKLEAKKRKNPKEVLNDE HGLLVFLN
11565	41933	A	11634	1	675	
11566	41934	A	11635	1	1032	

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11567	41935	A	11636	3	976	HEAKHQMADDAGGS/AGGPEG PGGPWDGKTPLLSGEVFGIVIR GRGSRP/RGRGRGR\GRGARGG KGPRIK/WIGMPVHQVGAALVK DH*RSKFPWKEIYLFSLP\IKGIK DS*FSFLAGPLSKDEGFEGLCPV QKQTRAGQAQQVSRPFVAIGG LQMAHVGSGVLSAPKE\VATG HPVGAIILAKLSIRPRAQKGIWG TKYWQSPNTVP\CKV\TGRCGF VVVRLIP\APRGSGIVSAPVA\K KLLMMAGIDDCYT\SAPGCTAT LG\NFAKGHPLIAIFK\TYKLP*P PDLWK\ETVFTKV\PYQ\EFT\DH LVKDPHPESSVQRDLRLQLVAT
11568	41936	C	11637	279	322	
11569	41937	A	11638	1	107	
11570	41938	C	11639	69	134	
11571	41939	B	11640	223	950	
11572	41940	B	11641	1	684	
11573	41941	A	11642	1	564	EFGTRDNRVLLPLVNPTVFFDI AVD/GVYPLGRVSFELFADKVP KTAENFRALSTGEKGFG\YKGS\ CFHRLFP\GFM\CQGW*L*SHHN GT\GGKSHLWGRNLKDENFI\L KHTGPGILS\MANAG\PNTNGSP VFLTSCTA\KTE\WLDGKH\AGL GKVKEGMNIVEAMER\FGSRN GKTSKKIISIA\DCGTTSN
11574	41942	A	11643	1	877	MSGALDVLQMKEEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYIINLKRTWEKFLLAAR AVVAIENPADVSVISSGNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIQAAFREPRLLVVTDPRA DHQPLTESSYVNLPTIALCNTDS PLRYVD/ICNNKGAHSVGLMW WMLAREVLRMRGTISRGHPWE VMPDLYFYRDPEEIEKEEQAAA EKAVTKEEFQGEWTAPAPEFTA TQPEVADLSEGVQVPSVPIQQF PTDDWSTQPATENWSAAPTAQ ATEWVGATTDWS
11575	41943	A	11644	1	1674	

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11576	41944	A	11645	1	1121	MLEAVLEESPREEAAFSWVMK GNLAAGKTIQAQDRDAVGILSS RTGESMENLQKNLLPKQRRRT RETFTMSGALDVLQMKEEDVL KFLAA\GTH\LGGTNLDFQMEQ YIYKRKSDGIYIINLKRTWEKLL \LAA\RAIVAIENPADVSVISSRN TGPEGLCLKF\AA\ATGATPIAG\ RFTPG\TFT\NQIQ\AAFREATGF LVVTWTPGLD\HQPLTEA\SYV YLPTIA\LCNTDS\PL\RYVDIAIP CNNKGAHSVGLMW\WML\ARE VLRMRG\TISREHPWE\VMPDL YFYRDPEEIEKEEQAAAEKAVT KEEFQGEWTAPAPEFTATQPEV ADWSEGVQVPSVPIQQFPTED WSAQPATEDWSAAPTAQATE WVGATTDWS
11577	41945	A	11648	1	396	
11578	41946	A	11649	1	567	
11579	41947	A	11650	1	226	
11580	41948	A	11651	3	377	
11581	41949	A	11652	19	450	PDRRWSSLDTMNHTGQTFFSPV NSGQPPNYEMLKEEHEVAVLG APHNPAPPTSTVIHIRSETSVPD HVVWSLFNTLFMNPCCLGFIAF AYSVKSRDRKMVGDVTGAQA YASTAK\ALNIWALILGILMTIL LIVIPGLIFQAYG
11582	41950	A	11653	210	2206	
11583	41951	A	11654	450	644	SLRLWVTERTAVTNLPSSSRGV GDKPPVGSPHLFLSLVVAFNPL QSTRNPASASQPQ\PCSAEQPAR RG*AEPALRTVLPIHAEMWLPR LHEFEEHRLVHRCFTLTFVDET DHCAVLPRGAGSGQGGGFERIL SQSPGSLWESC*PGLWLNILSNP PPCPLPAPLGRTAQ
11584	41952	A	11655	66	157	RGTWSIIA*KSQGISWDRFEEVT LCREPFT
11585	41953	A	11656	1	2538	
11586	41954	B	11657	68	1602	
11587	41955	B	11658	1	1464	
11588	41956	A	11659	587	1081	ILSWLTLWSILRLYIVTLTGKIC SLTSEASEATSPPRGTNNSRSVA LAVVTLVWRVCSFIFDSKAFIL AFAFFFSHWFSILPFPPQHGATL WYFWGDFECSRGPRNIHTDDR ARLVPMTERGGPPQGGEPART RSPRQGGRGGMEGGE*YPCPPH LGGQERKPG

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11589	41957	A	11660	180	583	YTEVLKGPDGAENHGTRTT** MHKPH*PIRSTGRKADKQLQQS LR\NKINVQKSQAFLYTNNRQT ESQIMSELPFTIASKRIKYLGIQL TMDVKDLFKENYKPLLKEIRG YKQMGEHSMLMGRKNQYSEN GHTAQ
11590	41958	A	11661	82	159	
11591	41959	A	11662	2	1008	NAAPLQQRNKAGCR/YDLDEL REEGFRRSNFFKLKAEVRTQCK ETKNLEKTLDKWLTRKTSVEK SLNDLMELKTMVQGLRDKCTN FSNGFDQLEERVSVIEEQMNEM KQEKKYREKKDRSMTQKVNK DIQELDSALHQEELIDIYRTVHP KSTEYTFFSAPHRTYFKIDHIVG SKALLSKCKRTEIITNCLSDHSA IKLELRIKKLTQNRSTTWKLNN LLLNDYWVHNEMKAEIKMFFE TNENKDTTYENLWDTFKAVCR GKFRALNVHKRKQERSKIDTLI SQLKELERQELTHSKASRMQEI TKIRAEQKEKETEKNIQKNQRI QELFLLKDQQN
11592	41960	B	11663	1	1529	
11593	41961	B	11664	111	1350	
11594	41962	C	11665	1	2127	
11595	41963	B	11666	1	1350	
11596	41964	A	11667	1	1506	

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11597	41965	A	11668	1	1855	MIIIVPLYSSLGDRVKSCEKKRE RERERRKKERKKERKKERKKE RKKASSKEREEGRKKERRKKL RKKEEKERKKRKKKRREGRKE RKKEKERKEGKKEERKNIPGKR RESTDPLKEMDHRCLLPEMLK GTWWTTPARASGPAVPLLCEF RQWTVDTTSVVPESTHMPGQM TQPIPAPDSHNMDEAGGHYPK QTNTRPENQILHVFTDKWELNT EYKDPKKRTTDTRAYLRVEAT LAADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRSSFVLATL AADWMVPTQTEGRSSFVLATL AADWMVPTQIEGRGRMTPHM AGYSSETKLPEERSGSSICGSPIS AVLQPPLLIPRQTGSGVDLQQT PTDLQLRVLMERSSSPATEQSW MENDFDEMRDEGFRRSNYSEL KEEVQTYCKEVCRGKFKALNA HKRKQETSKIDTLTSQLKELEK QEETHSKASRRQEITKIRAELKE IETQKTLQKINESRSWFFEKINK IHRPLARLIKKKTEKNQINAIKN DKWDITNNLTEIQATIREYYKH LYANKLENLEEMDKFLDTYTL PRL*N/CRQSLIAYQQIKVQDQ MDSQSNSTRGTRRSWYHSF
11598	41966	A	11669	2678	2897	PDGAKKHGKRT\RDERTSFSSEF NQLEERVSVIENQMNEMKREE KFREKRVKRNEQSLQEIWD\M* KDQMRSTS
11599	41967	A	11670	843	2004	NNQCREVLKGVDGAESQGSRT\ REERRSLRSRCDQLEERVSVIED QMNEMKREGKFREKRIKRNEQ SLQEIWDYVKRPNLRLIGVPES DGENGTKLENTLQDIIQENFPN LTRQANIQIQEIQRTPQRYSSRR ATPRHIVVRFTKVEMKEKMLR AAREKGRVTHKGKPIRLTADLS AGTLQARREWGPIFNILKEKNF PPRISYPAKLSFISEGEIKYFTDK QMLTIVHLKTLDIIYMYNIRRPK GGEKKADQEVNSEPRNNIVLET KGDRGPQAPASPGGPPPRRVRR SASGSRAGITFHPVHYLTRRPFA HRFHYQSHGYGVGSVQSAELR HKTNSAARAALRDGGVDCRGR ERGSACQKRSDDEAGGLVLSD LPRVMSGSWEVRR
11600	41968	B	11671	1	3221	

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11601	41969	A	11672	82	160	
11602	41970	A	11673	1	551	AAAMADSGTAGGAALAAPAP GPGSGGPGPRVYFQSPPGAAGE GPGGADDEGPVRRQGKVT\VS YDRKELRKRL\NL\EDWIL*QLN GAFYDCQ\EEEIPELEIDVDELL D\MESD\DARAA\RVKELLVDC YKPTEAFISGLLDKIRGMQKLS TPPEEVRVPDPGRTVAPTGQSL PPDLVATAITGGT
11603	41971	A	11674	362	650	
11604	41972	A	11675	1	651	
11605	41973	A	11676	1	3101	
11606	41974	B	11677	1	2838	
11607	41975	A	11678	1326	1980	TSEASRQSERVDSAALSALSLLS RSSKCRPWGTARVARAGGCLT PLLSRRFLETRPFTGPWDPGLG VTCWCCPPKRRLKSTPRPKFSV CVLGDQQHCDEAKAVDATFEV CLGDQVLSNANGFLSLSAKKY DAFLASESLIKQIPRILGPGLNK AGKFPSLLREEGQAICYSSTNLT *SSLPSSQVLCLAVAVGHVKMT DDELVYNIHLAVNFLVSLLK
11608	41976	A	11679	11	720	EAMSSKVSRDTLYEAVREVLH GTQRKRRKFL\ETVELQISLKNY DPQ\KDKRF\SGT\VRLKSHSPAL SFSVCVLGD\RQH\CD\EAKA\V DIPPHGPSEAAEKTSTKNKKLV QKSWPKKV*MPFLA\SESSDQA RFPRIPRAPGLNKAGK\FP\SLLT HNGKHGGPKVDEVKVPQSRFQ MKKVLCLAVAVGHVKMTD\DE LVFNIHLA\VNFL\VSLLK\KNW QKCSGALYYQEAPMGQSPKRL
11609	41977	A	11680	34	507	
11610	41978	A	11681	407	806	LRVGMLQRSKANGPDDDHLLG ASCTCGPSTGSPSPRLPSLPQRP QKGLLHQ/RATRMKPGNIAKGL WKRLSKGTVMKLWLLTAVPRL SGLLVCPLVHQLLLAFKFLKRF PIFCLWFRAANRHARFSILFKLS RP
11611	41979	A	11682	1	1551	

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11612	41980	A	11683	1	751	MAGYSSETKLPEERSDSSIRGSR KSTVLQTLLLIPRQTGIKKLTQN RSTTWKLNNLLLNDYWVHNE MKAEIKMFFETNENKDTTYQN LWD/YIQSSV*REIYSTKCPQEK AGKIQN\DTLTSQLKELEKQEQ THSKASRRQEITKIRAEPKEIQT QKTLQKINESRSLFFKRINKIDR PLARLIKKKREKNQIDAIKN\EK GISPPIPQNYKLPSENTTNTSMQ IN*KI*KKWINSWTHTPSQE*TR KKLNL
11613	41981	A	11684	49	551	VRATYFHHAPANCTEFVPRQL VSRAENLPQATSLPTEKASRAF RVLLIPRQTRSGVDLQQTPTDL QLRVLIVRRKTNKQKGHPHQN PICTSPLRRSNFFELKEEVRTHG KDAKNLEKRLDKWLTRISSVE KSLNDLMELRTMA*ELCDECTS FSS*FNQLEERVSVI
11614	41982	A	11685	1	1566	MNSLLTGQIPESQQIHRDSSAAT WWKKIYRQKMGNDIEKSEVRG GLTPHTAGYSSETKLPEKRSGS SICGSPISAVLQPPLLIPRQTGSG VDLQQTPTDLKLRVLTVRRKS NKQKGHPHQKPICTSPLSKTKD RSTRQKVNKDIQDLNSALHQA DLIDIYRTLHPKSTEYTFFSAPH HTCSKIDHIVGSKALL/EQM*KN RNYQKLSLRPQCNQ\LELRIKKL TQNHSTTWKLNNLLLNDYWM QKRPLKIQQCFMLKTLNKLGID GTYLKIIRAIYDKPTANIILNGQ KLEAFLLKTGTRQGCPLSPLLL NVVLEVLARAIRQEKEIKGIQL GKEEVKLSLFADDMIVYLENPI VSAQNLPKLISNFSKVSGYKIN VQKSQTFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLKEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRACIAKSILSQKNKAG GITLPEFRLYTRLQ
11615	41983	A	11686	1	4962	
11616	41984	B	11687	101	3772	
11617	41985	B	11688	1	1047	
11618	41986	A	11689	21	287	

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11619	41987	A	11690	131	723	LLEGKLTNRKDIHTKNPSVRH/ RSSKTKERVSAMEDEINEMKRE EKFREKRVKRNEQSLQEIWDYL KRPNLRLIGVPESDGENGTKLE NTLQDIIQENFPNLARQANIQIQ EIQRMPQRYSLRRATPRHIIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLT/ADLSAETLQARRE WGPIFNILKEKNFQPRISYPAKL
11620	41988	A	11691	1	1257	
11621	41989	A	11692	1	759	
11622	41990	B	11693	107	511	
11623	41991	A	11694	170	726	LLEGKLTNRKDIHTETPSVCHH HQRPKDIIQENFPNLARQANIQI QEIQRTPQRYSSRRATPRHIIVR FTK/VEMKEKMLRAAREKGRV THKVKPIRLTADLLAETLQARR EWGLIFNILKEKNFQPRISYPAK LSFISEGEIKYFTDKQMLRDFVT TRPALKELLKETLNVERNNRYQ PLQKHAKL
11624	41992	A	11695	1	569	MAGYSSETKLPEERSGSNICCSP ISAVLQPPLLIPRQTGSGVDLW QTPTDLQLRVLTVRRKINKQKG HPHQNPICTSPSSKTKGQIRAEL KEIETQKALQKINESRNWVFEK INKIDRPPARLIKKKREKNQIDA IKNDRGDITIDPTEIQTTIREYYK HLYANKLENLEERDKFLNTYTL PRLNQEEVESLNRPITGSEIEAII NSLPTKKSPGPDGFTDAFYQRY KEDLVPFLLKLFQSIEKDRILSN SFYEASIFLIPKLGRDTTKKEN* QTERTSTPKPHLYITIIEDQRPD QSRTEGNRDTKSPSKNQ*IQEL/ WFLKRSTKLI\ATSKTNKEEKRE ESNRCNKK**RGYHHRSHRNT NYHQRIL*TPLCK*TRKSGRKG* IPQHIHSPKTKPGRS
11625	41993	A	11696	3	1039	
11626	41994	C	11697	1	1251	
11627	41995	A	11698	1	807	

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11628	41996	A	11699	1	713	MNSLLTGQIPESQQIHRDSSAAT WWKKIYRQKMGNDIEKSEVRG GLTPHTAGYSSETKLPEKRSGS SICGSPISAVLQPPLLIPRQTGSG VDLQQTPTDLKLRVLTVRRKS NKQKGHPHQKPICTSPLSKTKD RSTRQKVNKDIQDLNSALHQA DLIDIYRTLHPKSTEYTFFSAPH HTCSKIDHIVGSKALL/KQM*K NRNYQKLSLRPQCNQTRTQD*E THSKPLNYMETEQPAPE
11629	41997	A	11700	1	1768	MNLSRHLNEVKGELLWSLEWR DPDGGSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGLQQKKMDLKGVFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIKRDKEGHYIMV KGSIQQEELTILNIYAPNTEAPR FIKQVLSDLQRDLDSHIIMGDF NTPISTLDRSMRQKVNKDIQEL KSALQQADLIDIYRTLHPKSTE YTFFSAPHHTYSKIDHIVGSKAL LSKCKRMEIITNCLSDHSAIKLE LRIKKLTQNRSTTWKLNNVLLN DYWVHNKMKAEIKMFFETNG NKDTTYQNLWD/YIQRSV*REI YSTKCPQEKAGRI*N*HPNI\QL KELEKQEQTHSKVSRRQEITKIR AELKEIETQKTLQKINESRSWFF EKFNKIDRRLARLIKKKREKNQ IDAIKNDK\GISPLIPQKYKLPSE NTINTSTQIN*KI*KKWINSSTHT
11630	41998	A	11701	535	666	KGRNIQLNGLVIGTLSN*LKCL KMFFTMPLGYINGGISSDFFLH
11631	41999	A	11702	20	262	
11632	42000	B	11703	1	1254	
11633	42001	A	11704	1	1032	
11634	42002	A	11705	481	1491	
11635	42003	A	11706	2	717	

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11636	42004	A	11707	348	1976	SRVRPVVHLRRAPMVCQGHTT PPVCGSLAGPGDCVHYSVPAG YSSETKLPEERSGSNICCSPISAV LQPQLLIPRRTGSGVDLQQTPT DLQLRVLTVRRKTNKQKGHPH QKPICMSPSSKTKGSNSHITILTL NVNGLNAPIKRHRLANWIKSQ DPSVCCIQETHLTCRDTHRIKIK GWREIYQANGKQKKAGVAILV SDKTDFKPTKIKRDKEGHYMM VKGSIQQEELTTLNIYAPNTGAP RFIKQVLRDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDIQ DLNSALHQVDLIDIYRTLHPKS TEYTFFSALHHIYSKIDHIVGSK ALLSKYKTTEIITNCLSDHSAIK LELRIKKLTQNRSTTWKLNNLL LNDYWVHNKMKAEINTLFETN ENKDTTYQNLWD/YIQSSV*REI HSTKCPQEKAGKI*N*HPNI\QL KELEKQEQTHSKASRRQEITKIR AKLKEIETQKILQKINESRSWFF EKINKIDRPLARPIKKKREKNQI DAIKN\EKGISPLIPQKYKLPSEN TINTSMQIN*KI*KKWINSSTHT PSQD*TRKKLNL*INTSMQIN
11637	42005	A	11708	1124	1717	LLEGKLTNRKDIHTKNPSVRHH HQRPKVDKTTKMGRKQSRKTG NSKNQSASPPPKERSSSPATEQN WTENDFDELREEGFRRSNYSEL KEEVRTNAKEVKNFEKKLDEW ITRITNAEKSLKDLMELKTTAR ELRDECTSPSSQCNQLEERISAM EDKMNEMKREEKFREKRIKRK E\QSLQEIWDYVKRPNLCLIGVP
11638	42006	A	11709	1	3549	
11639	42007	B	11710	209	403	
11640	42008	A	11711	3	248	
11641	42009	A	11712	61	594	IQPLVSVLDEKPSNGVLVHMVK LLIKTFLDGIFDDLMENNVLNT DEIHLIGKCLKFVVSNAENLVD DITETAQTAGKIFREHLWNSKK QLSSVHGSEHEDKALTCHWVG HPGFPEKLKERKKFCGIMVVGL FGFTTDSGKAGADIHGRFLQGN FCNDAVTKAHVEKDF\IAFKSST

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11642	42010	A	11713	1	430	FSAVREDGGCYLWQIYPIKERM DRIRLVLIICNKEFDHLPPRNGA DFAIMEMKKLLEDLGYSVDVE ENLTAR/HNVSQGETGTKGLPIF ITQLIACFQRYSWRCHL\EEVFW KVQQAFESPEATVQMPTIERVS MTRYFYLFPGN
11643	42011	A	11714	3	1195	
11644	42012	A	11715	35	1288	
11645	42013	A	11716	1	1641	
11646	42014	A	11717	1	2933	MVCSAAPLLLLATTLPLLGSPV AQASQPLWPMAKGQTMWAQT STLTLTEEELGQSQAGGESGSG QLLDQENGAGESALVSVYVHL DFPDKTWPPELSRTLTLPAASA SSSPRPLLTGLRLTTECNVNHK GNFYCACLSGYQWNTSICLHYP PCQSLHNHQPCGCLVFSHPEPG YCQLLPPVPGILNLNSQLQMPG DTLSLTLHLSQEATNLSWFLRH PGSPSPILLQPGTQVSVTSSHGQ AALSVSNMSHHWAGE
11647	42015	A	11718	1	357	
11648	42016	A	11719	73	1494	KSSHCIKMGPQIFHKTSELFLPA TSCPSCPDQNEEDVSQTQYKEC CGGGWCSHSIFAVWHFI*RPDA T*FG*SSAYGFVASDQCP*GSS* LYHLWYSYSGSENKQCG*R\AA LGAGFSDKTPAHTVTMACISAN QAMTTGVGLIASGQCDVIVAG GVELMSDVPIRHSRKMRKLML DLNKAKSMGQRLSLISKFRFNF LAPELPAVSEFSTSETMGHSAD RLAAAFAVSRLEQDEYALRSHS LAKKAQDEGLLSDVVPFKVPG KDTVTKDNGIRPSSLEQMAKLK PAFIKPYGTVTAANSSF/LLTDG ASAMLIMAEEKALAMGYKPKA YL/RRDFMYVSQDPKD\HLLLG PTYATPKVLEKAGL\TMNDIDA FEFHEAFSG\QILANFKAMDSD WFAE\NYMG*KKPRFGLPPLWR RFNNWG\GSLSLGHPFGATGCR LVMT\AANRLREEGRASMA*V A\ACAAGGQGHA\MIV\EAYPK
11649	42017	A	11720	1	642	

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11650	42018	A	11721	17	960	KSGARSLQPQFLRAPEDGGPLS LPNAAMARGPKKHLI\RVAA\P KHWMLDKLTGGCA\PRHSPVP HKL\RECLPLIIF\LRNRLKYALT GDEVKKICMQRFIKI\DGKV\RT *YNPTPAGFHGMSSAFDKTGEE NFPS*SIDTKGSAFA\VHPYLTTL EEGQSTSLVPKVKKRSFVGHKK GIPSSWVTS*WPATIR*PRSPSSK VN*YHFRLDLETWQRLLDF\IKF \DTGNL\CMGDWGGA\NLGRN WVLITN\RERHPGSFDPWFHV\K DANGN\SFATRLSNIFVIGKGNK PWISLPRGKGIRLTIAEERDKRL AAKQSSG
11651	42019	A	11722	1	460	
11652	42020	A	11723	1	243	
11653	42021	A	11724	94	311	
11654	42022	A	11725	400	792	
11655	42023	B	11726	473	596	
11656	42024	A	11727	1	1707	
11657	42025	A	11728	3	484	
11658	42026	A	11729	122	253	
11659	42027	A	11730	1	803	RGGRGGAGAAGAELAGPLPSP APFESPGFTPPGPWGSICPAAFA HALHSGTVPARSGRTMARGAA LALLLFGLLGVLVAAPDGGFDL SDALPDNENKKPTAIPKKPSAG DDFDLGDAVVDGENDDPRPPN PPKPMPNPNPNHPSSSGSFS\DA DLADGVSGGEGKGGSDGGGSH RKEGEE\ADAPGVIPGIVGAVV VAVAGAISSFIAYQKK\KLCFK\ EN\AEQGEVDMES\HRNAQRQK PAVQ\RTLLEKIEDCPEKQPQAF GSRVRTAA
11660	42028	A	11731	335	476	
11661	42029	A	11732	2	169	
11662	42030	A	11733	49	289	VPVVQVPAAPGPLPGPATGSCS ASAAPRPPDPPPGHPEGHHGHS P/GVLGFEVGIFSYCQEQPQKCV TIKIFESPPIRRRL
11663	42031	A	11734	22	412	ARVGFLLGQEGKAGARASGPA DDVC\GKGASAIRSHMRASRSP PSPRRCHHHHEATGTASGSAAG GPGAGCVWLCRLALTPSAQDG RNSTFQTYKKEVCLPRHSHPCW MHAAGTTAGGSAVMSACCPSS SR

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11664	42032	A	11735	250	571	KGPRVTQGATVPKRQAPSAGL D/GSPISQFPWSY/DV*AIAILCG QGVT*PLPVSPPGGPAPPESVAL AEWVCSGSRRPLSNSGIARRPIG VIQPLDFLQNWPKPVLRC
11665	42033	B	11736	1	1593	
11666	42034	A	11737	2	1175	
11667	42035	B	11738	206	354	
11668	42036	B	11739	850	1461	
11669	42037	A	11740	2	663	VLLDERSAALDGAKRDGTLAL AAGALCREARAAQVFFLKGGY EAFSASCPELCSKQ/INVSANCP NHFEGHYQYKSILCGMTTHKA DISSWFNEAIDFIDSIKNAGGRV FVHCQAGISRSATICLAYLMRT NRVKLDEAFEFVKQRRSIISPNF SFMGQLLQLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNFPV SIPDHSTNSALSYLQSLITTSSHC
11670	42038	A	11741	1	474	
11671	42039	A	11742	3	1354	WAVCATRVGGAVGGTAKKPR SPEPRVTLLSQSKSGFWFGAER PGGLAFPRKAPPCPWPREQTKS TAGPITLGALRPAMVMEVGTL DAGGLRALLGERAAQCLLLDC RSFFAFNAGHIAGSVNVRFSTIV RRRAKGAMGLEHIVPNAELRG RLLAGAYHAVVLLDERSAALD GAKRDGTLALAAGALCREARA AQVFFLKGGYEAFSASCPELCS KQSTPMGLSLPLSTSVPDSAES GCSSCSTPLYDQGGPVEILPFLY LGSAYHASRKDMLDALGITALI NVSANCPNHFEGHYQYKSIPVE DNHKADISSWFNEAIDFIDSIKN AGGRVFVHCQ\AGISRSATICLA YLMRTNRVKLDEAFEFVKQRR SIISPNFSFMGQLLQF*VPQD/VL VPHCSAEGWEAPDMAVL\DRG T\STTTVFNFPVFIPV\HST\NSAL SLPFRGPINGPFPAG
11672	42040	A	11743	196	1260	
11673	42041	A	11744	5	447	
11674	42042	A	11745	1	328	
11675	42043	A	11746	3	364	
11676	42044	A	11747	1	816	
11677	42045	A	11748	1	1377	

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11678	42046	A	11749	1	989	EGRTVLGGGLGSAAAMASRLL LNNGAKMPILGLGTWKSPPGQ VTEAVKVAIDVGYRHIDCAHV YQNENEVGVAIQEKLREQVVK REELFIVSKLWCTYHEKGLVKG ACQKTLSDLKLDYLDLYLIHWP TGFKPGKEFFPLDESGNVVPSD TNILDTWAAMEELVDEGLVKA IGISNFNHLQVEMILNKPGLKY KPAVNQIECHPYLTQEKLIQYC QSKGIVVTAYSPLGSPDRPWAK PEDPSLLEDPRIKAIAAKHNK\T TAQVLIRFPMQRNLVVIPKSVT PERIAENFKVFDFELSSQD\MTT LLSY\NRNWRVCALLSCTSHKD
11679	42047	A	11750	1	855	
11680	42048	A	11751	2	367	
11681	42049	A	11752	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLSAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
11682	42050	A	11753	1	1536	
11683	42051	A	11754	1	2541	
11684	42052	A	11755	1	1788	
11685	42053	B	11756	1	1014	
11686	42054	A	11757	1	777	
11687	42055	A	11758	1	1029	
11688	42056	A	11759	1	2052	
11689	42057	A	11760	1	1392	
11690	42058	A	11761	1	993	
11691	42059	A	11762	1	1240	PTDPAAEGPCLLDAKTNKRKGP STPILPFCPSPFIRGPKVDSTHGA WGQKQHR*TGIF*RSRAPSPP\P\ KEHGSSPATEQSWMENDFDEL REEGFRRI\NYSELKEEARTHGK EVINLEKK\LDEWITRITNAEKC LK\ELMELE\TKA\RELREECRS\ LRSRRNQLEERVSAMEDEMNE MK\QEEKFREKKNKKK*TKAL KELWDYVKRP\NLRLIGIPESDE ENGTKLENTLQDIIQENFPNIAR QAN\VQIRGNYRERPQRLPPRG RATPRTH/IIVRFTKVGNGREKM FKGQPGGKGR\VTLKGKPITLTT ADLSAETSTSQKTEWGPIFNILE GKEFSNPEISYLSQT*AFISGREE LNSFYRTSQMLRDFCHHQASRL P*KSTRPALKELLKEEALKHGK GNNPVPSHLQKFIA

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11692	42060	A	11763	1	1917	
11693	42061	A	11764	268	307	AHHTHLCLLTESPPEGR*VCWG CGLGWGVVLSLVCPP
11694	42062	A	11765	2	349	
11695	42063	B	11766	1	1734	
11696	42064	A	11767	1	603	
11697	42065	A	11768	1	420	
11698	42066	A	11769	115	796	EWSSVRRSLVEKRALRRPHPQC LCFRMKTILSNQT\VDIPENVD\I TLKGRTVIVKGP/REGTLRRDFQ SPSMENFTFLERKKKRLRVDK WWGNRKE\LATVRTICSHVQN MIKGVTLGFRYKMRSV\YAHFP HQPLLSRGNGSLV\EI\RNFFG*K NISARVRMRP\GVA\CSV\SQAQ KGEF/ISLEGNDI\ELVSNSA\ALI QQATT\VKNKDIRKFLDGIYVFE KGTVQQADE
11699	42067	A	11770	1	295	ASTAGVSYYVAQAGLKLLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFM YFAGTWMKLETIILSKLSQGQK TKHRMFSLVGGN
11700	42068	A	11771	3	342	
11701	42069	A	11772	1	182	
11702	42070	A	11773	1	439	
11703	42071	A	11774	1	325	
11704	42072	A	11775	2	91	
11705	42073	A	11776	167	861	IWAILADPRMAQGKLRMEIGTK LRCLIWTVHKGVHWVTFWWV ERSQTGNLEVRRLWLGLLTHL HSGVNSLFTRARIWNPSMIDW/I KKMWHIYTMEYYAAIKKNQF MSFAGTWMKLSAPAAPTVLFL ASFTNHYNLRASLLVESCLAPS YTSVEPRFSIPQSLTPARGSSDG HTCFSHQSHDSLLICADSTHFW LSAHIWIQANAPPVPRAPSELSL KTRLKCSPQLNLRRPP
11706	42074	A	11777	1	660	
11707	42075	B	11778	1	2633	
11708	42076	A	11779	1	2985	
11709	42077	A	11780	398	605	
11710	42078	A	11781	204	585	VTMCDRKAVIKNADMSEEMH QDSVECATQALEKYNIEKDIAA HIKKEFDKKYNPTW\HCI\VGEG TFGSLC*HIETKHFHLTSYLGAK WAISFCFKFWFKRHGTVATHPV IPFQKQGIAALNFQLPED
11711	42079	A	11782	1	810	
11712	42080	A	11783	188	534	

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11713	42081	A	11784	1	1188	
11714	42082	A	11785	1	1137	
11715	42083	A	11786	19	428	ERRNSGNMALRVERSVRAVLC SLHVVLAPAAPCLSRPWQLGM GAVW\YCNLPEVGTKLNKQDE FGALERVKAASELYSPLSGEVT EINEALAENPGLVNKSRYEDG WLIKMTLSNPS*LDELMSEEAY EKYIKSIEE
11716	42084	A	11787	66	631	RRDPRTPANMALRVVRSVRAL LCTLRAVPLPA\APCPPRPWQLG VGAVRTLRTGP\ALLSVRKFTE KHEWVTTENGIGTVGI\SNFAQ\ EALGDVVYCSLPEVGTKI*TKP SWSLVLLE\SVKAASELYSPLSG \EVTEIN\EAL\AENPGTCKTNFC Y\EDGWLIKMTLSNPSE\LDELM SEEAYEKYIKSIEE
11717	42085	B	11788	46	743	
11718	42086	A	11789	209	401	MKPPVRSLSTPPRSIIMGSSATEI EELENTTFKYLTGEQTEKMWQ RLKGMEIKKLN*G
11719	42087	A	11790	135	313	
11720	42088	A	11791	1	624	
11721	42089	C	11792	81	299	
11722	42090	A	11793	5	166	SPVMMSFFLFVCLLTT*RSPSSS SSSSSSSSSSSSSSSSSSSSPSPSSSFS GSVV
11723	42091	A	11794	3	173	
11724	42092	A	11795	169	291	SCNSSILSFLSLSLVADPQIATYR /S*CSRLGHKGTLLPGS
11725	42093	C	11796	1	429	
11726	42094	A	11797	1	279	
11727	42095	A	11798	3	376	
11728	42096	B	11799	1	736	
11729	42097	A	11800	753	2455	
11730	42098	A	11801	1	312	
11731	42099	A	11802	48	397	
11732	42100	A	11803	51	286	
11733	42101	A	11804	1	420	
11734	42102	A	11805	11	537	PDRPTRPCRQCARSFRRKLKAA VGVEGPSLSSGELGTRVPAAPS PTTRPRAMAFCLPSFACI\YSALI LHDDE\VT\VTEDKI\NALIKSSR V*MLSPFWPGLFAKAL\ANVN\ MGSLICNVGAGGPCCPASWVL QPAGRSLPPPLLAASSLREKKV\ EAKKEGFRGSFD*LTWGFGSF
11735	42103	A	11806	114	399	

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11736	42104	A	11807	3	599	AIRRLRISAREEERENQPRLLPL SLGAGGGVGGFVQQWPRFKAR DLRGKKKEEL\LKQL\DDLKVE LVPSARRQKRQGGAAS\KLSKI R\VVRKSIAPCSPRLFTQTQKEN LRKFYKGKKYKPL\DLRPKKTR AMRRRLNKHEENL\RTKKQQR KERLYPLRKYAVKALGGALSIK HKENLKTKKQQRKERLYPLRK YAVKA
11737	42105	A	11808	226	370	AGSP*FPQFSEA*RRGALGSGA DQDLSHPRITIETLTSCRSLQTSS PR
11738	42106	A	11809	3	7964	RGSGSSKFEPRSRSASVLAPSAL GPPNTSPRQLVAHCALPATRMP VTEKDLAEDAPWKKIQQNTFT RWCNEHLKCVNKRIGNLQTDL SDGLRLIALLEVLSQKRMYRKY HQRPTFRQMQLENVSVALEFL DRESIKLVSIDSKAIVDGNLKLI LGLVWTLILHYSISMPVWEDEG DDDAKKQTPKQRLLGWIQNKI PYLPITNFNQNWQDGKALGAL VDSCAPGLCPDWESWDPQKPV DNAREAMQQADDWLGVP
11739	42107	A	11810	1	636	
11740	42108	A	11811	3	261	QKKPLKQPKKQA*EMDEVRAG AEALAGAGALGDRPELNTLCLS P\EDKAFKQKQKEEQKKLEELK AKA\AGKGPLAT\GGIKKSGKK
11741	42109	A	11812	1	621	
11742	42110	A	11813	1	1024	
11743	42111	A	11814	174	332	SHCLANAPGDVKVRNDPESPRE L*HL*R*RINYTRWKRSI*EEWC QGHSWRG
11744	42112	A	11815	1	1323	
11745	42113	A	11816	1	2322	
11746	42114	A	11817	1	336	
11747	42115	A	11818	22	391	PPPPAAKTRRKKVLATKVLGTV KWFNVRNGYGFINRNDTKEDV FVHQTAIKKNNPRK\YLRSVG\D GETVEFDV\VEGEKGAEAANVT GPDGVPV/EKGSRYAA\DRRR\Y RRCY\YDR\RRGPPPEYW
11748	42116	A	11819	433	866	PPPPAAIDAEKKVLATKVLGTV KWFNVRNGYGFINRNDTKEDV FVHQTAIKKNNPRKYL\RSVGD GETVEFDVVEGEKGAEA\ANVT GPDGVPVE\GSRYAADRRRYRR \GYYGKARWPFPANYAGGGRR RKGAAQVEGFLPPLPLD

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11749	42117	A	11820	63	484	
11750	42118	A	11821	1	819	
11751	42119	A	11822	150	463	
11752	42120	A	11823	63	594	FAKLPNPKGKGGEATRYMFSR PF*ENHGVVPLGHNN*RF\YKK GDIVDIQGEWGTLFQKGNCPH KVVTHGQNLEGVLPMVTPAML VGHLL*TNQF*GKVFS\KRINVR IEPIK\HSKSR\DSFLK\RVKEND QKKKEAKEKGTWVQLKRQPA\ PPREAHFVRTNGKEPELLEPIPY
11753	42121	A	11824	2	1376	
11754	42122	C	11825	132	341	
11755	42123	A	11826	155	245	
11756	42124	A	11827	3	293	
11757	42125	A	11828	204	467	LRAPHVACSRCNQGPCMENCL NTDQTHTQTQRQG*EEKSSSSK/ PISSLMEYYKRSQCSVKSKARS VF*LKLRAQAQLLQETKKPVFR L
11758	42126	A	11829	1	768	
11759	42127	A	11830	348	568	REISYKERIGM*MPPSVILNSYV KSMLETYPHPLLRGVVAPGPLK KGFLTESLLALPDPSFSGRMTSF KITPV
11760	42128	A	11831	1	840	
11761	42129	A	11832	2	216	
11762	42130	A	11833	1	726	
11763	42131	A	11834	3	3231	PGGWLRRALPGRERLQSPVHA VPPQHGTSHSRLLVTWPGAGR DQDFSSPPLLLLGETDHLHLDL PLSPLPTSDELFLPGICDPYVKL SLYVADENRELALVQTKTIKKT LNPKWNEEFYFRVNPSNHRLLF EVFDENRLTRDDFLGQVDVPLS HLPTEDPTMERPYTFKDFLLRP RSHKSRVKGFLRLKMAYMPKN GGQDEENSDQRDDMEHGWEV VDSNDSASQHQEELPPPPLPPG WEEKVDNLGRTYYVNHN
11764	42132	A	11835	1	624	
11765	42133	A	11836	2	361	
11766	42134	A	11837	3	432	NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLLARAEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIAHDVDPIELV VFLPALCRKMGVPYCIIKGKAR LGRLVHRKTCTTVAFT
11767	42135	A	11838	1	684	

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11768	42136	A	11839	9	247	AVTSDEPKGKKAKAKKVAPAP AVVKNQEAKKVVDPLFEKRHK N\FGIGQDIQPKRASPRLCELPR\ YIRLQRQRAILYK\RLKGPFCDY PGFTRALDRQTV*SSLLKL\AHK YRP\ETKQEKK\QRLFARAREEG VLAKGDVPNERDPPV\LRARSL TPFHHPWVEKQEKLQLVVNWH TDV\DPI\ELVVLLALPLCREKW GVP\YCNYRREKARLWDRLVP QERPCTTCPPFTQGELRKTKGG FWLKLGWKLIRTQFTIDQILMR SRRH\WG\GNVLG\PKSVGS*SP KLEK\AKAKELAH*TG
11769	42137	A	11840	1	273	
11770	42138	A	11841	1	218	
11771	42139	A	11842	1	1522	
11772	42140	A	11843	136	441	
11773	42141	A	11844	24	274	SRQAWHEAASASARRRGTRSP ALSPARAPAGPIWTNARRSARA NSVSPAAAPPPRRPVSLS\DPGE SCTRDPRAPDPCGPFRCC
11774	42142	A	11845	194	365	
11775	42143	A	11846	1	782	LLVVGTTVVVYFPNGRFKEFM SRHVHLMCYRICVRALTAIITY HDRENRPRNGGICVANHTSPID VIILASDGYYAMVGQVHGGLM GVIQRAMVKACPHVWFERSEV KDRHLVVK\RLTEHVQDKSKLP ILIFPEGTCINNTSVMMFKKGSF EIGATVYPVAIKYDPQFGDAFW NSSKYGMVTYLLRMMTSWAIV CSVWYLPPID*ERQIEDAVQFA NRVKSAIARQGGLVDLLWDGG LKREKVKDTFKEEQQKLYSKM
11776	42144	A	11847	3	916	
11777	42145	A	11848	13	473	DPPTDSLSPDGGSIELEFYLAPE PFSMPSLLGAPPYSGLGGVGDP YAPLMVLMCRVCLEDKPIKPLP CCKKAVCEECLKVYLSAQIQCP TCQFVWC*CAGCAWKTSPSSPC LAARRPCARSASKST/SSAQIQC PTCQFVWCFKCHSPWHEGVNC KEYKKGDKLLRHWASEIEHGQ RNAQKCPKCKIHIQRTEGCDH MT
11778	42146	A	11849	92	1103	
11779	42147	A	11850	1	516	
11780	42148	A	11851	1	642	
11781	42149	B	11852	200	608	

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11782	42150	A	11853	1	1856	MEETGMCEGHGASPGMEASSG EREKRGTGEASPGDREKRGTGE ASSGEREKRRTGEASSGDREKR GTGKASSGEREKRGTGEASYG EREKRGTGAAGGQESCAHCGG WLMPRAKPSTHRETNPRGTEA TAMAMDHVGQQADTTDSTDG SQWDPSEHSPNCGIREVGAGDP DTQQTGRHHCYYPAKETNEKT NTNRNSNTFIEQLLHAKQQRGN SGVPFKPGHMVRALTTNALSW AKLYPDPWCLRMGGTGNEVFE NEIKTGSCWIKEQEGQPRPQSP RSQVRPEADPGPSPLTKMSAEN EYRPPSPPKLAAERDKPSPRLRP RGVPWRRESRVRAGRECALLR VAAEGARPPPAGMSYDRAITVF SPDGHLFQVEYAQEAVK\RGST AVGVRGRDIVVLGVEKKSVAK LQDHRPVRKICT\LHDN\VCMA FAGL/TPADARIVIQTGPGVEFQ\ SHRA*T\VEGPRVTVE\YITPLTF ASLKASVYTQSKWGARPFG\IS GPHRGFSTFDGTP*LYQTDPSG TY\HAWKA\NSIG\RGAKSSARS SWEKN\YTDKAIETDDL\TI\KLV IKALLEVVQSGGKNIE\LAVMR RDQSLKI\LNPEEIEKYVA\EIEK EKEEN\EKKKQKKAS
11783	42151	A	11854	12	432	

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11784	42152	A	11855	1	1775	MSYPADDYESEAAYDPYAYPS DYDMHTGDPKQDLAYERQYE QQTYQVIPEVIKNFIQYFHKTVS DLIDQKVYELQASRVSSDVIDQ KVYEIQDIYENSWTKLTERFFK NTPWPEAEAIAPQVGNDAVFLI LYKELYYRHIYAKVSGGPSLEQ RFESYYNYCNLFNYILNADGPA PLELPNQWLWDIIDEFIYQFQSF SQYRCKTAKKSEEEIDFLRSNP KIWNVHSVLNVLHSLVDKSNIN RQLEVYTSGGDPESVAGEYGR HSLYKMLGYFSLVGLLRLHSLL GDYYQAIKVLENIELNKKSMYS RVPRVPRSPTYYYVGFAYLMM RRY\QDAIRVFANILLYIQRTKS MF\QRTTYKYEMINKQNEQMH ALLAIAL\TMYPMR\IDESIHLQL REKYG\DKMLRM\QKGDPQVY EELFSYSCPKFL\SPVVPNYDNI\ HPN\YHKE\PFLQ\QLK\VFSDEV Q\QQAQLSTIRSFLKLLHPPCLV AKPGLASLDLTEQEF\RIQLLVF KHKMKNLRVDSAVSQALDGEF QSASEVDFYI\DKDMI\HIADTK VARRYGDFFIRQI\HKF\EELNPN P*RRMG\QRPWMIFTTHSGNLV
11785	42153	B	11856	1	537	
11786	42154	A	11857	98	334	WATERWKGRKNHEISWKCFPG KAIS*MRSSKQMKPNFPRCSSIT VLSVRGMVLFLTLACPRFKMSS RTDFRFGNPQVT
11787	42155	A	11858	4	422	
11788	42156	B	11859	1	2567	
11789	42157	A	11860	2	364	
11790	42158	A	11861	1	501	
11791	42159	A	11862	1	402	
11792	42160	C	11863	30	673	
11793	42161	C	11864	195	1263	
11794	42162	A	11865	3	648	
11795	42163	A	11866	200	420	ILPSALRPPNPNWNVG/YVQTQ LVSKPLSLPTGIPCSTTSNILKPV ITKDARLHRVIVHGWGIKGTIPI AKIAIS

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11796	42164	A	11867	1	502	MQLPGRGHSFVCKANAGSTQA RQGASAGVAGCRGWLNYAAS EQIVLRVPHMRCEIPHKCVRRK SRIRPHSPFRLRNCWKGRSVRA FSLLRQLAKGGCAARRLSWVT PGFSQSRRCKTTASAKLACLQV RAQSEDISTVPIHYAYNMTRVG RMQMLGKYNPQSAKLVREAIL PTKATLDLSNQNNEDFSAFQLG LAQALHIKVHTMTREVMSDEL TKLLEGNLKPAIDMMVEFNTT GSLPENAVDVLNTALGDRKSF VALMALMEYSRYLVAEDKSAF VTPLYVEADGVTNGPINAMML MTGGLFTPDWIRNIAKGGL*FQ YTFTFNRNSRSQCFHIFQETSKK FFSMCF*SSLLTKHCHSSRDVW VFSTSFQHIRHTLIDGISNRTNQ LTCNTTSTRTIDGNSQRVLSNTT
11797	42165	C	11868	1	3831	
11798	42166	A	11869	1	5370	
11799	42167	A	11870	1	3999	
11800	42168	B	11871	1	12036	
11801	42169	B	11872	1	16395	
11802	42170	A	11873	1	19997	
11803	42171	A	11874	1	70	
11804	42172	A	11875	44	613	AGTHLRPFSPSLSAAMALRYPM AVGLNKGHKVTKNVSKPRHSR RR\GRL\TKHTKFVRDMIREVCG FAPYERRAMELLKVSKDKRAL KFIKKRVGTHIRAKRKREELSN\ VLAAMRKAAAKKDLGPSPCPL PEIKDKLDRSPGSPAVRGWVW VCRGPAVPCLVPALSHTLSGCC LVVNQKPWPAHPSRGSR
11805	42173	A	11876	1	150	FRGRCCVQRYRGCTLASA/CLL VGEAEAPSPVDPLERSRPYAVL RGQNLE
11806	42174	A	11877	447	725	
11807	42175	A	11878	2	206	RPVAYLLLQGWGRCCVQRYRG CTLASA/CLLVGEAEAPSPVDPL ERSRPYAVLRGQNLDQTLH*ST HQA
11808	42176	A	11879	1	413	
11809	42177	A	11880	122	268	
11810	42178	A	11881	1	555	

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11811	42179	A	11882	221	419	LQTILQGYSNQNSMVLVPKQR YRPMEQNRALRNNAAYLQKSP *ADKQLQQ/ECQDTKSMCKNH KHSYTPITDKQRAKSRVNSHSQ LLQRE*NT*ESNLQGA*RTSSRR TTNHCSMK*KRIQTNGRTFHAH G
11812	42180	A	11883	1	2464	MDEFLNTYTLPRLNQEEVESLN RPITGSEIVAIINSLPRKKSPGPD GFTAEFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIILIPKPG RDTTIKENFRPISLMNIDAKILN KIILANRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHINRT KDKNHMIISTDAEKAFDKIQQP FMLKTLKKFGIDGTYLKIRIKYL GIQLTRDVKDLFKENYKPLLNE IKEDTKKWKNIPCSWVGRINIM
11813	42181	A	11884	2104	2637	MFQRGHISQWWVVVGALTVFT SVLDTDPMRDNKRSGSEILPFC REHGTSFTYNHAHSPLSCSPSCL FSGLALFSPENNSGFLCMTLPAS FTAGNRLFSSAGQPWWIQQGF KAHAKARRLILLAFHHYCCRPF LAVELKPSPVSTPTFLFA*LLPP CSVPGAILHESFGEAITWLDAE
11814	42182	A	11885	69	417	QTHSQHYTEWGKVESIPPENW NNTRMPIFTISIQHIIRSSSESNQT RERNQGHPNG*RGSQTVAFC*R YDRIPRKP*RLIQKTPRTASAAD TQANRVWSGPPASSNRPAAEGP DC
11815	42183	A	11886	376	597	ENKIPRNPTYKGCEGPLQGELQ TAAQGNKRGHKHMEKHSRLM DRKNQYPSAADTQANRVWSGP PANSNRPAAEGPD*PGQNFQYH VE
11816	42184	A	11887	5	292	LTVSCPCSRMLFLTTDVLLPLM FIKKLGANVASPSSKKPLFVIRL VITTLLPLACGTLPTSSVSRTTFF RTMLPQA\PEFAPPSTGTESHYY CCIW
11817	42185	A	11888	320	596	YPGKQGLEWTSSKLQQTCRKY RERHKDTP/TRRATPR/RHNCQV HQS*NEGKNVKGSQRERSGYS QREAHQTNSRSLGRNSTSQKRV GASIQRS
11818	42186	A	11889	3	239	EASRGRIRQQHLPFCNICCSAAS TGDTQANRVWSGPPANSNRPA AEGLDC*KEN*QTERTSTPKPD LYITIIKDQSLL

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11819	42187	A	11890	3	278	EASRGRIRQQHLPFCNICCSAAS TGDTQANRVWSGPPANSNRPA AEGLDC*KEN*QTERTSTPKPD LYITIIKDQRLIPGLFTSPWISARI
11820	42188	B	11891	394	1213	
11821	42189	A	11892	856	1217	VDRSRLQKVSNNKLVQAKGGC SNPLQGS*KLDNPKDANS/RQQ PERTWKWIFPQPHR*GAFGPRH C*ESHLYQFGLDLLNSAGSGIG KNEVQEQKRAEVGARAAPEKE LPEALSWFLKVLW
11822	42190	B	11893	1	894	
11823	42191	B	11894	93	938	
11824	42192	A	11895	149	508	LLEGKLTNKKDIHIKTPSVRHH HQRPKPKISLS**ATSAKSQDTK SMCKNHKHSYTTITDKQRA\NH E*TPIHNCFKESKIPRNPTYKRC *G/RSSRRTANHCSRK*KRTQTN GRTFHTHG
11825	42193	C	11896	1	1257	
11826	42194	A	11897	183	1065	YWRCNGFLS*\YAEAAEEIVDCI TESLSILKTPLPKKMNEEMLCQ EFGRFGPLASVKIMWPRTDEER ARERNCGFVAFMNRRDAERAL KNLNATAFRPALSHFPSLPMDT TSQIPKH\PVTVSSTNKLILIIKTH FQAQSSLNQNIHPMDPSHGIQY SAFSPSTPNPSHPALP*PLAIQVH HAVCDGFHVGRMLNELQQYC DEWQRDKLEEILRGLTPRKNDI GDAMVFCLNNAEAAEEIVDCIT ESLSILKTPLPKKMNEEMLCQE FGRFGPLASVKIMWPRTDEERA RERNCGFVAFMNRRDAERALK NLNATAFRPALSHFPSLPMDTT SQIPKHSSHRQFNKQAHSDHQD SLSGPVQSESKYPSHGSIPWDSI LSLLTLNTQPIPPSLALTHMEME SGLHFHCPFTASPPSAVPPPELE KTTLKFIWNQKRARIANSILSQ KNKAGGITLPDFKLYYKATVT KTAWTGSPTAIRQARTTRQEKE MKGIQIGKEEVKLSLFTDDVNL QVRENK
11827	42195	C	11898	138	644	

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11828	42196	A	11899	2	3088	ADKTPGGSQKASSKTRSSDVHS SGSSDAHMDASGPSDSDMPSRT RPKSPRKHNYRNESARESLCDS PHQNLSRPLLENKLKAFSIGKM STAKRTLSKKEQEELKKKEDEK AAAEIYEEFLAAFEGSDGNKVK TFVRGGVVNAAKEEHETDEKR GKIYKPSSRFADQKNPPNQSSN ERPPSLLVIETKKPPLKKGEKEK KKSNLELFKEELKQIQEERDER HKTKGRLSRFEPPQSDSDGQRR SMDAPSRRNRSSG
11829	42197	C	11900	413	823	
11830	42198	A	11901	263	1246	NPGKQGLEWTSSQTPADLQLR VLTVRRNTNKQKGHPHQNPICT SPSSKTKEVENLEKRLDKWLTR LTNVEKSLNDLMELKTMAREL HDEGTSFSSQFDQLEERVPVME DQMNEMKQEEKFREKRMKRN EQSLQEIRDYVKRPNLRLIGVPE SDGE\KEPSWKTLCRILSRRTSP A*QGRPTFKFRKYRECHKDTPQ GEQLQDT*LSDSPKLK*RKKY* GQPERKKYRLPSANT\KTSLRK* TRKSRRNG*ITGHIHPPKTKPGR S*IPE*TNSRL*N*GNN**PANQK KSRTRRIHSQILPEAQRGAGTIP SETIPINGKRGNPPKLIL
11831	42199	B	11902	67	2584	
11832	42200	A	11903	1	3793	MSDAEDERFLQFQLRYRVYLT GDCRTVGAGQWVQRTEREPKQ GEALPHPGSARGWGVPFPRDD GWHLENRVTPTLILRFSHSLSK QHTRRPYSAPGSEGPTPTEPCSL LAQQSEIKLQDGSEAGGGPLLLI PRQTGSGVDLRQTPTDMQLRV LTVRRKTNKQKGQPHQNPICTS PSSKTKAPHHTYSKTDHIVGSK ALLSKCKRSEIITNCLSDHSAIK LELRIKKRIQNRSTTWKLNNLL LNDYCVHNEIKAEI
11833	42201	A	11904	1	441	

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11834	42202	A	11905	312	3705	FIMPAVASVPKELYLSSSLKDL NKKTEVKPEKISTKSYVHSALK IFKTAEECRLDRDEERAYVLYM KYVTVYNLIKKRPDFKQQQDY FHSILGPGNIKKAVEEAERLSES LKLRYEEAEVRKKLEEKDRQE EAQRLQQKRQETGREDGGTLA KGSLENVLDSKDKTQKSNGEK NEKCETKEKGAITAKELYTMM TDKNISLIIMDARRMQDYQDSC ILHSLSVPEEAISPGVTASWIEA HLPDDSKDTWKKRGNV
11835	42203	A	11906	1	609	
11836	42204	A	11907	3	755	LRVDNAPAHASGLFFCAGAAG TVLFAMAPSRNGMVLKPHFHK DWQR\RVATWFNQPAR\KIRR\R RPRQAKARRIGPAPRGGGPIRPI VRCPTGRVHNGSWRPGRGFQP GRSSRVAGHSPRKVAPDPSGIS VDPK\RRETSSHGSPLQAQRAS GLKE\YRSQTQSSSPRKPSAS/PL *GDSSAEELKL\ATQ\LTGPVMP VRNVYKKEKARVI\TEEV\KNF KAFASLRMARA\NARLFGIRAK RAKEAAEQDVEKKK
11837	42205	A	11908	1	327	
11838	42206	A	11909	1	756	
11839	42207	A	11910	1	219	
11840	42208	A	11911	2	227	
11841	42209	A	11912	1	567	
11842	42210	B	11913	99	799	
11843	42211	A	11914	61	342	
11844	42212	B	11915	1	945	
11845	42213	A	11916	92	133	DPPSQKLKTLRKD*TNG*LQ*P MKRSP*MT*WS*KP*HENYVTH AQASVPDSINWKKGYQ*LKIK* MK*SKKRSLEKKE*KETNKASK KYGTM*KD
11846	42214	B	11917	1	368	
11847	42215	B	11918	1	106	
11848	42216	A	11919	1	705	
11849	42217	B	11920	1	834	
11850	42218	B	11921	1	1305	
11851	42219	A	11922	1	1187	
11852	42220	A	11923	228	619	

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11853	42221	A	11924	1499	2238	KGKKKVINQISLGQRMRLSQSS HGKVQACQVPFHPNAPPAVQF QSRELQSGSRPRSCGEKATRCL RQGPREVPLPKNAWA*QRKQE KKRSRKGS/GREPGLRRPPNAQ ARDRSSRAPATHRKELKPEREH ISCSRSHIRYQEWSVLRDTVHR NLVLDTKRHPALILVEYKERTS SPATEQSCMENDFDELREEGFR RSVITNFSELKEDVQTHHKEAK NLEKRLDKWLTRINSVEKSLND WMELKTMA
11854	42222	A	11925	699	796	
11855	42223	A	11926	1029	1223	ERELPDPLRFPSEGNASALLSAS RTVRASTDLRPLSGTP*RDEPGT SDGNAEITRLLRRSGWEL
11856	42224	A	11927	186	1597	
11857	42225	A	11928	1	1200	
11858	42226	A	11929	1	600	
11859	42227	A	11930	1	663	
11860	42228	A	11931	908	1331	GDMRGRREGGFGLGRRTAMRC GCSPGIVREADNLVKLSRPSTV RVTRSSASVMVLTMPLAPATFL RVNCWAG/RGR/C*SQNETVSR TRCEEGR**KDYRVEEQRLRKN WDLARPGEEQLAPSPEKRDLPL RVKDQGRHPCVV
11861	42229	A	11932	1	1707	
11862	42230	A	11933	1	1012	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQPDLIDIYGTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITSYLSDHSAI KLELRIQNLTQNHSTTWKLNNL LLNDYWLHNEMKAEIKMFFET NENKDTTYQNLWDAFK/RSV*R EIYSTKCPQEKAGKIQN*HPNID QQN**TTSKANKEKKREDSNRC NKK**RGYHHRSHRNANYHQR ILQ/YTSMQIN*KI*KKWINSSTH TLSQD*TRKKLNL*IDQ*QELKL WQ*SIAYQPKRVQDQMDSQPN STRVASKRIKYLGIQLTRM*RTS SRRTTNHCSMK*KRIQTNGRTF HAHG
11863	42231	C	11934	1	1788	
11864	42232	A	11935	550	827	DVSWAGRSEDHRWIFLKEQRT GGPPK/ERSRSESRHQISCMCAA STWMERTAYGGSHRELLLQQL PQEHTRKTLPLQQTSAWTYRLF HTSCEI

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11865	42233	A	11936	584	1094	NWIPSLHLTQKLIQDGLKT*ML DLKP*KP*KKT*AIPFRT*AWAR TSCLKHQKQWQQKPKLTNGI*L N*RVSA/PAKETTISMN/EATYR MGENFCNLLI*QRANIQNLQ*T QTNLQEKNKQPHQKVGKGHEQ TLLKKRHLCSQKTHEKMLIITG HQRNANQNHNEMPFHTS
11866	42234	A	11937	797	1044	EESIS*KWPYCPR*FVDSMPSPS SYR*VSSQNWKKLL*SSYGTKQ EPTLPSQS*AKRTKLEASHYLTS NYTTRLQ*PKQHGT
11867	42235	A	11938	176	374	LTNQKKSRTRWIHSQILSEVQR GADKQPNRE*TPIHNCFKENKIP RNPTYKGCEGPLQGELQTTAQ
11868	42236	B	11939	1	1843	
11869	42237	A	11940	3227	3391	DPLPGQRQLLLQKQRRP*TQAG LLSFQPGPQPHGSVPPTLSQPW LPGGWPELSG
11870	42238	B	11941	1	1479	
11871	42239	B	11942	1	2097	
11872	42240	A	11943	654	1341	KNRNYNKLSLRPQCNQTRTQD *ESHSKPLNYMETEQPAPE*LL GT*RNEGRNKDVL*NQREQRH HIPESLGRIQSSV*REIYSTKCLQ E/I/MQERSKIDTLTSQLKELEKQ EQTHSKASRRQE/DN*NQSRTE GNRDTKNPSKNQ*IQELVF*KD QQN**TASKTNKEKKREESNRH NKK**RGYHHRSHRNTNYHQRI LQTPLRK*TRKSRRNGYIPRHIH SPKTKTGRS
11873	42241	A	11944	471	611	
11874	42242	A	11945	1	585	
11875	42243	A	11946	3	1029	GRQHGGSQRMGGTASARASSG RLAPRGRGAFAFRRRCPSPRRW RLTCGPAAVEHSFCHNVGPGV RATADKYTCMFTYASQGGTNE QWQMSLGTSEDHQ\HFT\CTIW RPPRGKSYL\YFT\QFKAEVAGR LRFEYRHGLTFKAA/SLKRESD VPLENLRNFEVNQNSSGLTRPG GISKAELSKLVIVGQGIRALSCD QQPLLRGGTFSSPVKLKGACVP ERAQHITGFLGGTLKFSTWADV ALSRRGFSGWLKPWGREQRVQ GPPGSQQLFRFPLPVKLFWTQD RRSRGTKRVGNMGAMLGKAA MLPPTSSRASFMSLQNCFPMFT QGTSFQMNWEEMKCFFIFK
11876	42244	A	11947	1	1206	

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11877	42245	A	11948	1	654	
11878	42246	A	11949	849	1089	SPEGKHYRCYLVHMPSDTERSS L*MRPRAGRSSAEGPGCRQRSL ALDHMVQQAQRCWRYQWWR RFSKEFNQWWRRFSEEL
11879	42247	A	11950	5	1376	
11880	42248	A	11951	2	278	VPQPDTRKGSVLKWISKRGKPL AVEIEESHCL\CLPLRTECLGIKP \IVHLFSCTRPVIVPSLELNYDV DSIAHMFVADLLLMITLPSYDIP
11881	42249	A	11952	3	267	
11882	42250	A	11953	1152	1338	FKRGQYGRLLRPRFHHGQILYA RRQGA\EPLAIQVHHAVCDGFH VGRMLNELQQYCDEWQGGA
11883	42251	A	11954	394	615	ASDPLRGLLCGPSLLDERHPLL HGAQSHRPPKG*GVRANNAGL AGSSIYLQPRCGIHEVKPSGLLS REGLQLQS
11884	42252	C	11955	114	362	
11885	42253	A	11956	1	211	
11886	42254	A	11957	395	547	
11887	42255	C	11958	412	641	
11888	42256	A	11959	3	905	SNNSPTSASRVAGITGVRHCVR NWWVLGLTDFKNEAVDPRAW TTKSKTPPQNKTKQENKNEDV GRDQRVEWLVTEEVSELSLKG EKLHWKEKEVQSTGKETDARS SMRNYLMLLGPEVQEKEPVKR RLARGKAFVELAEPTRAPGNSG FPVSGGVFTPSLGALTWICKFR VKSWAILNSQLLLDTMKKGIV YKNGDRIQGNRSADNRNNGVP LTGARDMQPAMPEPPTHSMGS CAARAFPMSAASCFRAPSPIDH PKAEE\WGARRGTGGQ\PTCSP GAGIHWVKPAGLLSREGLQLH
11889	42257	C	11960	482	709	
11890	42258	A	11961	1	734	MRLESD/KHLVQFVPIHKSKG\L EYPIGPWLPFITNSRVQEQAFYH DRHSFEAVLDLNAAPESVDLAE AERLAEDLRLLYVALTLSAFAP LVRRRGDKKGDTDVHQSALGR LLQKGEPQDAAGLRTCIEALCD DDIAWQTAQTGDNQPWQVND VSTAELNAKTLQRLPGDNWRV TSYSGLQQRGHGIAQDLMPRL DVDAAGVASVVEEPTLTT\HQF PAGASRGTFW\HSLFEDLDFTQ PVDPNWRL
11891	42259	A	11962	21	898	
11892	42260	A	11963	1	1962	

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11893	42261	A	11964	1	313	MRFYGQLAEDPGQQKAGETTR HTEDYISQLPLQRQGIPELALQK DLFINKIYGKEFNVCRSTLEDPR VHVLCRDMDEAGNHHSEQTIA RTENQTPHVLTHRRELNNENT WTQGGEHHTPEPVMGWG*RPR AAKSWGNNKAY*RLYFSAAFA ETRDPRTCPSERSFY*QDLWK/ MSSMSAGRL*RIPEFMSFVGTW MKLETIILSKLLQGQKTKHRMF SLIGGN
11894	42262	A	11965	47	178	QQLVHTAFVIRLIRGTTEGAWR NCKQMAR*QSISLECKFMPRT
11895	42263	A	11966	2	223	
11896	42264	A	11967	2	133	
11897	42265	B	11968	179	6003	
11898	42266	A	11969	1	1125	
11899	42267	A	11970	1	360	
11900	42268	A	11971	677	1238	
11901	42269	C	11972	193	471	
11902	42270	A	11973	17	280	
11903	42271	B	11974	1	654	
11904	42272	B	11975	526	597	
11905	42273	A	11976	1	1261	
11906	42274	A	11977	170	998	
11907	42275	A	11978	1	1130	
11908	42276	A	11979	1	369	
11909	42277	A	11980	1	300	
11910	42278	C	11981	207	451	
11911	42279	A	11982	1	348	
11912	42280	A	11983	2	469	RGIREGEEFDVDLAGMEVAVG GWGRGLWLHRHQAGIRGQSLG WRCRPWVGAGGVQAASERPD LAGSIMGPEVGALRRASPVIVIQ SQAGAFLSSNTTCQQFRDPGFR GRYPASPHTLSLPPETAHL*LLL CLPAAGVLPHTWPLLDRQGWH RGHAR

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11913	42281	A	11984	1	937	MAAPLVLVLVVAVTVRAALFR SSLAEFISERVEVVSPLSSWKRV VEGLSLLDLGVSPYSGAVFHER QYIPVKMKSKAFWIFSWEYAM MYVGS/HSGNHLPLLLPSQLLG FHPRSL/VALYFLFQISLQTLVIF WYFFAEMFEHFSLFFVCVFQIN VFFYTIPLAIKLKEHPIFFMFIQI AVIAIFKSYPTVGDVALYMAFF PVWNHLYRFLRNIFVLTCIIIVC SLLFPVLWHLWIYAGSANSNFF *GITLTFNVGQRPHRLKAPRASS AARSDRGPAASPASPGDAARPV SGRRPWDAPPHNYLNAVPPPSR
11914	42282	A	11985	1	521	
11915	42283	A	11986	1	207	
11916	42284	A	11987	1	867	
11917	42285	C	11991	1	225	
11918	42286	A	11992	72	425	
11919	42287	A	11993	1	354	
11920	42288	A	11994	460	752	
11921	42289	A	11995	93	401	PQKKYIHIFLDSLALLPRLECSG AISAHCKLHLLVSSDSPASASQ VAGITGARHHAWLIFVFLVEM GFHH/VGQAGLELLTSGDPPAL ASQRAGVSIFIYLFIF
11922	42290	A	11996	2	315	
11923	42291	A	11997	615	1180	
11924	42292	A	11998	3	151	
11925	42293	A	11999	2126	2241	
11926	42294	A	12000	1	765	
11927	42295	A	12001	924	995	
11928	42296	A	12002	1	789	
11929	42297	A	12003	2	132	FFFFFLVEMGFHHVGQAGLKLL TSSD\RPPWPPKVLGLQARAT
11930	42298	A	12004	504	755	

WO 01/075067

PCT/US01/08631

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11931	42299	A	12005	1	1322	MAILPKVIYRFNAIPIKLPVTFFT ELGKTTLRFIWNQKRACIGKSV LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT ESSEIMLHIYNHLIFDKPDKNKK WGKDSLFNKWCWENWLAICR KLKLDPFLTSHTKINSRWIKDL NVRPKTIKTLEENLGNTIQAIG MGKDFMTKTPKAMATKAKID KWDLIKLKSFCTAKETTIRLLG RPPALFTASSSVLKQLALEGILI LDSRALLGFLYEARHSHSNSPN HDAQNATSKKNIRDGYDKIYR QEQVLARMEEKTLITAGGNVK WCSHFRKQIGGQWLTLETKTK TPQPFSSTSQISTDKDKGLNPQL LKMDPGHMGWCPPGMGIPWQ LSSDDRVWVLAAAGSGRHPGS GFKSL/PGLLHEGSYGH****S*I *GGNS*GSSGGPQCISGEERVFR
11932	42300	A	12006	12	143	
11933	42301	A	12007	1	534	
11934	42302	A	12008	1	591	
11935	42303	A	12009	2	353	
11936	42304	A	12010	1	1923	
11937	42305	A	12011	1	465	
11938	42306	A	12012	1	784	PGWEKRMSRSSVVNTQEALPT AAIPRDAKGRVYYFNHITNASQ WERPSGNS\SSGGKNGQGEPA\R VRCSHLLVKHSQSRR\PSSWRQ EKITRTKEEALELINGYIQKIQS GEEDF\ESLASQFSDCKHQPKA RG\DLGAFQQKVRLQKPF*RTP RFALADGGR*AGPCFTD\SGIHII LPHLSEGWGAQAWPRGRAGRL GRPAPPCPPASGRTPHSLPPSHSI YCSHNGWEGALPDWGPFQTGG PGVPHSLSVPSWGCDLQTLH
11939	42307	A	12013	1	319	PRERAPRGSVGAGGEICHTSVC CCQPSWTRLLLLITWMLL/YYS ECKPFHCSREEPDNHILLLKI*EF GPPSTQGQHAAPLSRSRYSCCP DRYLLRKLGICQEHQLL
11940	42308	A	12014	1	1058	
11941	42309	A	12015	1	861	

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11942	42310	A	12016	1	431	IVLGGVATTVCQLNEFIMTDNA VPADVLVLTKPLGTQVAVAVH QWLDIPEKWNKIKLVVTQEDV ELAYQEAMMNMARLNRTGGL LICLPREQAARFCAEIKSPKYGE GHQAWIIGIVEKGNRTARIIDKP RIMEVA\HKWPLKM
11943	42311	A	12017	1	1020	
11944	42312	A	12018	247	1436	GERGPRTMSTRESFNPESYELD KSFRLTRFTELKGTGCKVPQDV LQKLLESLQENHFQEDEQFLGA VMPRLGIGMDTCVIPLRHGGLS LVQTTDYIYPIVDDPYMMGRIA CANVLSDLYAMGVTECDNML MLLGVSNKMTDRERDKVMPLI IQGFKDAAEEAGTSVTGGQTVL NPWIVLGGVATTVCQPNEFIMP DNAVPGDVLVLTKPLGTQVAV AVHQWLDIPEKW\NKIKLVVTQ EDVELGLPGRRLMNMARLNRT AAGLMHT\FNAHAAT\DITG\F\G ILGHAQNLGQASRRNDVSFVIH NLPGAWPRWLAVSKACG\NMF GLMHVTCPETSGG\LLICLPR\E QAARFCAEIKSPKYGEGHQAWI IGIVEKGNRTARIIDKPRIIEVA\ HKWPLKM
11945	42313	A	12019	219	380	RPLQIRSHSELLGVWTPTSEF*E DTTQSVTAGLLEVSWGRVVLC SKSFPALQS
11946	42314	A	12020	1	516	
11947	42315	A	12021	1	228	
11948	42316	B	12022	56	656	
11949	42317	A	12023	1	488	
11950	42318	A	12024	3	419	
11951	42319	A	12025	1	348	
11952	42320	A	12026	1	708	
11953	42321	A	12027	25	213	
11954	42322	A	12028	1	1165	
11955	42323	A	12029	1	411	
11956	42324	A	12030	1	996	
11957	42325	B	12031	1	744	
11958	42326	A	12032	1	444	
11959	42327	A	12033	1	555	
11960	42328	A	12034	1	2241	
11961	42329	A	12035	1	408	
11962	42330	B	12036	1	423	
11963	42331	B	12037	1	507	
11964	42332	A	12038	3	529	
11965	42333	A	12039	191	319	
11966	42334	A	12040	1	660	

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11967	42335	A	12041	1	579	
11968	42336	A	12042	1	2940	
11969	42337	A	12043	1	4280	MEYYAAIKKDEFMSFVGTWM MLETIILSKLSQGRKPKRRMLSL IGSQLLTNKGTSWMENEFDELT EVGFRRTLHPKSTTEYTFFSAPH CTYLKIDHIIASKTLLSKCKRTEI ITNGLSDHSVIKLELKIKKFTQN CTTTWKLKNLLLNDYWVNNEI KAEIKMFFETSENEDTMYQNL WDTFKPLCRGKFIALNAHKRK QRRSKIDIQTAQLKELEKEQQT NSKASRRQEITKIRAELKVTETR KTLQKINESRSW
11970	42338	A	12044	1	645	
11971	42339	A	12045	3	362	LDQLLDMSYE/QLMQLYSCAQ RRRLNPGLRRKQHSLLK\RLRK AKK/EAPPMEKPEVVKTHLRD MIILPEMVGSMVGVYNGKTFN QPEMIGHYLGEFSITYKPVKH/G RPGIGATHSSRFIPLK
11972	42340	A	12046	1	519	
11973	42341	A	12047	2	599	PPPRSSEDPAKMAEVEHEEGSG PFRKFTLPAAVDL\DQ\LLDIVPT KQFDAAVQVAAQRRRLEPGGL RRKQ\HSPA*KRLRKAKKGGPA PWRKPEVVKT/HTLRDYDHSYP EMVG\SMVG\VYNGK\TF\NQV GDQGVCGRPCRLGWAGVA*CR RDQLTPSFALGLPQPEMIGHYL GEFSITYKPVKHGRPGIGATHSS RFIPLK
11974	42342	A	12048	8	224	RTASYPRRFPWDHLLICPCQQL LICFLSLWIRLVFTKVSCT*NHN NMFSCVWLLLLSMIFLRFTHIA CIRNI
11975	42343	C	12049	65	163	
11976	42344	A	12050	3	187	
11977	42345	A	12051	3	689	HASDQKEIIIEPFQAVDEVERVP EDYYTGPVYLTEVTTLQQRLLQ PDFQPVCASQLYPRHKHLLIKR SLRCRKCEHNLSKPEFNPTSIKF KIQLVAVNYIPEVRIMSIPNLRY MKESQVLLTLTNPVENLTHVTL LECEEGDPDDINSTAKVVVPPK ELVLAGKDAAAEYDELAEPQD FQDDPDIIAFRKANKVGIFIKVT PQREEGEVTVCFKMKHDF\KNL \AAPISP
11978	42346	A	12052	1	882	
11979	42347	C	12053	152	404	

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11980	42348	A	12054	3	398	LRKIKIDLGKFSDNPDGYIDVLQGLRQSFDLTWRDIMLLLDQSLTPNEKSAAKTAAREFGDLWFV/SFQN*SCKTTNRSSNGAPDAVHD*D/PTADPWTGPLAHALMLMTLKAPLTRKSQLHDPYYAPIQQEAV
11981	42349	A	12055	2	286	
11982	42350	C	12056	261	482	
11983	42351	B	12057	1	1133	
11984	42352	A	12058	438	575	NKTRMPSLTTPLQHSTESPSQSSQTREGNKGYPNW*RGSHTVTVC
11985	42353	B	12059	50	309	
11986	42354	A	12060	1	870	
11987	42355	A	12061	148	368	ELSSCSLMSHRAIHHPSEERATTT/NQQSEPGSW*GWVGANRWCHKMSSGGSLGTEPCGSCLACSAWTVTVQAQ
11988	42356	A	12062	405	707	RLSLQTAGCSDVPVFPSAPSGPPSPA*AP*SGSAASPWPPFAPSAAHVAMPAPPRHWPQLSLKMPPWPPDSPVPPGCLA*AEAPPPHCPVHLPASRSALS
11989	42357	A	12063	90	470	KSVHSLPPSFSSLLPWTCNRTLSKPPALPSPSRQPECRRRLLHCSGSRHSSCPSSSSSPSFSSSPSPSSSSSASASPPPPPSPSPAPP*LWLQPLFCSQ*QLCHCQELVHLESRLTYPYHSSNQPF
11990	42358	B	12064	1	474	
11991	42359	A	12065	1	383	MEYYAAMKNDEFMSFVGTWMKLETIILSKLSQGQKPNTACSHSWMDPQRRGKRQSLSISEAGANQFPKSVFRFFGLGDSKVGSKWSATCACEPIHTSEYCGDRVICKTTSSLRGASFAWCSSGNGE*WFPASSMSLQRT
11992	42360	A	12066	1	384	MIITGLEDYEMGLRMEGTLEIPGHYQKDKFLAQSTPDLLLPKTSLTNPFSINQILAERQIVTFTVYPDTERDRETRNLADLKQIKIDLGKFSDNPDGYIDILRGLRQSFDLTW\RDIMLLLNQTLAPN
11993	42361	A	12067	152	238	
11994	42362	A	12068	89	544	
11995	42363	A	12069	62	199	SWKPSFSANYHKDRKPNTACSHS*DPAFLAPSPVP*SRPLRPPQD

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11996	42364	A	12070	1	655	SVSGLVEKVTFEQRLKGGEGDS TVGSSGNEIFRQWPCWELSNGC SLQGDAGCSCLVVHVTFPAGSL SGDGLPTAQWLQSLLVLAGGR RVNSTQGHRCHHWGSVAEPCV LVKRHHAAQEGLCSFQKTPRS QVPFHLFWDPGHHTLLCSYCPS \GVAGTQPAVQAVSTAV*TAAE GEPLPMSENMRCLVFCPCDSLL RMMVSSFIRVPTKDMNSSFFM
11997	42365	A	12071	1	987	MLVLGYNRKNTEGTQKQKGT NASDFHFLSQVLEQVVSPKGSK EAQCCVLRHLGCESSESAPGIPP NLGIQLLTWAVMWDPFPTTLA RAPSLALELMTQYFNNWNWV YNNITDQGESKMSKLKGKERR QREGERRERKREREKRERESQR KERKREKKGKKREREKDRSDL KQIKIDLGKFSDTPDGYIDVLQ GLGQPYYLTWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKP\IN*SMISTI TQGKEENPTAFLERLREALRKH
11998	42366	A	12072	1153	1379	CLASWKEKSLLHCPQRKQRLR GEELEKLKKWKETATQIKRSYC WI*PSKSPHYLTS*KR*WNY**L GNYNSIPAS
11999	42367	A	12073	1	864	
12000	42368	B	12074	8	441	
12001	42369	A	12075	62	332	TDSPHCTDPPSRPTVPASCLKRK CCGSTMPTARPIMPTLMETR*M PISPRVSWAGPRPTSWPALISST LFPRMANHWRD*SRITWFQGQ A
12002	42370	A	12076	34	409	TRAAGIRHEGKPEKTGLKRNFT N/DCRKS*TSG*RSTTSSRSRSPS PAPRSRSCSR\RDLPAPPPLSRSG DRPQTAPSCPMWRARLPSCPGS AIPIPRPAWTRSACCGAASTRLR PFSGSSTSPQWM
12003	42371	A	12077	1054	1368	
12004	42372	A	12078	298	514	PNWFKHDVSKSESFSNKMWIA KILKA/ARPAPLTQCV/RNSCFL QCRHLSSVSASDLT*DNVKRQF CVSPHTES
12005	42373	A	12079	2	1613	
12006	42374	A	12080	2	106	

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12007	42375	A	12081	42	305	YNTVLPKACLCGSLICWMN*SH SDQNMQVSVERSNLRVRLYAC CGLLLCTAYPQHFAHRYVDKIP GYPSRAGTLTGLHPMQVCRCR
12008	42376	A	12082	206	6038	
12009	42377	A	12083	1	4316	MQWEEAEKDPSGSCVFQRPPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSDN
12010	42378	A	12084	393	991	
12011	42379	A	12085	324	438	
12012	42380	B	12086	528	598	
12013	42381	A	12087	52	574	
12014	42382	A	12088	1235	1366	
12015	42383	A	12089	1	1800	
12016	42384	A	12090	1	513	
12017	42385	A	12091	3	77	
12018	42386	A	12092	1923	2171	GAFCPFTLLHGYQVLQWPGSSL PHKEGPAPALEGGHVYPRWI*A SADSQSTEAGRIGPASTG*RQYP GGEEHACCLPALLHS
12019	42387	A	12093	1	360	
12020	42388	B	12094	21	3636	
12021	42389	A	12095	1	936	
12022	42390	A	12096	1	599	
12023	42391	A	12097	1	248	VGKSSIVCRFVQDHFDHNISPTI GASFMTKTVLCGN/ELHKFLIW DTAGQER/SRQIPPLDPHENGNN GTIKVEKPTMQASRRCC
12024	42392	A	12098	1426	1572	
12025	42393	A	12099	367	513	
12026	42394	A	12100	31	661	APALPGCEHMMAIRELKVCLL GDTGVGKSSIVCRFVQDHFDH NISPTIG\ASFMTKTVPCENDFT KFLIWDTAGQERFYSLAPMYY RGSGAAVIVYDFTEAGFHFHPL KKWV\KRLKELGPE\NIVMAIA GNKCDLSDI\REVPLKGC*RNTA ESIGAIVVETSAKNA\INIE\ELFQ G\ISRPDPHPWTPHENGNNGTIK VEKPT\MQAS\RRCC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12027	42395	A	12101	1	487	MDKFLDTYTLPRLNQEEVESLNRPITGAEIVAIINSLPTKKSPGPDGFTAEFYQRLISNFSKVSGYRINVQES\QAFLYTINRQTESQIMSALPLTIASKRIKYLGIQLTRDVKDLFKENYKPLLNEIKEDTNKWKNIPCSWVGRINIVKMAILPKNWKKLL
12028	42396	A	12102	1	1563	
12029	42397	A	12103	1	1449	
12030	42398	A	12104	3	1606	
12031	42399	A	12105	2	402	
12032	42400	A	12106	172	329	
12033	42401	A	12107	1	720	
12034	42402	A	12108	97	206	
12035	42403	B	12109	1	1248	
12036	42404	A	12110	1	1419	
12037	42405	A	12111	1	1387	MDKFLDTYTLPRLNQEEVESLNRSITGSEIVAIINSLPTKKSPGPDGFTAEFYQRYKEELVLLLLKLFQSIEKEATLPNSFYEASIILIPKPGRDTTKKENFRPISLMNIDAKILSKILANQIQQHIKKFVHHDEVGFIPRMQGWFNIHKSKNVIQYINRTKDKNYMIISIDAEKAFDKIQQLFMLKTLSKLGIDGTYLKIIRAIYDKPTVKIILNGQKLEEFPLKTGTRQGCPLSPLLFNIVLEVLARAIRQEKEIKGILLGKEEVKLSLFADDMIVYLENPIVSAQNL\LKLISNVS\KV*GYKINVQKSQAFLYTTNRQTESQIMSELPFTIASKRIKYLGIQFTRDVKDLFKENYKPLLNEIKEDTNKWKNIPCSWVGRINIVKMAILPKPPLLIPRQTGSGVDLQQTPTDLQLSVLTVRRKINKQKGHPHQYLIWTSPSSKTKGRQLLASNRTKLDGE
12038	42406	B	12112	1	711	
12039	42407	A	12113	1694	4489	IYRFNAIPIKLPMTFFTELEKTTLKFIWNQKRARIAKAIRSQKNSGGITLPDFKLYYKATVTKTAWYWYQNRDIDQWNRTEPSEITPHIYNYLIFDKPEKNEQWGKDSLFNKWCWENWLAICRKLKLDPFLTPYTKINSRWIKDLIVRPKTIKTLEENLGITIQDIGMGKDFMSKTPKAMATKAKIDKWDLIKLKSFCTAKETTIRVNRQPTKWEKTFATYSSDKGLISRIYNELKQIYKKKTNNPIKKWAKDM

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12040	42408	A	12114	1	115	
12041	42409	A	12115	58	414	
12042	42410	A	12116	6	389	VMTTGTNSRVEPRVRGRVYKK KMDKKRQEKITEAKSKDKSQM DEEKTD/DEKPKLQVELEQEYQ DKFKRLPLEILEFVQEAMKGKI SEDSNHGSAPLSLSSDPGKVNH KTPSSEELGGDIPGKEFDTPL
12043	42411	B	12117	50	5137	
12044	42412	A	12118	1	1194	
12045	42413	A	12119	1	2559	
12046	42414	A	12120	3	406	
12047	42415	A	12121	119	423	TSSCSSEKFVITHLLKPTSVNSS KSFSFQLCSIG/VQGAAILWRRR GSLVFRIFSFSALVSPHLCGFIYL WSLTMVTYFSLSNGGRPSPCQA AAPQVNLGLLC
12048	42416	A	12122	3	597	ISASASDNVFMSVSSPSCSSCFF TLYRYLWKSEKPLYYSFVDKP VAYKKREMVVNLQKQFKHTG RVQ/SSNLLEKKAPSSFQFNWT EEDTDRTCF\HGHSLQGVLKEK GQSLLTKNSLYWLSTQKF*RCY GHHVPPYEESIYFLSNRFNLNLF SFLLRIKTSFL\HEEVSLVEK\KL FEEKIQCKKERNQDPRKVRTTL
12049	42417	A	12123	1	883	
12050	42418	A	12124	23	362	FAFNMPEPGKIVPAP*KGSKKA VTKAQNKDGEKRMLSRKESYS VYVYKVLKQVHPDTGVSSKG MGIMNSFVDDILERIAGEAFRL AHYNKRSTITSREIQTDVRLLLT REMVK
12051	42419	A	12125	2	405	
12052	42420	A	12126	1	398	LHSAMPEPAKSAPAPKKGSKK AVTKAQKKDGKKRKRSRKESY SIYVYKVLKQVHPDTGISSKAM GIMNSFVNDIFERIAGEASRLAH YNKRST\ITLPREI\QTAVRLLLP\ GELAKHAVSEGTKAVTKYTSA K
12053	42421	A	12127	1	401	
12054	42422	B	12128	48	424	
12055	42423	A	12129	3	462	DAWVSGRLTELPSSCFFPPIFRQ LLPVMPEPSKSAPAPKKGSKKA VTKAQKKDGKKRKRSRKESYS VYVYKVLKQVHPDTGISSKAM GIMNSFVNDIFE\RIAGEASRLA HYNKRSTITSREIQTAVRLLLPG ELAKHAVSEGTKAVTKYTSSK

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12056	42424	A	12130	74	504	FAFNMPEPAKSAPAPK\KGS\KK AVTKAQKKDGKKRK/RSRQGR AYSVYVYKVLKQVHPDTWHL LLRPWGIMELLSFNDIFRNGIAG LRVSRLGRI*QQGVSTIHLPGEI HDGPLRLACLPGGVWPSKAVF RGAPRPFNQVNTSV
12057	42425	A	12131	53	471	
12058	42426	A	12132	1	241	FKDTCTRMFIAALFTIAKTWNQ PKCPTMWHIYTMEYYAAIK/SD EFMSFVGTWMKLETITLSKL*Q GQKTKHRMFSLIGGT
12059	42427	A	12133	1	244	
12060	42428	B	12134	1	2142	
12061	42429	A	12135	1	1962	
12062	42430	A	12136	3	393	IWMKLETIILSKLSQG*KTKHR MFSLTGGNLTMRTLGHRLLPSL PHRLRPCARLHLRCPPWPPPSR RRCARSTTPTATPPSTATSRWSS TPPTCTCLWPSTSTGTTWPWRT SSATSCACRTTKWSMPRS
12063	42431	A	12137	2	87	
12064	42432	A	12138	1	270	
12065	42433	C	12139	1	214	
12066	42434	A	12140	1	684	
12067	42435	C	12141	1	333	
12068	42436	A	12142	1	189	
12069	42437	A	12143	215	310	
12070	42438	A	12144	2	91	
12071	42439	C	12145	1	229	
12072	42440	A	12146	1	268	
12073	42441	A	12147	1	278	
12074	42442	A	12148	2	274	WMKLETIILSKLSQRQKTIHHLF SLIALFTIAKKWKPPRYLSVDK WIKKLWY/HTYTMEYYSAFKK EAILPIAIAWMGLKDIMLSEISQ TWP
12075	42443	A	12149	2	136	
12076	42444	A	12150	2	95	
12077	42445	A	12151	1	233	
12078	42446	A	12152	377	484	
12079	42447	A	12153	2	91	
12080	42448	A	12154	1	891	
12081	42449	A	12155	1	1194	
12082	42450	A	12156	785	892	
12083	42451	A	12157	191	317	
12084	42452	A	12158	410	520	
12085	42453	A	12159	683	796	
12086	42454	A	12160	830	927	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12087	42455	A	12161	18	539	PTDP*LGIYQKE\YKSCYYKDIC T/RVCVPAALFTIANTWNQPKC TSMIDWVKKMWHIYTMEYYA AIKTDEFMSF\AGTWMKLETIIL RKLSQGQKTKHRMYSLIGGNL TMRTFGHSAGSHHTPGPIMRCG AGGGIALGEIPNVNDELMGTAN QHGTCIPMQQNCTLCTCTLKLK V
12088	42456	A	12162	1	108	ASTAGVSYYVAQAGLKLLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFM YFAGTWMKLETIILSKLSQGQK TKHRMFSL*GVSYYVAQAGLK LLGLSLSKCRDYRCEPPCPE
12089	42457	A	12163	1	701	
12090	42458	A	12164	274	435	
12091	42459	A	12165	1	3658	
12092	42460	A	12166	749	856	
12093	42461	A	12167	1	598	
12094	42462	A	12168	538	664	
12095	42463	C	12169	1	873	
12096	42464	B	12170	177	325	
12097	42465	B	12171	1	1245	
12098	42466	A	12172	1	3313	
12099	42467	A	12173	1940	2060	
12100	42468	A	12174	1	1213	
12101	42469	B	12175	155	559	
12102	42470	A	12176	2	321	PAPRGGAYRGRQTSLSCGGLHP V*ASWLLCLPKQAWAM/VGRP PQASLLPCSLISDCCASNQRDSV GVGPSEPCAGYNLLLCRFLSQS EKHSIRVGAVDCSCSYLAIL
12103	42471	A	12177	1	519	
12104	42472	A	12178	1	477	
12105	42473	A	12179	119	375	KRTQT*AIAGAPPPASLPPCSLIS DCCASNE*GSVGIGPSKPGAGY NLLLCHLISPSISPTSSPKSDTCPI ADFSNKSPDRSSAGDILLAMQS LGSMAIFLILILPTREHGKFFHLF VSSFISLSSGL
12106	42474	B	12180	1	363	

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12107	42475	A	12181	1	1309	MAEGEEGTSYMAAGERVVAIA LIDGFRPLTLESTFFNSGSCSKL EQHSTYLGDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVPEP KQHGIGPKQKYRSTGPNRALR NNAAYLQFLIFGNLEKTKPWG KDSLLIKVFEAAVLWIECFAFIF YDARGVLIVVQVDSCSKLEQHS TLSRAILLIYKGFCRFRNHHQTG FSPAGANQRGPLAATLSGPGGE GQSAVARLTGEKKNHPGAQYA NRLSPRVGRFINAAGTTGFPTG KRAVSATQLMDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQA VKGNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGHLISDCCASNQPDSVGVG PSEPGAGYNLVVRHFLSPSEKH SIRVGVTRFSRCRPSPLPLTQKG NSLTPCASQLRQCLALLRLR*R AISCCPSHW*KEKPPWRPIRKPP LPARWPIH*CSWHDRFPD/CESG HLISDCCASNQPDSVGVGPSEP GAGYNLVVRHFLSPSEKHSIRV GVTRFSRCRPSPLPLTQKGNSLT PCASQLRQCLALLRLRH
12108	42476	B	12182	1	1335	
12109	42477	A	12183	1	1675	
12110	42478	B	12184	57	1530	
12111	42479	A	12185	1	1419	
12112	42480	A	12186	1	574	RVDDFVRQTRPSAQAALAEKM AANQPPPLMMKHSQTDLVSRL KT\RKILGVGGEDDDGEV/HRSP ISQALGTEIKFTIREPLGLTVWQ FVSAVLFSGIAIMALAFPDQLY DAVFDGAQVTSKTPIRLYGGAL LSISLIMWNALYTAEKVIIRWTL LTEACYFGVQFLVVTATLAETG LMSLGIRLTRSSRRGR
12113	42481	B	12187	79	387	
12114	42482	A	12188	1	908	
12115	42483	A	12189	2	70	
12116	42484	A	12190	1	1158	

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12117	42485	A	12191	2	611	FVSVPSVLLGLQFWRSERD/TARLQSARWRVERGRLKELLSRQRPRRREEVVVGREVCRTEMEVRASLQKIVSNGDEQLEKAMEEILRDFEKRPSSLLVDCQSSSEISDHSFGDIPASQTNKPSLQLILDPSNTEISTPRPSSPGGLPEEDSVLFNKLTYLGCMKVSSPRNEVEALRAMATMKSSSQYPFPVTLYVP
12118	42486	A	12192	3	497	
12119	42487	A	12193	1	804	
12120	42488	A	12194	1	1243	MAPVEHVVADAGAFLRHAALQDIGKNIYTIREVVTEIRDKATRRRLAVLPYELRFKEPLPEYVRLVTEFSKKTGDYPSLSATDIQVLALTYQLEAEFVGVSHLKQEPQKVKVSSSIQHPETPLHISGFHLPYKPKPPQETEKGHSACEPENLEFSSFMFWRNPLPNIDHELQELLIDRGEDVPSEEEEEEENGFEDRKDDSDDDGGGW\ITPSNIKQIQQELEQF\DVPEDVRVWLA*PPDFAMQNVLLQMGLHVLAVNCMLIREARSYILRCHGCFKTTSDMSRVFCSHCGNKTLKKVSVTVSDDGTLHMHFSRNPKVLNPRGLRYSLPTPKGGKYAINPHLTEDQRFPQLRLSQKARQKTNVFAPDYIAGVSPFV\ENDISSRSATLQVRDSTLGAGRRRLNPNACRKKFVKK
12121	42489	C	12195	164	350	
12122	42490	A	12196	1	378	
12123	42491	B	12197	265	1539	
12124	42492	A	12198	1	2511	
12125	42493	A	12199	1	1077	
12126	42494	B	12200	38	1451	
12127	42495	A	12201	1	207	
12128	42496	A	12202	1	197	
12129	42497	A	12203	1	216	
12130	42498	A	12204	1	335	
12131	42499	A	12205	1	174	
12132	42500	A	12206	1	1309	
12133	42501	A	12207	1	1266	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12134	42502	A	12208	1	590	IDRFDAPCGLEELEDHEDEFNE EDERAIEMYRRRRLAEWKATK LKNKFGEVLEISGKDYVQEVTK AGEGLWVILHLYKQGIPLCALI NQNLSGLARKFPDVKFIKAISTT CIPNYPDRNLP\TILVYPG\GDIN G\QFIGPLSV\GGMNLTRDELEW KLSESGAIMTDLEENPKKPIEDV LLSSVRRSGPHEEGQRFRG
12135	42503	A	12209	291	416	SHYLKIHAEKLSEYDQISPPNSQ PDKENPVLST**SIQRRHMTLFK MNLKIILKYRKPEA*SQRLVSK R*KHSIRGSGINLSFVPTGFQIVP FHLFETSLWL
12136	42504	A	12210	437	773	DYTITGELKTAIQRSKINFCPILH SHSSHNAKSFVI*TVTLLHRHLL *KVSVNKVQSLFIQCGIFSEAGA GVYNYCPPPRQRRQPGDKPRW RWRRGRNNRCSANSHGLQLYA
12137	42505	A	12211	1	1183	
12138	42506	A	12212	1	459	
12139	42507	A	12213	1	513	
12140	42508	A	12214	91	1168	
12141	42509	A	12215	323	429	
12142	42510	A	12216	870	1305	SPGLPHCWQPCRARSRGTDVW NVLVS\GSGSGAYKEPAILVGPE NLTLTVHQTAVLECVATGNPRP IVSWSRLGWPPNPTAKEQEQRA KTESQRKQPRDKARENQPKAA RPKRAAPKSHEAARKTNPPTAS TKRQAAPTNTPKESS
12143	42511	A	12217	1	2695	
12144	42512	A	12218	1	258	
12145	42513	A	12219	1	624	
12146	42514	A	12220	247	425	
12147	42515	A	12221	31	858	LLEIVNSSIQPEKQAGWLSQAV HGAPDGPNRPMLHPETSPGRG HLLAVLLALLGTTWAEVWPPQ LQEQAPMAGALNRKESFLLLSL HNRLRSWVQPPAADMRRLDW SDSLAQLAQARAALCGIPTPSL ASGLWRTLQVGWNMQLLPAG LASFVEVVSLWFAEGQRYRHA AGE*ARNATCTHYMQLVWATS SQLGCGRHLCSAGQAAIEAFVC AYSPRGNWEVNGKTIVPYKKG AWGSLCTASVSSLLKAWDHAR GLLGGPRETLGKEPTEPWTALK
12148	42516	A	12222	1	1519	
12149	42517	A	12223	1	789	

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12150	42518	A	12224	1	505	ATEDPGVAMGRRPARCYRYCK NKPYPKSRFCRGVPDAKIRIFDL GRKKAKVDEFPLCGHMVSDEY EQLSSEALEAARICANKYMVKS CGKDGFHIRVRLHPFHVIRINK MLSCAGAD/RIHISKKWGFTKF NADEFEDMVAEKRLIPDGCGV KYIPSRGPLDKWRALHS
12151	42519	A	12225	135	828	RFWVSPHGPAAPARCY\RYCKN KPLPKVLRFCR\GVP\DAKIRIFD PGAEKRQKVE*VFRFCGHMVS DE\YNQLSS*ALE\AARNLCPIS TMVKS\CGKDGF\HIRV\RLHPF HVIPHQTRCCSCAGADRLQTG MRG\AFGKPQGTVARVHIGQVI MSI\RTKLQNKEHV\IDALRRAK \FKFPGRQ\KIHISKKWGFTKFN ADEFEDMVAEKRLIPDGCGVK YIPSRGPLDKWRALHS
12152	42520	A	12226	2	367	
12153	42521	A	12227	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLSAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
12154	42522	A	12228	1	714	
12155	42523	A	12229	122	939	YPGKQGLEWTSNKIQQTCS*GS SLLEGKLTNRKDIHTKTPSVRH/ RSSKAKERVSVIEDQMNETKRE EMFREKRVKRNEQSLQEIWEY VKRPNLRLIGVPESDGDNGTKL ENTLQDIIQQYFPNLARQANIQI QEIQRMPQRCSSRRAAPRHIIVR FTKAEMKEKMLRAARGKGRV THKGKPIRLKVDVLAETLQARR EWGPIFNILKEKNFQPRISFPAK LSFISKGEIKSFTDKEMLRDFVT TRPALQELLKEALNMERNNRY QPQQKHAKL

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12156	42524	A	12230	1	1043	MGDFLHSTDRNYLIKFWAKLS AKKTPANSSSPLGDHQHPCITK NLQIPEKWLIGLLLPLKADLLK EDAGTHCKEAKNLDERLDEWL TRINSVEKFLNDLMELKTMAQE LHYACTSFSSQFDQLEERVSVIE NQMSEMKREEKFREKRVKRNE QSLQKIWDYVKRPNLRLTGVPE SDWENGTKLENSLQDIIQENFP NLARQANIHIQEIQRMPQRYSS RRATPRHLIVRFTKFEMTEKMV RAAREKGQVTHKGKPIRITADI SAETLQARREWGPIFNILKEKN FQPRISYPAKLSFISEGEIKSFTD KQMLRDFVTTRPTLQELLKEAL /NMERNNQYQPLQKHAKL
12157	42525	B	12231	1	1275	
12158	42526	A	12232	1	1584	
12159	42527	B	12233	1	1023	
12160	42528	A	12234	1	2052	
12161	42529	A	12235	5160	6183	VSKHPQASAGDTQTNRVWSGP PANSDRPAAEGPDC*KEN*QTE RTS\NQNPICMSPSSKTKEAKNL DKRLDEWLTRINSIEKTLNDLM ELNTMARKLRDACTSFSSQFDQ VEERVSVIEDQMNEMKREEKF REKRIKRNKQSLQEIWDCVKRP NLRLIGVPESDGENGTKLENTL QDIIQENFPNLARQVNIQIQEIQ RTPQRYSSRRGTPRHIIVRFTKV EIKEKILRAAREKGRVTHKGKPI RLTAVLLAETLQARREWGPIFN ILKEKNFQPRVSYPAKLSFISEG EVKSFTDKQMLRDFVTTRPAL QELLKEALNMERNNRYQLLQK HATLSRPSMLG
12162	42530	A	12236	1	975	
12163	42531	A	12237	3	1186	
12164	42532	A	12238	1	906	
12165	42533	A	12239	1	1882	
12166	42534	A	12240	1	1394	

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12167	42535	A	12241	1	4935	MGPGARLAALLAVLALGTGDP ERAAARGDTFSALTSVARALAP ERRLLGLLRRYLRGEEARLRDL TRCNDETITYLLDKRLTVLTAA NIPYSSPENGAKRRRQDAFPPIH YNTQDALLQYLSGVGWGAPPA AQAHRDAPFVDSIAQVLLRTSG GSAEASGWSLRSRWAVGGATG SWVLSKGDRASLGERVVTGWA TLNVGRSFAYCLTTCVQPPLDV GPRKEHAPRPPSLSPTSTRQRGQ SERSQDANGRRKQKT
12168	42536	B	12242	88	1014	
12169	42537	A	12243	686	1920	IKPQRWGKKQNRKTGNSKKQS ASPPPKERSSSPATEQSWTENDF DELREEGFRRSVITNFSELKEHV VTHRKEAKNLEKK\LDEWITRI TNAEKSLKDLMELKTTAQELR NECTNLSNRCDQLEETVSAME DQIN/EMNEMKQEGKFREKRIK RNEQSFQ\EIGDYVKRPNLH\LI GVPESDGQNGTKLENTLQDIIQ ENFPNLARQANIQIQEI\QRTPQ RYSLRRATPRHIIVRFTKVEMK EK\MLSAAREKGR\VTHKGKPIR LTTADLSAETLQAQKTEWG\PIF NIL\KEKNF\QPRIS\YPAK\LSFIS EGEIKYFTDKQMLRDFCHHQG LPLKELLKEEALKHWKGTTRY QPLAKTLPKYRSTRQKVNKDT QELNSALHQADLIDIYRTLHTK STEYTFFQHHTTPIPKLTT
12170	42538	A	12244	1	633	
12171	42539	A	12245	3	109	
12172	42540	A	12246	2	575	
12173	42541	A	12247	1	237	
12174	42542	A	12248	1	1065	
12175	42543	A	12249	2	338	
12176	42544	A	12250	1	1319	
12177	42545	A	12251	1	744	MQKALCAAPDLGTFVTVLTPPP GAQIGSRRERSKVPYIVRQCVE EIERRGMEEVGIYHVSGR\VAA DIQALKAAFDVN/NRTMHSSWE ESDELLKARDDPHSGQHSRDG ALAKAGMADKKDMSVMMSET DMNAIAGTLKLYFRELPEPLFT DEFYPSFAEGIDRLERVAEKEA VNKMSLHNLATVFGPTLLRPSE KESKLPANPSQPITMTDSRSLEV MSQVEVLLYFLRLEAIPALDSK RQSILFSTDV

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12178	42546	A	12252	1	507	
12179	42547	A	12253	1378	4280	STPMAVAGPLGRPWSTSPTRAS TSGASWKGRARARSCAARAPL SRRSALPGPAGPTPPGVLRIAEA AIPRTAAPMRTSPPARRTSPLAS PAACPQAPPPTACSGTKAALPR RTRNSPSTAAVPPRRSAISGTGT ARLSCPRPPSWASARPGRSGPT MTRAPSMETQMARSEHHLDTA ALQTGQRSSAGTKMGCPTLMT RPPHRPTSAARAGAAGMRWSR EP*SPLK/RSELDLEKGLEMRK WVLSGILASEETYL
12180	42548	A	12254	1	1109	MRTPYKTSPMRMLYMTSLMTP TRHANEDAVDDIAYKDTVQDI TSEDAVYDIANEDVVYDIANED ALQDIANEVAVYDIANEDIVYD IANEDALYDITNEDAVYNIANE DAVYGIANEDAVYEFANKHAV YDIANEDTVQDICKKEDAANK CYFPGFFPIRCRHEHLPVCIIDVI CSLIKCRHEHLPSSLIGQDRLGA QASRRERSKVPYIVRQCVEEIER RGMEEVGIYRMSGVAADIQAL KAAFNVSECRPAQDGMEVWA VVSAMRSQSAPRPRHVTSFSVS FLHLSGSSRRPLHFRALS\NNKD VSVMMSEMDVNAIAGSLKLYF RELPEPLFTDEFYPNFAEGIGEH WRPWPHGRRLLHVHCCPQRL
12181	42549	A	12255	1351	4308	WKGRARARSCAARAPLSRRSA LPGPAGPTPPGVLRIAEAAIPRT AAPMRTSPPARRTSPLASPAAC PQAPPPTACSGTKAALPRRTRN SPSTAAVPPRRSAISGTGTARLS CPRPPSWASARPGRSGPTMARA PSMETQMARSEHHLDTAALQT GQRSSAGTKMGCPTLMTRPPH RPTSAARAGAAGMRWSREPWS PLK/RSELDLEKGLEMRKWVLS GILASEETYLSHLEALLLPMKPL KAAATTSQPVLTSQ
12182	42550	B	12256	1	1017	
12183	42551	A	12257	2310	2834	EEKYNMQTRLRRAEDVFPPVIG VAAHKGGVYKTSVSVHLAQDL ALKGLRVLLVEGNDPQGTASM YHGWVPDLHIHAEDTLLPFYL MLR\LAIETVAHDYDVIVIDSAP NLGIGTINVVCAADVLIVPTPAE LFDYTSALQFFDMLRDLLKNV DLKGFEPDVRILLTKYSNSNGW

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12184	42552	A	12258	106	108	NFLFVLRRQLWVGGLCW*AAE LNKVCL
12185	42553	A	12259	1	901	
12186	42554	A	12260	23	482	KPRELGPISPVWLPPDRLPERPQ RRRPSGVDPGSWLGSGSCGSTG CSALMSCSCGSTPLLSLALKVT PGGVLGAPSGSEDGS*PNRKAC GSEMEICLTTRGVWGPEVALG VGGGLQQSCRAPCGGLPKLLRS WSQSSLSPNSPGRGASSGEAA
12187	42555	A	12261	1	1938	
12188	42556	A	12262	1	2235	
12189	42557	A	12263	43	1827	THVRLAGARASPRAPRLRPRKP RPQGLPCLPGLRRARLEGGARG RADEMFLLPLPAAGRVVVRRL AVVRSGSRSLSTADMTKGLVL GIYSKEKEDDVPQFTSAGENFD KLLAGKLRETLNISGPPLKAGK TRTFYGLHQDFPSVVLVGLGK KAAGIDEQENWHEGKENIRAA VAAGCRQIQDLELSSVEVDPCG DAQAAAEGAVLGLYEYDDLK QKKKMAVSAKLYGSGDQEAW QKGVLFASGQNLARQLMETPA NEMTPTRFAEIIEKNLKSASSKT EVHIRPKSWIEEQAMGSFLSVA KGSDEPPVFLEIHYKGSPNANE PPLVFVGKGITFDSGGISIKASA NMDLMRADMGGAATICSAIVS AAKLNLPINIIGLAPLCENMPSG KANKPGDVVRAKNGKTIQVDN TDA\EGRLILADALCYAHTFNP KVILNAATLTGAMDVALGSGA TGVFTNSSWLWNKLFEASI\ET GDRV*RMPLFDHYTRQ\VVDC QLAD\VNNIGKYRSAG\ACTAA AFVKEFVTHRKWAHLDIAGVM TNKDEVPQSTGKA*LGRPTRTL I\EFL\LRFSQDNCLVQILKNVFH SVLNWTVELKKVFE
12190	42558	A	12264	1	405	GIRSAEVGKHLAHILLSRQQGR RPVTLIGFSLGARVIYFCLQEM AQEKDCQGIIEDVILLGAPVEGE AKHW\SLSGRVVSGRIINGYCR GDWLLSFVYRTSSVQLRVAGL QPVLLQDRRVENVDLTSVVSG
12191	42559	A	12265	1	1072	
12192	42560	A	12266	105	514	

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12193	42561	A	12267	44	872	NARPWVRGLLIEFRRRGSLCRE RAREMEMGRRIHLELRNRTPSD VKELVLDNSRSNEGKLEGLTDE FEELEFLSTINVGLTSIANLPKL NKLKKLELSDNRVSGGLEVLA EKCPNLP\HLI*GGNKIKDLSTIE PLEKLENLKSLDLFNCEVTNLN DYRENVFKLLPQLTYLDGYDR DDKEAPDSDAEGYVEGLDDEE EDEDEEEYDEDAQVVEDEEDE DEEEEGEEEDVSGEEEEDEKGY NDGEVDDEEDEEELGEEERGQ KRKREPEDEGEDDD
12194	42562	A	12268	1	388	KRGAAMDGRVQLIKALLALPIR PATRRWRNPIPFPETFDGDTDR LPEFIEQTGSYMFVDENTFSSDA LKT\ALPQSLPSIASHRQTAAPS DLDSPRRYLGWPQSLDSDSDS WPPPKGSVTFSETYFLPTP
12195	42563	A	12269	1	127	
12196	42564	A	12270	5	434	ISLRYLDGLAGPTHASAATEAS DRSEDLRWT/VCAQLIQALLAL PIRPATRRWRNPIPFPETFDGDT DRLPEF\IVQTCSYMI\VDENTFS SDALKVTFLITRLTGPAL\QWVI PYIKKESPLLNDYRGFLAEMKR VFGWED\DEDF
12197	42565	A	12271	515	1137	
12198	42566	A	12272	1	762	
12199	42567	A	12273	1	468	
12200	42568	A	12274	2716	3411	KREEETKKKSKREMEVVKKKQ CTYSFKSQGKFLSTHARQFSIGS QPISASQTVEEIMKSILTLQSQI\ NSLAAVTLQNR*GLDLLTAEKG GLCTFLGEECCFYTNQSGIA*D ATQRLQEKASEIRRLSNSYTNL WSWATWLLPFLGPVAAILLLL AFGPRIFNLLVKFVWSRIEAIKL QMVLQIEPQMSSTNNFYRGPLD *PAGTSPGLESSPLKDTTTAKPL LRPYPAGSS
12201	42569	A	12275	8312	9221	
12202	42570	A	12276	74	471	
12203	42571	A	12277	4043	4159	LFCQSGFHSLLTPSTATCSTIR* VATSRLRPVFTCRRS
12204	42572	A	12278	1	1332	
12205	42573	B	12279	29	1316	
12206	42574	A	12280	1	580	
12207	42575	A	12281	2	710	
12208	42576	A	12282	1	1559	
12209	42577	A	12283	1179	1490	

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12210	42578	A	12284	2	313	
12211	42579	A	12285	599	743	GALART*PPQQRWVSCPR/GVP/ GAL*REFTMFLSLQAENSIDFVS RELCAHSIRKLQAHVLLIK*VFI K
12212	42580	A	12286	208	398	
12213	42581	A	12287	716	1069	
12214	42582	C	12288	326	577	
12215	42583	A	12289	188	590	
12216	42584	A	12290	860	1121	VPFLTSWVNVGFKSSALHSSAL LQFWLTLWE*LPAWARCCCCL PNGSFWGPRSSRLDVAWERPV APGWREVSPLLSELWTAASGP YG
12217	42585	B	12291	1	1614	
12218	42586	B	12292	1	1080	
12219	42587	A	12293	3	219	
12220	42588	A	12294	890	1094	VESGTHLGQYKIYFGFLYQKKF SLQSHGYILFGCPQYW/ITSTDC PSIPCMWYSRTL*VTWSKKQVT SE
12221	42589	C	12295	1	3912	
12222	42590	A	12296	881	1151	
12223	42591	A	12297	1	1323	
12224	42592	A	12298	1817	2284	VWDGSILYQKLGALDGLSS*VI PLASSLQSLQYPLPSSFIQRILNT YSVKGLRSWTVNEDRVDAVSS GGIWLQVEASLVLY*MLYFSIIT LLILGLVHVNFKILDSSSELITD KLCGGLGFTLYTGSKLI*SDVTF PRAFSASTQTSMLTKYTVE
12225	42593	A	12299	1	1109	
12226	42594	A	12300	1	367	
12227	42595	A	12301	1	531	
12228	42596	C	12302	1371	1746	
12229	42597	A	12303	1	645	
12230	42598	C	12304	387	680	
12231	42599	A	12305	655	2498	
12232	42600	A	12306	1	528	ENLGNTIQDTGMGKDFMTETP KAMTTKAKIDKRDLIKLKSFCT AKETTIRVNRQPTEWEKIFAVY PSDKGPISRIYKQLKQIYKKKSN NPIKKWAKNRNRHFSKEDIYV AKKHMEKSSSSLVIRKMHIKTT VGYHLMPVRMAIIKKSGNNRC WRGCGE\C*WEGQLVQPLWKT VWQ
12233	42601	A	12307	1	1359	

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12234	42602	A	12308	1968	2648	TQTNLQEKNKQLHQKVGKGYE QTLLKRRHLCSQQTHMQPTDT WKNAHHQLAIREMQIKTTMRY HLTPLRMAIIKKSGNNSCWRGC GEIGTLLHCWWDCKLVQPLWK TVWRFLKDLESEIPFDLAIPLLCI YPKDYTSFCYKDTCTCMFIAAL FTIAKTWN*PKCSSVIDWIKKM WHIY/TTMEYYGAIKRNKIMSF AGTWMKLDAIILSKLTQKQKT KLRMFLLISRS
12235	42603	A	12309	1	403	
12236	42604	A	12310	3	264	FFYAHIMFIAALF\TIAKTWNQS KCTSMIDWIKK\MWHIHTMEY YAAIKR\RGFMSFTRTWMKLEA IILSKLTQEQKTK\HHMFSLIRGS
12237	42605	A	12311	79	432	
12238	42606	A	12312	1	933	
12239	42607	A	12313	70	675	
12240	42608	A	12314	1	339	
12241	42609	A	12315	3	422	
12242	42610	A	12316	1	471	
12243	42611	A	12317	1	963	
12244	42612	A	12318	375	542	ENDKARRSDTPSML*WVEGMK *SVKAPHTLHLASDYVLEPWG GESATFIPASWDC
12245	42613	C	12319	1	2148	
12246	42614	A	12320	1	1881	
12247	42615	B	12321	1	1074	
12248	42616	C	12322	143	439	
12249	42617	C	12323	123	362	
12250	42618	A	12324	474	603	NHKNPRRKPRQYHSGHRHGQG LHV*NTKNNGNKSQNGQMGSN
12251	42619	A	12325	5169	5756	CPSLPPPHGKPAAACPRSPPGGC CTPRSARTVPRGLSENSQTKCH SADLPPEGPRVFWTPPGTGAAP APPAPAPGPARCGPRRCHAWPP QRRSSGAGRSPPPRHFAEFLKM VAFLRILILRAVSLLRSLDLEIS* G*RP*GPSWGGPPQSTPSAASA ASKTSSPRRWSTPAWAFLARA HPRWVAPSTAAQCTAAP

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12252	42620	A	12326	21	98	ESWLVLGRRKAGRLIGACGFEP PHFLTLDLEMHRDSCPLDCKVY VGNLGNNGNKTELERAFGYYG PLRSVWVARNPPGFAFVEFEDP RDAADAVRELDGRTL\CG\CRV RV\ELVRMGEK\RSRNRGPPPS\ WGRRPRDDYRR\RSPPPR\RRSP R\RRSFS\RSRSRSLS*ERVGWC WAGGKREDSSERVDLSRRIF
12253	42621	A	12327	919	1043	
12254	42622	A	12328	460	657	CFSPGMWQKTHSRKHSPGAICP INPVGECLVRKIKQLD*ITWINA I*LPLRDGLFYFLNFPFCCRG
12255	42623	A	12329	1	2235	
12256	42624	A	12330	1	255	
12257	42625	A	12331	2	429	CRADLNSRIDDFVPNPSVAVSG ASYAVAAVTMAHYKAADSKR EQFRKYFEK\SGVLDTLT\KVLV ALYEEPE\KLNSALDF\LKHHLG AATP\ENPEIELLRLELAEMKEK YEAIVEENKKLKAKLAQYEP\P QEEKRAELGFFSV
12258	42626	A	12332	670	860	
12259	42627	A	12333	2	450	VNKAGGLIYQLDSYAP/RAEAE KTFSYPLDLLLKLHDERVLVAF GQRDGIRVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANYP VSIRFGRPRLTSNEKLMLASMF HS\IKFVVLADP\RQAGIDSLLRK IYEIYSDFALKNPFYSLEMP
12260	42628	A	12334	1	2034	
12261	42629	A	12335	1	324	
12262	42630	A	12336	2	694	FGTRGKAAMAIFSVYVVNKAG GLIYQLDSYAPRAEAEKTFSYP LDLLLKLHDERVLVAFGQRDGI \RVGHAVLAINGMDVNGRYTA DGKEVLEYLGNPANYPVSIRFG RPRL\TSNEKLMLASMFHSLFAI G\SQLSPE\QGSSGIEMLETDTFK LHC\YQTLTGIKF\VVL\ADPR\Q AGIDSLLRKIYEIYSDFAL\KNPF \YSLEMPIRCELFDQNLKLALEV AEKAGTFGPGS
12263	42631	A	12337	2	1658	

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12264	42632	A	12338	3	997	VQKPNRQWRLVQDLRIINEAV VPLYQAVRNPYTLLSQIPEETG WFTVLDLKDALFCIAVHPDSQF LLAFEDPLNPTSQLTWTVLPQG FRDSPHLFGQALAQDLSQFSYL DTLVLRYVDDLLLAAPSETLCH QATQVLLNFLATCGYKVSKLK AQICSQQVKYLGLKLSKGTRAL SEERIQPILAYPHPKTRKQLRGL LGITGFCQIWIPRYSEIARPLHTL IKKTQKANTHLVRWTPEAEAA FQVLKKALTQAPVLSLPTGQDF \SLYVTEKTGIALGVLTQHYGE ERNS*LPTEYLSNIRKPLGDYY WLYRNLKRWQSYTARVIRKER
12265	42633	A	12339	3	421	
12266	42634	A	12340	3	4804	KRLENIQKTLEVAFSEAVWMQ PSVVLLDDLDLIAGLPAVPEHE HSPDAVQSQRLAHALNDMIKE FISMGSLVALIATSQSQQSLHPL LVSAQGVHIFQCVQHIQPPNQE QRCEILCNVIKNKLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSISTREKLVL TTLDFQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
12267	42635	A	12341	1	2223	
12268	42636	A	12342	1	3864	MQWEEAEKDPSGSCVFQRPPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSDN

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12269	42637	A	12343	204	963	DCACTFHCRSATKIVKDLKAQ GLVKPCNSPCSTPILGVQKPNG QWRLVQDLRIIDEVVVYVDDL LLAARSKTLCHQATQALLNFLI TCDYKVSKPKAQLCSQKVKYL GLKLSKGTRVLSEERIQPIPAYP HPKTPKQLRGFLGITGFCRIWIP RYSEIARPLYTLIKKTQKADTH LVEWTPEAEVAFQALKEALTQ APVLSLPMGQDVPLYVTEKTGI ALGVLGVLTQVRG/LSLQPMAY LSKEMDVVAKGWPH
12270	42638	A	12344	1	1178	MPESPTPLLGRDILAKAGAIIHL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFPYQRQYPLRPEAQQGLQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPAVPNPYTLLSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPQG FRDSPHLFHHTLAQDLSQFSYL DTLVLCLPLRNQQECHQATQV LLNVLATCGYKVSKQKAQLCS QQVKYLGVKLSKGTRAL/QQ*R TDRT*LSTSNCSNLRHSRGPSRG SLD*SQPQLVY*WKFFCRKRTS KRGVCSGQ**WNT*KKSPHSRN *CSAGGTNSPPSGTRIRRRKKGL IRIYMLPLILSAPYDHLH
12271	42639	A	12345	1	841	
12272	42640	A	12346	3	1428	
12273	42641	A	12347	2	268	
12274	42642	A	12348	1	897	
12275	42643	B	12349	1	1650	
12276	42644	A	12350	232	1002	TPGSTVHAPEADQGLQKIVKDL KAQGLVKPCNSPCSTPILGVQK PNGQWRLVQDLRIIDEVVVYV DDLLLAARSKTLCHQATQALL NFLITCDYKVSKPKAQLCSQKV KYLGLKLSKGTRVLSEERIQPIP AYPHPKTPKQLRGFLGITGFCRI WIPRYSEIARPLYTLIKKTQKAD THLVEWTPEAEVAFQALKEAL TQAPVLSLPMGQDVPLYVTEK TGIALGVLGVLTQVRG/LSLQP MAYLSKEMDVVAKGWPH
12277	42645	A	12351	1	2217	

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12278	42646	A	12352	1	6530	MWGSDRLAGAGGGGAAVTVA FTNARDCFLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSDQGENVAEINRQVGQKL GLSNGGQELHAVSLEQHLLDQI RIVFPKAIFPVWVDQQTYIFIQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADAEYKKLHS YGRDQKGMMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSIFSFQSEKKQETSWG LTEINAFKNMQSKVVPL
12279	42647	A	12353	1734	4349	MPNRACFQCGLQGHFKKDCPS RKPQVCLTIESQEVNCLLDAGA AFSVLLSCPGQLSSRSVTIRGVL GQPVTRYFFQPLSCDWGALPFS HAFLIMPESLTPLLEREILVKAG AIIHLNIGEGTPICRLLFEEGISPE VWATEGQYGQAKNAHFVQVK LKDSTSFPYQRQYPLRPEAQQR LQKIVKDLKAQGLVKPYSSPCN TPILGVQKPKRQWRLVQDLRII NEAVFPLYPAIPSPYTLLSQIPEE AEWFTVLDLKDAFFCIPVHPDS QFLFAFEDPSNPTSQLTWTVLP QGFRDSPHLFGQALAQDLSQFS YLDTPVLQCMDDLLLAARSET LCHQATQALLNFLTTCGYKVS KPKAQLCSQQVKCLGLKLSKV TRALSEERIQPILAYPYPKTLKQ LRGFLGITGFCRIWIPRYGKIAR PLYTLIKETQKANTHLVRWTPE AEAAFHALKKALMQAPVLSLL TGQDFSSYVTKNKQTKKKK\T* IALRVLALV*GTSLQPVAYL/SK EIDVVAKGQPHCLRVVVAVAV LVSEAVKIIQGRNLTVWTSHDV NGILTAKGDLWLSDNHLLKYQ ALLLEGPMLRLCTCAALNLDTF LPHNEEKIEHNCQQVIAQTYAT RGDHLEVPLTDPNPNLYTDGRS FVEKGLQKVGYAVVSDNGILES NPLTPGTSAQLAKLTRALELGE GKRVNIYTDSKYAYLVLHAHA
12280	42648	A	12354	5	138	
12281	42649	A	12355	1	909	
12282	42650	A	12356	3	245	
12283	42651	A	12357	1	1080	

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12284	42652	A	12358	3	955	VPRKSVHSGDAEYHKVLKEEA SDSRENKVGTTWLQILSGSFAS RVTEHITQPLQESVSLWISSEQN IPPKFMGRLNKLRKATYKRKYS AAKSKVEKKKKEKVFATVTKP VG\GDKNGGT\RVVQTR\KLPR YHPTEDVPRKIVEPPQKNLFSQ HVRKTAKTALPPGTILIILTG\RH RGK\RVVFLK\QLASGLILV\TAP LVLNRVPLRRTHQKFVIATSTKI DISNVKIP\KKKDKTPLLTDAYL \KKKKLRKPR/HPRKGEIFDTVK RGNMRITE\QRTIDQKAVDSQIL PKIKAIPQA/LQGYLRILCLL*RN GIYPHKLVF
12285	42653	A	12359	1	555	
12286	42654	A	12360	1	300	
12287	42655	A	12361	1	588	
12288	42656	A	12362	1	264	
12289	42657	A	12363	1	870	
12290	42658	C	12364	239	400	
12291	42659	A	12365	9	98	SWKPSFSAN*HRNRKPNTTCSH SQVGVDL
12292	42660	A	12366	9	81	
12293	42661	A	12367	3	169	
12294	42662	A	12368	134	481	GCCGGTIKNSFSFPPLPNWPRFV MFPSLCVLIVETCETWICTLIVQ LPLMSENMRCLIFCSCVSLLRM MVSSFVHVHDHKVKSHSRPS/G NLRSKEASPSPKTSKVGKLTVQ PSVCG
12295	42663	A	12369	41	388	SYGQMMKCQPFTFPSPGYGAG VFSSDKIGQMTFMERT*RMSCK EAAQDHTAREKEKVELKFPSLP FRRKELL*PCTWLGSPISLVTLD FPWPQGSGRLSMPVLWTCLIPG SLEIG
12296	42664	B	12370	1	909	
12297	42665	C	12371	295	2025	
12298	42666	A	12372	14	260	
12299	42667	A	12373	1	142	TCTCVFIAALFTIAKTWN*SKCP SMRDWIKKNVAHTHHGILCSH KKE
12300	42668	A	12374	1	395	

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12301	42669	A	12375	2	976	REHLAEGMAVGTASADLNISA CWLRREQQISQHSARALLRDRL PPQENSSWHPAGAPLGRNFQRK EQAAIFAVLQPPLVIPRKTGSGV DLEQTPADLQKRGLTVTRKTN KQKAIASTSTERTPTQKPPFKSH QHQRPNVDKSAKMRKNQSKK AENSKNQNTSSPPKDHNSSPAR EQNWMEN\EFDELTEVGFRRW VITNSSELKKHVLTQCKEAKNL EKRDMDEAGNHHSQQTNTGTE NQTPHVLTHKWELNNENTRTRI YKKHGAAICLASGIYHSVDLPF WGLDLPFWDLEDSGSTILGSGG QWPSSHSSTRQCTSVDSVWGL
12302	42670	B	12376	1	111	
12303	42671	A	12377	34	346	
12304	42672	A	12378	1	585	
12305	42673	A	12379	3	14703	
12306	42674	A	12380	1	636	
12307	42675	A	12381	1	1626	
12308	42676	A	12382	1	3246	
12309	42677	C	12383	62	202	
12310	42678	A	12384	1	286	
12311	42679	A	12386	1	1176	
12312	42680	C	12387	1	942	
12313	42681	A	12388	785	892	
12314	42682	A	12389	2	91	
12315	42683	A	12390	1	708	
12316	42684	A	12391	3	96	TWMKLETIILSKL*QRQKTKHR MFLLIGGN
12317	42685	B	12392	1	1954	
12318	42686	A	12393	1550	1830	DTISHQLEWQSLKSQETTALLTI AKTWNQPKCPSMIGWIKKMW HIYTMEYYAAIK/SDEFMCFAW TWMKLETIILSKLSQEHKTKHH MFSLTSGS
12319	42687	A	12394	3	553	
12320	42688	A	12395	1	1428	
12321	42689	A	12396	642	753	
12322	42690	B	12397	1	759	
12323	42691	B	12398	1	900	
12324	42692	A	12399	623	775	
12325	42693	A	12400	992	1156	
12326	42694	A	12401	86	349	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12327	42695	A	12402	1	2521	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NIVQHINRTNDKNHMIISIDAEK AFDKIQQRFMLKTLNKLGIDGT YLKIIRAIYDKSTANIVLNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLRKEE IKLSLFADDMIVHLENPIVSAQN LLKLIDNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SERIKYLGIQLTRDVKDLFKEN YKPLLNDIKEDTNKWKNTPRS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIWN QKGARIAKSILIYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPDKNKKWGNDS LFNKWCWENWLAICRKLKLDP FLIPYTKINSRWIKDLNVRPKTI KTLEENLGNTIQDIAMGKDFMS KTPKAMATKAKIDKWDLINLK SFCTAKETTIRVNRQPIEWEKIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSSLAIREMHI KTTMRHHLTSVRMAIIKKLGN DWCWRGCGEIGRLLHCWWDC KLVQPLWKSVWRFLRDLELET PFDPASPLLGIYQKE\YKSCYYK DICT/RVCVPAALFTIANTWNQP
12328	42696	B	12403	80	5612	
12329	42697	B	12404	68	505	
12330	42698	A	12405	1	471	
12331	42699	A	12406	194	430	IAIMRLLLQISIIILSSCLREVKSM QAYRKALRKLKLADVKRYQKS LVVQKRS*ER*SLVLILILPARTF QSYLAPIC
12332	42700	A	12407	1	546	
12333	42701	A	12408	2	418	
12334	42702	A	12409	302	746	ETSHQVMDRSNPVKPALDYFS NRLVNYQISVKCSNQFKLEVCL LNAENKVVDNQAGTQGQLKV LGANLWWPYLMHEHPAYLYS WEDGDCFTPKALDPLPACDLC DQL\HLRSRQGGSVCGCDPCEQ LLLL\VSQLQAPAIDSAAAGRPV
12335	42703	A	12410	83	552	
12336	42704	A	12411	1	459	
12337	42705	A	12412	34	588	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12338	42706	A	12413	1	466	
12339	42707	A	12414	950	1230	CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGQ
12340	42708	A	12415	497	847	
12341	42709	A	12416	1	337	MGVVPEELFLEELNLSGLKWD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPR\ALADS LMQLARQVSRLESGQHPEFAPP SHGD
12342	42710	A	12417	716	961	
12343	42711	A	12418	1	1218	
12344	42712	A	12419	1	1104	
12345	42713	A	12420	548	1078	
12346	42714	B	12421	83	345	
12347	42715	A	12422	1	681	
12348	42716	A	12423	1	1431	
12349	42717	A	12424	566	871	
12350	42718	A	12425	145	980	
12351	42719	A	12426	2	702	
12352	42720	B	12427	1	1156	
12353	42721	A	12428	188	584	
12354	42722	A	12429	1	1194	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12355	42723	A	12430	170	1855	LLEGKLTNRKDIPHQNPICTSPS SKTKGILPISEPPSNRIFACWGK PAWTACCN/FSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADSL MQLARQVSRLESGQINHTPNSF HIGAGGSWCLSESPCVVLNYK YPLVCGYTDGNAEVSKFGNFFL DLSRTRCLAEGNYTSGDNHTLR DPHYVEDKGHKYLVFEANTGT ENGYQGEESLFNKAYYGGGTN FFRKESQKLQQSAKKRDAELA NGALGIIELNNDYTLKKVMKPL ITSNTVTDEIERANVFKMNGKW YLFTDSRGSKMTIDGINSNDIY MLGYVSNSLTGPYKPLNKTGL VLQMGLDPNDVTFTYSHFAVP QAKGNNVVITSYMTNRGFFED KKATFAPSFLMNIKGNKTSVVK NSIRREGFCRFRNHHQTGFSPA GANQRGPLAATLSGPGGEGQS AVARLTGEKKNHPGAQYANRL SPRVGRFINAAGTTGFPTGKRA GFCRFRNHHQTGFSPAGANQR GPLAATLSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGTTGFPTGKRAV
12356	42724	A	12431	851	2237	
12357	42725	A	12432	2	2346	
12358	42726	B	12433	329	479	
12359	42727	B	12434	656	2404	
12360	42728	B	12435	486	834	
12361	42729	A	12436	1	693	
12362	42730	A	12437	1	114	
12363	42731	A	12438	152	391	AGGWALPSLGLPSWTSRCPWR RGSAGLLLEASVPVQQ*PKLLD RLSRRWPGEGHPRPARVRSCM ALGPRRLGVLCQEPS
12364	42732	A	12439	1	1707	
12365	42733	A	12440	1	897	
12366	42734	A	12441	36	420	
12367	42735	A	12442	2	217	
12368	42736	A	12443	1	903	
12369	42737	A	12444	1	1626	
12370	42738	B	12445	107	757	

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12371	42739	A	12446	1	1655	MGTVPRSAGQETWVLCEHIIGG ERSFTEYSLCHRIESSTSSIKLEL GGNNVEPLESSRVFDSTVQNEE ADAVSTGEEGVTHEGTQGGKV IPQMHMGSGLQPKSFSQNRSQV NNDMIVTDNNGAVKFPQLCKF CDVRFSTCDNQKSCMSNCSITSI CEKPQEVCVAVCWMSEEICTN VMYSPLPCKFLHLSPIEVLPIIRS PVNQSGRCKIRHIGSNNRLQRS TCQNTGWESAHVMKTPGFREY NTSNPDLLLVIFQVTGISLLPPL GVAISVIIIFYCYRVNRQQKLSS TWETGKTRKLMEFSEHCAIILE DDRSDISSTCANNINHNTELLPI ELDTLVGKGRFAEVYKAKLKQ NTSEQF*DSGQFKILFPIE\EYAS WKTEKDIFSDINLKHENILQFLT AEERKTELGKQYWLITAFHAK GNLQEYLTRHVISWEDLRKLGS SLARGIAHLHSDHTPCGRPKMP IVHRDLKSSNILVKNDLTCCLC DFGLSLRLDPTLSVDDLANSGQ CYEVCSSGRFLVTIFKGNRLRE RTEKNTRITPRDWVYEWLW
12372	42740	A	12447	1555	3277	RAAGSAMGRGLLRGLWPLHIV LWTRIASTIPPHVQKSVNNDMI VTDNNGAVKFPQLCKFCDVRF STCDNQKSCMSNCSITSICEKPQ EVCVAVWRKNDENITLETVCH DPKLPYHDFILEDAASPKCIMK EKKKPGETFFMCSCSSDECNDN IIFSEEYNTSNPDLLLVIFQVTGI SLLPPLGVAISVIIIFYCYRVNRQ QKLSSTWETGKTRKLMEFSEH CAIILEDDRSDISSTCANNINHN TELLPIELDTLVGKGRFAEVYK AKLKQNTSEQFETVAVKIFPYE EYASWKTEKDIFSDINLKHENIL QFLTAEERKTELGKQYWLITAF HAKGNLQEYLTRHVISWEDLR KLGSSLARGIAHLHSDHTPCGR PKMPIVHRDLNSSNILVKNDLT CCLCDFGLSLRLDPTLSVDDLA NSGQVGTARYMAPEVLESRMN LENAESF\KHTDVYSMALVLWE MTSRCNALGEVKDYEPPFGSK VREHPCVESMKDNVLRDRGRP EIPSFWLNHQGIQMVCETLTEC CDHDPYARLTAQCVAERFSELE HLDRLSGRSCSEEKIPEDGSLNT

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12373	42741	A	12448	3	1354	
12374	42742	A	12449	1	168	
12375	42743	A	12450	2	147	
12376	42744	A	12451	3	523	LQFFRRSEVKMKNHLLFWGVL AVFIKAVHVKAQEDERIVLVDN KCKCARITSRIIRSSEDPNEDIVE RNIRI\IVPLNNRENISDPTSP\LR TRFVY\HLSDLCKK\CDPTEVEL\ DNQIVTAT\QSNICGWMTVPQS TCYTLSTGNKCYTAVVPL\VYG GETKMVETALTPDACYPD
12377	42745	A	12452	3	274	
12378	42746	A	12453	1	120	
12379	42747	A	12454	119	461	PVPQDLQAAVLGRTTALFK\AV KTGTLQVCKRLLLSF\VCL/CPA PRGRQASLSCGGLHPVRASWLL CLPKQAWAMAGAPPPAWLPPC SLISDCCASNQRDSVGVRPSEPG VGYSLV
12380	42748	A	12455	2	370	
12381	42749	A	12456	1	3135	
12382	42750	A	12457	1	942	
12383	42751	A	12458	1	462	
12384	42752	A	12459	1	297	
12385	42753	A	12460	935	1338	CTDGFLVWMSFLFVSFPLPPCS LISDCSASNERDSVGVGPSEPG AGYNLVVRRFLSPSEKRSIRV* VTRFSRCRPSPLSLTRKGNSLTP CASQVRQCLALFRLAHGVRTH SPAPTVWHSLPKVGPFLENSVP
12386	42754	A	12461	1	268	
12387	42755	A	12462	3	479	
12388	42756	A	12463	1	262	
12389	42757	A	12464	1	304	MAGAPAPASLPPCSLISDCCAS NQRDSMGVGPSEPGAGYNLVP V\EKRSIRVGVTGFSRCCPSPLSL TRKGNSLTPWASQVRQCLALL QLAHGRGSPNPRP
12390	42758	A	12465	1	512	
12391	42759	B	12466	1	1257	
12392	42760	A	12467	1	705	
12393	42761	A	12468	1	3039	
12394	42762	B	12469	66	467	
12395	42763	C	12470	360	747	